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<p>(54) Title: BIALLELIC MARKERS</p> <p>(57) Abstract</p> <p>The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.</p>		

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## BIALLELIC MARKERS

## RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/030,455, filed November 6, 1996,  
5 the entire teachings of which are incorporated herein by reference.

## BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution,  
10 generating variant forms of progenitor sequences (Gusella, *Ann. Rev. Biochem.* 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and  
15 is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In  
20 many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism  
25 (RFLP) is a variation in DNA sequence that alters the length of a restriction fragment (Botstein et al., *Am. J. Hum. Genet.* 32, 314-331 (1980)). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment.

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RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; W090/11369; Donis-Keller, *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 85-99 (1989)). When a heritable trait can be linked to a particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the animal will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-nucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (US 5,075,217; Armour et al., *FEBS Lett.* 307, 113-115 (1992); Horn et al., W0 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Some single nucleotide polymorphisms occur in protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective or other variant protein and, potentially, a genetic disease. Examples of genes, in which polymorphisms within coding sequences give rise to genetic disease include  $\beta$ -globin (sickle cell anemia) and CFTR (cystic fibrosis). Other single nucleotide polymorphisms occur in noncoding regions. Some of these polymorphisms may also result in defective protein expression (e.g., as a result of defective splicing). Other single nucleotide polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same manner as RFLPs and VNTRs, but offer several advantages. Single nucleotide polymorphisms occur with greater



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frequency and are spaced more uniformly throughout the genome than other forms of polymorphism. The greater frequency and uniformity of single nucleotide polymorphisms means that there is a greater probability that such a  
5 polymorphism will be found in close proximity to a genetic locus of interest than would be the case for other polymorphisms. The different forms of characterized single nucleotide polymorphisms are often easier to distinguish than other types of polymorphism (e.g., by use of assays  
10 employing allele-specific hybridization probes or primers).

Only a small percentage of the total repository of polymorphisms in humans and other organisms has been identified. The limited number of polymorphisms identified to date is due to the large amount of work required for  
15 their detection by conventional methods. For example, a conventional approach to identifying polymorphisms might be to sequence the same stretch of DNA in a population of individuals by dideoxy sequencing. In this type of approach, the amount of work increases in proportion to  
20 both the length of sequence and the number of individuals in a population and becomes impractical for large stretches of DNA or large numbers of persons.

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## SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a polymorphic site. Complements of these segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying the polymorphic site in the segments can be the reference (Table, column 3) or an alternative base (Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table, column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases present at the polymorphic sites in the individuals tested.

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DETAILED DESCRIPTION OF THE INVENTION  
DEFINITIONS

An oligonucleotide can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally occurring or synthetic, but are typically prepared by synthetic means. The oligonucleotides of the present invention can comprise all of an oligonucleotide sequence presented in column 7 of the Table or a segment of such an oligonucleotide which includes a polymorphic site.

Oligonucleotides can be all of a nucleic acid segment as represented in column 7 of the Table; a nucleic acid sequence which comprises a nucleic acid segment represented in column 7 of the Table and additional nucleic acids (present at either or both ends of a nucleic acid segment of column 7); or a portion (fragment) of a nucleic acid segment represented in column 7 of the Table which includes a polymorphic site. Preferred oligonucleotides of the invention include segments of DNA, or their complements, which include any one of the polymorphic sites shown in the Table. The segments can be between 5 and 250 bases, and, in specific embodiments, are between 5-10, 5-20, 10-20, 10-50, 20-50 or 10-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in the Table.

Hybridization probes are oligonucleotides which bind in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., *Science* 254, 1497-1500 (1991).

As used herein, the term primer refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and an agent for

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polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template.

10 The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with

15 the complement of the 3' end of the sequence to be amplified.

As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same

20 chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site

25 is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include

30 restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats,

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and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic or biallelic polymorphism has two forms. A triallelic polymorphism has three forms.

10 A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Typically the polymorphic site is occupied by a base other than the reference base. For example, where the reference allele contains the base "T" at the polymorphic site, the altered allele can contain a "C", "G" or "A" at the polymorphic site.

Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

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conditions, are suitable for allele-specific probe hybridizations. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleotide sequence and the primer or probe used.

The term "isolated" is used herein to indicate that the material in question exists in a physical milieu distinct from that in which it occurs in nature. For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstance, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present.

#### I. Novel Polymorphisms of the Invention

The novel polymorphisms of the invention are listed in the Table. The first column of the Table lists the names assigned to the fragments in which the polymorphisms occur. The fragments are all human genomic fragments. The sequence of one allelic form of each of the fragments (arbitrarily referred to as the prototypical or reference form) has been previously published. These sequences are listed at <http://www-genome.wi.mit.edu/> (all STS's (sequence tag sites)); <http://shgc.stanford.edu> (Stanford STS's); and <http://ww.tigr.org/> (TIGR STS's). The Web sites also list primers for amplification of the fragments,

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and the genomic location of fragments. Some fragments are expressed sequence tags, and some are random genomic fragments. All information in the websites concerning the fragments listed in the Table is incorporated by reference  
5 in its entirety for all purposes.

The second column lists the position in the fragment in which a polymorphic site has been found. Positions are numbered consecutively with the first base of the fragment sequence as listed in one of the above databases being  
10 assigned the number one. The third column lists the base occupying the polymorphic site in the sequence in the data base. This base is arbitrarily designated the reference or prototypical form, but it is not necessarily the most frequently occurring form. The fourth column in the Table  
15 lists the alternative base(s) at the polymorphic site. The fifth column of the Table lists a 5' (upstream or forward) primer that hybridizes with the 5' end of the DNA sequence to be amplified. The sixth column of the Table lists a 3' (downstream or reverse) primer that hybridizes with the  
20 complement of the 3' end of the sequence to be amplified. The seventh column of the Table lists a number of bases of sequence on either side of the polymorphic site in each fragment. The indicated sequences can be either DNA or RNA. In the latter, the T's shown in the Table are  
25 replaced by U's. The base occupying the polymorphic site is indicated in EUPAC-IUB ambiguity code.

## II. Analysis of Polymorphisms

### A. Preparation of Samples

Polymorphisms are detected in a target nucleic acid  
30 from an individual being analyzed. For assay of genomic DNA, virtually any biological sample (other than pure red blood cells) is suitable. For example, convenient tissue

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samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For  
5 example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); PCR (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren et al., *Science* 241, 1077 (1988),  
20 transcription amplification (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification  
25 methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

### 30 B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis of target DNA for detecting polymorphisms. The first type of analysis,



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sometimes referred to as de novo characterization, is carried out to identify polymorphic sites not previously characterized (i.e., to identify new polymorphisms). This analysis compares target sequences in different individuals to identify points of variation, i.e., polymorphic sites. By analyzing groups of individuals representing the greatest ethnic diversity among humans and greatest breed and species variety in plants and animals, patterns characteristic of the most common alleles/haplotypes of the locus can be identified, and the frequencies of such alleles/haplotypes in the population can be determined. Additional allelic frequencies can be determined for subpopulations characterized by criteria such as geography, race, or gender. The de novo identification of polymorphisms of the invention is described in the Examples section. The second type of analysis determines which form(s) of a characterized (known) polymorphism are present in individuals under test. There are a variety of suitable procedures, which are discussed in turn.

#### 1. Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., *Nature* 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe

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hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

## 2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in WO 95/11995. One form of such arrays is described in the Examples section in connection with de novo identification of polymorphisms. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described in the Examples, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference

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sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

### 3. Allele-Specific Primers

5       An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in  
10       conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows  
15       a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of  
20       the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

### 4. Direct-Sequencing

25       The direct analysis of the sequence of polymorphisms of the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual*, (Acad. Press,  
30       1988)).

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## 5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

## 10 6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

## 25 III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

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## A. Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See  
5 generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). The more sites that are analyzed, the lower the probability that the set of polymorphic forms in one individual is the same as that in  
10 an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with polymorphisms in distal genes. Preferred polymorphisms for use in forensics are biallelic because the population  
15 frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic  
20 analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of  
25 polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime  
30 scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a

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match of suspect and crime scene sample would occur by chance.

$p(\text{ID})$  is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies  $x$  and  $y$ , the probability of each genotype in a diploid organism is (see WO 95/12607):

- 10 Homozygote:  $p(\text{AA}) = x^2$   
 Homozygote:  $p(\text{BB}) = y^2 = (1-x)^2$   
 Single Heterozygote:  $p(\text{AB}) = p(\text{BA}) = xy = x(1-x)$   
 Both Heterozygotes:  $p(\text{AB}+\text{BA}) = 2xy = 2x(1-x)$

The probability of identity at one locus (i.e., the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

15  $p(\text{ID}) = (x^2)^2 + (2xy)^2 + (y^2)^2$ .

These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity  $p(\text{ID})$  for a 3-allele system where the alleles have the frequencies in the population of  $x$ ,  $y$  and  $z$ , respectively, is equal to the sum of the squares of the genotype frequencies:

25  $p(\text{ID}) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$

In a locus of  $n$  alleles, the appropriate binomial expansion is used to calculate  $p(\text{ID})$  and  $p(\text{exc})$ .

The cumulative probability of identity ( $\text{cum } p(\text{ID})$ ) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus.

30  $\text{cum } p(\text{ID}) = p(\text{ID}1)p(\text{ID}2)p(\text{ID}3) \dots p(\text{ID}n)$

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The cumulative probability of non-identity for  $n$  loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$\text{cum } p(\text{nonID}) = 1 - \text{cum } p(\text{ID}).$$

- 5        If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

10        B. Paternity Testing

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced.

- 15        Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

- 20        If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child  
25        attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

- 30        The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him

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incompatible as the father) is given by the equation (see WO 95/12607):

$$p(\text{exc}) = xy(1-xy)$$

where x and y are the population frequencies of alleles A and B of a biallelic polymorphic site.

(At a triallelic site  $p(\text{exc}) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)$ ), where x, y and z are the respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

$$p(\text{non-exc}) = 1 - p(\text{exc})$$

The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$\text{cum } p(\text{non-exc}) = p(\text{non-exc1})p(\text{non-exc2})p(\text{non-exc3}) \dots p(\text{non-excn})$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded)

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

### C. Correlation of Polymorphisms with Phenotypic Traits

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the



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circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria). Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance

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(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of  
5 individuals who have been tested for the presence or  
absence of a phenotypic trait of interest and for  
polymorphic markers sets. To perform such analysis, the  
presence or absence of a set of polymorphisms (i.e. a  
polymorphic set) is determined for a set of the  
10 individuals, some of whom exhibit a particular trait, and  
some of which exhibit lack of the trait. The alleles of  
each polymorphism of the set are then reviewed to determine  
whether the presence or absence of a particular allele is  
associated with the trait of interest. Correlation can be  
15 performed by standard statistical methods such as a  $\chi^2$ -  
squared test and statistically significant correlations  
between polymorphic form(s) and phenotypic characteristics  
are noted. For example, it might be found that the  
presence of allele A1 at polymorphism A correlates with  
20 heart disease. As a further example, it might be found  
that the combined presence of allele A1 at polymorphism A  
and allele B1 at polymorphism B correlates with increased  
milk production of a farm animal.

Such correlations can be exploited in several ways. In  
25 the case of a strong correlation between a set of one or  
more polymorphic forms and a disease for which treatment is  
available, detection of the polymorphic form set in a human  
or animal patient may justify immediate administration of  
treatment, or at least the institution of regular  
30 monitoring of the patient. Detection of a polymorphic form  
correlated with serious disease in a couple contemplating a  
family may also be valuable to the couple in their  
reproductive decisions. For example, the female partner

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might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \dots \beta_{17} + PE_n + a_n + e_p$$

where  $Y_{ijkpn}$  is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy record;  $\mu$  is an overall mean;  $YS_i$  is the effect common to all cows calving in year-season;  $X_k$  is the effect common to cows in either the high or average selection line;  $\beta_1$  to  $\beta_{17}$  are the binomial regressions of production record on mtDNA

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D-loop sequence polymorphisms;  $PE_n$  is permanent environmental effect common to all records of cow  $n$ ;  $a_n$  is effect of animal  $n$  and is composed of the additive genetic contribution of sire and dam breeding values and a Mendelian sampling effect; and  $e_p$  is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used as parents for breeding the next generation of the herd.

#### D. Genetic Mapping of Phenotypic Traits

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84, 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6 (1992).

Linkage studies are typically performed on members of a family. Available members of the family are characterized

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for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction  $\theta$ , versus the situation in which the two are not linked, and thus segregating independently (Thompson & Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions ( $\theta$ ), ranging from  $\theta = 0.0$  (coincident loci) to  $\theta = 0.50$  (unlinked). Thus, the likelihood at a given value of  $\theta$  is: probability of data if loci linked at  $\theta$  to probability of data if loci unlinked. The computed likelihoods are usually expressed as the  $\log_{10}$  of this ratio (i.e., a lod score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod scores for differing values of  $\theta$  (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See

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Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of  $\theta$  at which the lod score is the highest is considered to be the best estimate  
5 of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of  $\theta$ ) than the possibility that the two loci are unlinked. By convention, a combined lod  
10 score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared.  
15 Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

#### IV. Modified Polypeptides and Gene Sequences

20 The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some  
25 nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component)  
30 except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the

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corresponding codon in any of the alternative forms shown in the Table.

Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, *supra*. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, e.g., mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

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The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, i.e., 80, 95 or 99% free of cell component contaminants, as described in Jacoby, *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, *Science* 244, 1288-1292 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate



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the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide-fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

#### V. Kits

The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10,

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100 or all of the polymorphisms shown in the Table.  
Optional additional components of the kit include, for  
example, restriction enzymes, reverse-transcriptase or  
polymerase, the substrate nucleoside triphosphates, means  
5 used to label (for example, an avidin-enzyme conjugate and  
enzyme substrate and chromogen if the label is biotin), and  
the appropriate buffers for reverse transcription, PCR, or  
hybridization reactions. Usually, the kit also contains  
instructions for carrying out the methods.

10 The following Examples are offered for the purpose of  
illustrating the present invention and are not to be  
construed to limit the scope of this invention. The  
teachings of all references cited herein are hereby  
incorporated herein by reference.

15

## EXAMPLES

The polymorphisms shown in the Table were identified by  
resequencing of target sequences from three to ten  
unrelated individuals of diverse ethnic and geographic  
backgrounds by hybridization to probes immobilized to  
20 microfabricated arrays or conventional sequencing. The  
strategy and principles for design and use of such arrays  
are generally described in WO 95/11995. The strategy  
provides arrays of probes for analysis of target sequences  
showing a high degree of sequence identity to the reference  
25 sequences of the fragments shown in the Table, column 1.  
The reference sequences were sequence-tagged sites (STSs)  
developed in the course of the Human Genome Project (see,  
e.g., *Science* 270, 1945-1954 (1995); *Nature* 380, 152-154  
(1996)). Most STS's ranged from 100 bp to 300 bp in size.

30 A typical probe array used in this analysis has two  
groups of four sets of probes that respectively tile both  
strands of a reference sequence. A first probe set

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comprises a plurality of probes exhibiting perfect complementarily with one of the reference sequences. Each probe in the first probe set has an interrogation position that corresponds to a nucleotide in the reference sequence.

5 That is, the interrogation position is aligned with the corresponding nucleotide in the reference sequence, when the probe and reference sequence are aligned to maximize complementarily between the two. For each probe in the first set, there are three corresponding probes from three

10 additional probe sets. Thus, there are four probes corresponding to each nucleotide in the reference sequence. The probes from the three additional probe sets are identical to the corresponding probe from the first probe set except at the interrogation position, which occurs in

15 the same position in each of the four corresponding probes from the four probe sets, and is occupied by a different nucleotide in the four probe sets. In the present analysis, probes were 25 nucleotides long. Arrays tiled for multiple different references sequences were included

20 on the same substrate.

Multiple target sequences from an individual were amplified from human genomic DNA using primers for the fragments indicated in the listed Web sites. The amplified target sequences were fluorescently labelled during or

25 after PCR. The labelled target sequences were hybridized with a substrate bearing immobilized arrays of probes. The amount of label bound to probes was measured. Analysis of the pattern of label revealed the nature and position of differences between the target and reference sequence. For

30 example, comparison of the intensities of four corresponding probes reveals the identity of a corresponding nucleotide in the target sequences aligned with the interrogation position of the probes. The

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corresponding nucleotide is the complement of the nucleotide occupying the interrogation position of the probe showing the highest intensity (see WO 95/11995). The existence of a polymorphism is also manifested by

5 differences in normalized hybridization intensities of probes flanking the polymorphism when the probes hybridized to corresponding targets from different individuals. For example, relative loss of hybridization intensity in a "footprint" of probes flanking a polymorphism signals a

10 difference between the target and reference (i.e., a polymorphism) (see EP 717,113). Additionally, hybridization intensities for corresponding targets from different individuals can be classified into groups or clusters suggested by the data, not defined *a priori*, such

15 that isolates in a give cluster tend to be similar and isolates in different clusters tend to be dissimilar. Hybridizations to samples from different individuals were performed separately. The Table summarizes the data obtained for target sequences in comparison with a

20 reference sequence for the individuals tested.

From the foregoing, it is apparent that the invention includes a number of general uses that can be expressed concisely as follows. The invention provides for the use of any of the nucleic acid segments described above in the

25 diagnosis or monitoring of diseases, such as cancer, inflammation, heart disease, diseases of the CNS, and susceptibility to infection by microorganisms. The invention further provides for the use of any of the nucleic acid segments in the manufacture of a medicament

30 for the treatment or prophylaxis of such diseases. The invention further provides for the use of any of the DNA segments as a pharmaceutical.

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All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and  
5 individually indicated to be so incorporated by reference.

1	2	3	4	5	6	7
						TGTGAACCTCCACTTGAAGCCAAAGAAAGAACTCACACTTAAACACATGCCAGTTGGGAAGGCTCT
						GAAAACTCAGTGCATAATAGGAACACTTGAGACTAATGAAAGAGAGAGTTGAGACCAATCTTTATTT
						GTACTGGCCAAACTACTGAATAACAGTTGAAGGAAGACATTGGAAGAGCTTTTGGGATAATGT
WI-7070	226	C	T	---	---	TACTAGACTTTATGCCATGGTGCTTTCTAGTTTAATGCTGTGCTCTGTGACAG
						AAGCCATTGACGTAACTCATCTCAGAGGTTATTGCGATGGATTGACTCCTGGGACAAAAGGAC[G/C]AA
						AAACACTCTTCTGTGGATATCTGTGCAGATAGATGACCCAAAGATCAGATGCTACCCAGATGTGTTT
						GATAATACATAAGCCCTAGGATTAGATACAAATCTTGAAGAAACTGAGACAGATAATTCTGAATT
WI-10744	61	G	C	---	---	AAATGAGGTAAAGTTTCAGGCACCTCA
						GGGCAAAATTACCAGCAAAAAGTCAAAATTACCAGCATCAAAAGTCAGGTGCAAAAGGAGGTAGAACAA
						TTACAGTAACATATGCAATCTTTTGTATATTAGTATTATCTGCCCAATGCCAGTAATGCTAGATA[C/T]AGTG
						GGTCCCTAATAGTATTAGTTCCTTTTCTCCCTCTCTCTCAITCTCTGAATTTATTTTATACTTAA
WI-9975	126	C	T	---	---	GGGATTAGTTACCACCAAAATGTTATGATCAATTTGATTTACTGAA
						GCTAGGTTTGTCTTCTGTGGCTGTCTTCACTAGACTTGAGATGACTTGATTACAGTAATCCCTATGT
						GATGTAACTAGCTAGACCTTCCCTTCTCCGCAATTCAGCTCCAGGTTTCAGAAAGTATGCCACAC
						TCAACCCCTCTCTCCAGTTTCATCTCTGTATTAAATTTCTCCCATATTAAATCAAAGGGAGTGGACAGGT
WI-8010	247	G	T	---	---	CCCTGGCTGAAAAGAAATAAGAGATCCCCAAAGGTGGGG[G/T]CTT
						GCCGGCCTATCTTTTAAATTTAACTTGTATCTTTGGTGTCTTCTCCATCCTAGGATTCGCCTTATAAT
						CTTTGTCTGTCTGTAG[C/T]ATTAACCTGATCTACTTTTGTATACACAAGGCTGATGGCTCACAATGT
						AGTAGGCCAAATCTTCAGGCTCTTTGAAATTTTCTGCTATTGAGGACATTTCCACTTTCTACTTA
WI-5222b	85	G	C	---	---	TCTCGACTCTATAACAACCTCCAACAGAA
						GCCCGGCTATCTTTTAAATTTAACTTGTATCTTTGGTGTCTTCTCCATCCTA[G/C]GATTCTGCCCTAT
						AATCTTTGCTCTGTCTGTAGATTACCTGATCTACTTTTGATACACAAGGCTGATGGCTCACAATGT
						AGTAGGCCAAATCTTCAGGCTCTTTGAAATTTTCTGCTATTGAGGACATTTCCACTTTCTACTTA
WI-5222	52	G	C	---	---	TCTCGACTCTATAACAACCTCCAACAGAA
						TATGCACCTCCACAAAAGCGATATAATTTAAAAGTTTTTTCATTAGAAATAAATGTATAAAAATAA
						ATATGTTATTATAGGCATTTATTACTAACTATAGTCTTCTTGGAAAGAACACCCAAACCAATACTT
						ATAAAGTACATGTAATTTATAGTAACATATTTACTATATACATATGGAATAATCATATTTCTCACA
WI-8007	242	C	A	---	---	GAAGAGCTGAACAGACATTCACCAGGATACGACTGTGTTGGAC[C/A]AGCTGCTG
						TCAGTTGCAAAAATTTGCTGCCATAAACATGCTTTGCTTATCTCTGTGCATATGATGTTTGTAG
						TCTATATTCACACATATGAGTGAATTTCTGTTGGGCATGGGAATACATCTTTATGAGACATTGA
						ACTGCTCACCACATCATAGTATCCATTTAAACAGACCAACAATGTATAAGAAATCCCTTTGTTTAC
WI-9823	97	C	T	---	---	ATGCTTCCAAATCTGATTTGTATGACTATTGTATGCACAGTTGGATCACC

WI-9651b	105 A T ---	---	TCTACATCTATGGACAACTCCATGCCCTTTGCACATGCTGATCCCTCCCTCCTGGAATCCTTCTCT ACTTGCTCCTCATGTACAAATTTCTGCTGCTCTTCAJ/TJGGGCGAGCTTGAAGCCCTCCCTTTAGAC ACCTCTACAGGTACAGCCGACCATGCCCTACCTCCATGGCACTGCCAGGGGACCCCTTATAGGCCTCTG TCTTTAAACCTGTAATGGTATATTAACTCTGGTGTTGAATGCTCTC
WI-9651	139 T C ---	---	TCTACATCTATGGACAACTCCATGCCCTTTGCACATGCTGATCCCTCCTCCTGGAATCCTTCTCT ACTTGCTCCTCATGTACAAATTTCTGCTGCTCTTCAAGGGGAGCTTGAAGCCCTCCCTTTAGACACCT CTTACAGGTACAGCCGACCATGCCCTACCTCCATGGCACTGCCAGGGGACCCCTTATAGGCCTCTGT CTTTAAACCTGTAATGGTATATTAACTCTGGTGTTGAATGCTCTC
WI-7676b	309 A C ---	---	GTGACCTTCTGACAGGTGGAGATGGACATCCTTGTCTGGGACTTGGCCCTGCTATTTATTTTG TATTTATGCTTAACTCTTCCACTGATGCATCCTCCAAGGTAGATGGGAGGGTCTGTGTGAAGGG GCCGCTTCTCTTGGTCCCTGCTGGTTGCAGGGGAGGAGCGGTGGACTGCAGCTTCTGCTGGTGC TCCCCCGTCTCTGAGGCGAGTATAGGAGAGAGCAAGGATTGAGT
WI-7676	139 C T ---	---	GTGACCTTCTGACAGGTGGAGATGGACATCCTTGTCTGGGACTTGGCCCTGCTATTTATTTTG TATTTATGCTTAACTCTTCCACTGATGCATCCTCCAAGGTAGATGGGAGGGTCTGTGTGAAGGG GC/TJGGCTTCTTGGTCCCTGCTGGTTGCAGGGGAGGAGCGGTGGACTGCAGCTTCTGCTG GTGCTCCCCCGTCTCTGAGGCGAGTATAGGAGAGAGCAAGGATT
WI-10072	105 G A ---	---	CATTATCTTGCTTGGTCTGTTCATTCTCTCTCTCCAATGAAGGATATTTAAGCATCATT CATCTGGCCCTTTTGGAGTTTGAATATTTTGT/GAJTGACTCCTATGCACATGATAAATTTGTTA TGCTTGCTCTTATCTTATCTTTTGTATAGGAGTTTGGCCATGACCTTTATGAGGAGAAAGGA TCACCCCTTTTGGCTCTACAACCTTATAGATATTTAAATATCTTT
WI-9986	42 T C ---	---	TTGGTGTGAATCAGAAATATAGGAAATAGACAAATTTGAA/T/A/CJGTACCCCGAGAAACAAGAG CCCTGCACCTTGACTCCAAAGGAGTTCTATTCTGGCTGTTCAGACTTTATTTGATCTTTGAGAA GAGAACTGTTTCCCTCTAAATCAGTTTCATCATCTGTATCCAGGGTAGTACTACAAGAACATGTCA ATATCAATAGCATGCATATGGGTGTGGATTCTTAGAACTTATTGCAATT
WI-7041	174 C A ---	---	GTCTATTGCAGGAGAAACGTCCCTTGCCTCCACTCCCTCTCATCAGGCCAAGTGGAGGACTGGCCAGA GGGCTGCACATGCAAACTCCAGTCCCTGCTTCAGAGAGCTGAAAAGGGTCCCTCGGCTTTTATTT CAGGGCTTTGCATGCGCTCTATTCCCTCTGCTCTC/CJCCACCTTCTTTGGAGCAAGGAGATGC AGCTGATTGTGTGAACAAGCTCATTTGTACAGTGTCTGTTCATGTAATAA
WI-7224	134 T C ---	---	ATAAACCTTGTGTATGATCACCCTCACTCAATTAATCAACTTATGTGCTATCAGATATCCTCTCT ACCCTCAGCTTATTTGAAGAAATCCTAAACATCAAACTTTCATCCATAAAATGTACGATTTT /CJATTAATAAACAAATAACTTTTAAAGAAACATAAGGACACATTTTCAAAATTAATAAAATAAAG GCATTTAAGGATGGCTGTGATTATCTTGGGAGCAGAGTGATTCATGCTAG

WI-10826	132 A C ---	---	TCTTATTTGCATTTCACAGTAGCCCCATGAAGTAGGTATAACCCAGCCTCTATTTTAAACATGAGAAGATGGAGGCCCTTTCCAAATGGACTAAGTAATGTGTCTCAGGTTTTCTTAATAAGCAAGACCTGCAJVCJCCCTGGCTTCCCTGACTCCAAAGCTTATCCCTTCTCATGCTGTGCTCAGCCAGGACCCCATGCGCA
TIGR-A004S25	145 G A ---	---	GAAAGCCCAGCCTCTCCATCCCCACAGATCTGCCATTAGTATTTATTCCTTTGAAGATACCTTTGGAGATTCAATTTCTTGAGTGGCACTGCGATGCTCATTGAGTGAAGAACTTTGGGGGTATAGAAATGGAATGGAGAGTTTCAACACAGCTTTGCTGAAAC
WI-1021	24 A T ---	---	TGTAATTTGGGJAJCTCCAGACTTCACTGTCCCTTAGGCATTGAAACCATCACCTGGTTTGCAATTCATGACTGAGGTTAACTTAAATGACTGAGGTTAACTTAAAC
WI-4687	121 G T ---	---	AAACACACAGAAATCATCAAGCACAJATCTGTGTTTGAGATAAATGATAGTCTGAGTCACCTATGTAAGAAAGTAACCTCTGAAATAGTAGGATAGTATATCAATTTCTGTAATAGATTCACCTCTCAGCAAT
WI-4719b	107 T G ---	---	TGGTCTGTTTTCATTTCTATGGAACCTCTCCGTACTGTAAATTTTCAATCTATGGAACCTCCCCATACTGTAAATGGACAGTTTGGTTCCAC
WI-4719	70 G A ---	---	TAGTATGTCACCTGCCATGGTAAGGACTTTGATCACTAGGAAATAAGAACACACTTTGAATGGTCTTGCCCTTTCAATAAAAGAGTGACATGATTGAACATGTGTTTTAGATAAAGGGCACCTTGTJGCAGGAGTGT
WI-9484b	216 G C ---	---	TTAGGATGAAGAGAGAGAGATTAAAGGAAGATCAGGAAGAAAGTAGCAATGGGAATGAAATAAGGAGGCTGAGATCCACTGGATAATCTAAACCAAGAGAGAAACCTTGAT
WI-9484	178 G A ---	---	TTCAATTCCTTCCAAATCCTTAGGAAATTTACATTTATGGCTAGTGTCTTGGGTGTGAGCGGATTATGTCTGACGCCATGGGTGTTTCATAAGTGACTTGAGAGTTACTGTAGAGGCTACACAGAAATCTCTGTGAGGGGCATGTAATTGTATTCATTCAACAATCTGCTATGCTTCTCAGATTGCAGAAAAATCAC
			TGCTCAAAATCCCCACTTGTCACCTTATCCTTAAGACATTTTTCACAGGA
			TCAACACGCTTTTATTGCCACTCTGGCTCCCTCGTCCCAGCAAGATTCTACCTCTTACCCCTGTAGGAATACTGAGCTCCGATGCAGGGGAATGGGGTGGGGGTGTACCATTCTCCTCTGCACACTGCCAAGT
			TAAAGAAACCCCTGCTTGTCTGGAGAGGGAGGGCCAGACAGGAGGAATCAAGGGCATGTATGGCTCAGTCCCACTTCTGJAJCTGCAGAGTATAGGGACCCAGGGTCCCAACTTT
			TCAACACGCTTTTATTGCCACTCTGGCTCCCTCGTCCCAGCAAGATTCTACCTCTTACCCCTGTAGGAATACTGAGCTCCGATGCAGGGGAATGGGGTGGGGGTGTACCATTCTCCTCTGCACACTGCCAAGT
			TAAAGAAACCCCTGCTTGTCTGGAGAGGGAGGGCCAGACAGGAGGAATCAAGGGCATGTATGGCTGCTCAGTCCCACTTCTGJAJCTGCAGAGTATAGGGACCCAGGGTCCCAACTTT
			TCAACACGCTTTTATTGCCACTCTGGCTCCCTCGTCCCAGCAAGATTCTACCTCTTACCCCTGTAGGAATACTGAGCTCCGATGCAGGGGAATGGGGTGGGGGTGTACCATTCTCCTCTGCACACTGCCAAGT
			TAAAGAAACCCCTGCTTGTCTGGAGAGGGAGGGCCAGACAGGAGGAATCAAGGGCATGTATGGCTGCTCAGTCCCACTTCTGJAJCTGCAGAGTATAGGGACCCAGGGTCCCAACTTT



WI-7330	207	C T ---	---	---	AGGATGGAAGGAGACACGGGGCAGGAGAACTCTCTTCTGCTAAATCGATAGGAGTCAGTTTTGTCT TAAATGCTGACTACAGCCACTGACATGGTTGGCTGGAAATTTCTTTTAAATGTGGCATATAGGTTT GTGACACAAGAAGTCATACTTTGGTGGCTAAGTTTACTAAGGAAAATAACTGAAAAGATTAAAG TGAGAG[C/T]TGAAAGAGAAATGATAATGCTTCCAAACTGTAGCTGTACACAG
WI-9443	211	G A ---	---	---	TTAAAACAGTTCAGGTTGGTGAAGCAGAAAAGGGATGTGATTACAATTTAAATGAATCAGTCACCTT GCACAATTAATCCTCTTGGCATCATACAACTGGTTTTAATGGCAAATGATGACATCATAGCATGA CCAACTCATGGAAGGCAGTCTAGAGTCATACGCTCACACCTGAGGGGAAGGCACCTGCACCCA CTGACGAGAC[G/A]CAGAGACCTTGGACTACAGATGACACCACATGCCCACTT
WI-7166	59	C T ---	---	---	TCCTCTAAAAGAGAAAACAAACCCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTA[C/T]GGAT CATCAACAAGATTTCCTTGTGCAAAATATTGACTATTCTGTATCTTTTCATCCTTGACTAAATTCGTG ATTTCAAGCAGCATCTTCTGGTTTAACTTGTGCTGTGAACAATGTGCGAAAAGAGTCTTCCAAT TAATGCTTTTTATATCTAGGCTACCTGTTGGTTAGATTCAAGGCCCGAG
WI-7259b	189	T C ---	---	---	GCTTCTCCCCAGGAAGCGGGTCTTGGCCTGGAACCTTCAGAGAGGAGCGGGAGCAATTTAGCC CCACCTGCTCCCATCTGCCCCCTGCAACAGCTGCAGGCTGCTTCTCTCTCTGAGTTCTCTGGGCT GCGCAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTAACCTGGCCACAG[T/C]TGGGGAGCAG AGCCAGCAGTGGACAGGTGTTTGCAGGGGCCAACCTTCCCTGGAGCTC
WI-7259	188	G T ---	---	---	GCTTCTCCCCAGGAAGCGGGTCTTGGCCTGGAACCTTCAGAGAGGAGCGGGAGCAATTTAGCC CCACCTGCTCCCATCTGCCCCCTGCAACAGCTGCAGGCTGCTTCTCTCTCTGAGTTCTCTGGGCT GCGCAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTAACCTGGCCACAG[G/C, I]TGGGGGAGCA GAGCCAGCAGGTGGACAGGTGTTTGCAGGGGCCAACCTTCCCTGGAGC
WI-7322	275	A G ---	---	---	GTACTTTAGGCTGTGGAGGTGGCATTTAGTGTGACCCCTGCACCAGGGTTTCTAACAGATGAC CCTGTGAATCATAAATTTAAACCTGCATATATTTATAGCCAGTCACATTTGCCCTCTCACCCATATG GCCATAAACTGCCTAAGCACTCAGGCCCTCCACTCATCAACCCCTTTGACCAGAGAAAGCACTC TGGTTCTCTATCCCTTGTACATAGAGAGTTTGTGATGGGGCCTCTGGCTG
WI-7685	46	T C ---	---	---	TCAGTTCTAGTCTCTCTGGGGCCACACAGAAACTCTTTTGGGCTC[T/C]TTTCTCCCTCTGGATCA AAGTAGGAGGACCATGGGACCAGGCTTGGAGCTGAGCCCTCACCTGTACTCTCCGAAAAATCCT CTTCTCTGAGGCTGGATCTAGCCTTATCCTCTGATCTCCATGGCTCTCTCCCTCTCTGCGGACTC CTGGTTGAGCTGTTGCTCAGTCCCCAACAGAIGCTTTCTGTCTC
WI-563	87	G A ---	---	---	TGTGACCAATTGTTATTTAGAGGGTTTAAACATGGCCTGACTATCACCTGATGGTCGCCAGAAATTC CTGGGGAGGGCTCCCTT[G/A]CCCTGATCATGTCTACCTAACTGCTACTCTAACATACTACTCTCC TGTGGTATGGGGATCCTAAGCCAAAAAGCTGAAATGAACATGTTCTAGCACTACAGAAATCCATACT GCCCTCAGTAAAGGCAAAATTTAAATCTCTTTGGATAACCCAGGGCACAT

WI-931c	191 C A ---	---	GACCAGGGCACCAGAAAGCCACGGAAAGCCACAGCCACTAGCCCTGAACCTTGACACCCCTGGAGTT TCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGTATTCTGCTGTGCAAAATGATCCTTCT GTTGCTGCACGTGTCAATTACTGTGTATGGATTTATAATTATGTCACAAAAGCC[C/A]CGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAAG
WI-931b	81 A G ---	---	GACCAGGGCACCAGAAAGCCACGGAAAGCCACAGCCACTAGCCCTGAACCTTGACACCCCTGGAGTT TCTCTCCCTCCCT[A/G]TCCCTCACCACACCTTCCAGTGTATTCTGCTGTGCAAAATGATCCT TCTGTTGCTGCACGTGTCAATTACTGTGTATGGATTTATAATTATGTCACAAAAGCCCGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAAG
WI-931	31 A G ---	---	GACCAGGGCACCAGAAAGCCACGGAAAGCCAC[A/G]GCCACTAGCCCTGAACCTTGACACCCCTGGA GTTTCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGTATTCTGCTGTGCAAAATGATCCT TCTGTTGCTGCACGTGTCAATTACTGTGTATGGATTTATAATTATGTCACAAAAGCCCGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAAG
WI-10870b	91 C T ---	---	GGATGACTTACCCAAATAGCAGGGTGGGTACATTCATGGGTAACAACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGG[C/T]ACCTACTTAGAGCAGTGGAGTACCCTGAGTACGACCCCC TTAGCAGCAGAAATTACAAGAAATCTTGGGACCTGTACTCCTGATACAAAATAAGGACATGGGTACGC CTGAGCCACTCTTAAACCATGAACCATCACCATTTAAATAACGTTGCCCCCC
WI-10870	103 G A ---	---	GGATGACTTACCCAAATAGCAGGGTGGGTACATTCATGGGTAACAACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGGACCTACTTAGA[A/G]ACAGTGGAGTACCCTGAGTACGACCCCC TTAGCAGCAGAAATTACAAGAAATCTTGGGACCTGTACTCCTGATACAAAATAAGGACATGGGTACGC CTGAGCCACTCTTAAACCATGAACCATCACCATTTAAATAACGTTGCCCCCC
WI-7719b	281 T C ---	---	AGTTTATCTTCCAGATGACCAGCAGTAGACAAATGGATACCTAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTGGGCATTGGTCTGGCCAAAGTCTACAATGTCCCAATATCAAGGACAACCCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCCATTAGATCAAGACTACACGGTCTATGAGCAATAATGTG ATTTCTGGACATTGCCCATGTATAATCTCACTGATGATTTCAAGCTAAAGCAA
WI-7719	163 A G ---	---	AGTTTATCTTCCAGATGACCAGCAGTAGACAAATGGATACCTAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTGGGCATTGGTCTGGCCAAAGTCTACAATGTCCCAATATCAAGGACAACCCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCC[A/G]TTAGATCAAGACTACACGGTCTATGAGCAATAAT GTGATTTCTGGACATTGCCCATGTATAATCTCACTGATGATTTCAAGCTAAA
WI-10396	72 C A ---	---	GCCTTGGAGTATATCTAAACTGTGGCTCCACTTTCATTTTCTTGAACATTGCTATCAACTGGAA GAGT[C/A]GTGACTTTATGCCCAGTTTCCCTCTCAGATTTTATGACGGTTGTTTTCTTTTGTGA TGCCATTTGAGGGATTGATGTTTCTTAAACTATGAAGTACTTGGCTGTCTCTCTCCATTGCTGTCAGG TTAACAGCCACCATTTGTAAACACATTGT

WI-10673	94	C G ---	---	TCCCTTTATGCACCCAAAGAGATATTTATTAAACACCAATTTACGTAGCAGGCCATGGCTCATGGGAACC CACCCTCCGTTGGCACTCATGGAGGGG[C/G]TGAGGTTGGAACATATGCAGTGTGCTCCGGCCACACA TCCTGTGGGCCCCCTACCCTGCCCAATCAATCCCTGCCAATAAATCCTGTCTTATTTGTTTCATCCTG GAGATTGAAGGGAGGTCAGTGTGTTGTCATGATTTGTCAGAGAACCCT
WI-7842	57	T C ---	---	CACAGCAATGCCCTTGAGGAGCCGCCACAGATGCTGAATCCCTATCCCATTCGT[C/G]GTATGAG TCCCATTTGCCCTTGCAATTAGCATCTGTCTCCCCCAAAAGAAATGTGCTATGAAGCTTTCTTTCTCT ACACACTCTGAGTCTCTGAATGAAGCTGAAGGTCTTAGTACCAGAGCTAGTTTTCAGCTGCTCAGAAAT TCATCTGAAGAGAGACTTAAGATGAAAGCAAATGATTGAGCTCCCTTATA
WI-7721	145	A C ---	---	CTGCCATCATCAGCCACTGGAGTCCACACTTGAATTTGGGCAGCTACCACGGGTCTGCCATGCTCTGG AGGAGCAAGGGGGCCACATCCCCACCCAGCTGTTACCCAGCCCGGCGAGGTGCAGCCCTTCTCTCC TGCTCTG[C/A/C]CTGACTCTCTTTGAGGTCCCTGTATGCTACCTCTGACTTCTGTGGTCCCTCTG TGCTGCTCTCATCCATTCCTTACTGGGGCTGGGGCTCTAGCCCAA
WI-4767b	173	C A ---	---	TTTCCAGTCTGTTTTATCCTTTTCATTGTCAAAAGATGCTCTTAGACTGAAATTCATAAAGAGTTCCCT CAGGTCTGGTAAATCCTAGATCTTCTATATCCATTGAGTGTGAGGTGGAGAGAGGGTATGTTT CTTGCCCTTGAGAAATCCTAGAAAGCACAGGGATGACA[C/A]AAATCACTAAGGAATTCCTACTAAGA CTCTCTAACCACAGAGATTTTAACTT
WI-4767	50	A G ---	---	TTTCCAGTCTGTTTTATCCTTTTCATTGTCAAAAGATGCTCTTAGACTGA[A/G]ATTCATAAAGAGTT CCTCAGGTCTGGTAAATCCTAGATCTTCTATATCCATTGAGTGTGAGGTGGAGAGAGGGTATG TTTCTTGCCTTGAGAAATCCTAGAAAGCACAGGGATGACACAAATCACTAAGGAATTCCTACTAAGAC TCCTCTAACCACAGAGATTTTAACTT
WI-7718f	222	C T ---	---	ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAAACTGATGCCAAGGGGTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAGATG ACTTTGCAGATGGAAGAGGTGAAATGAAGAGGAAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAA[C/T]CATGCAGGAAGGAAAACTAIGTATTAAAT
WI-7718e	60	T C ---	---	ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGAT[C/G]CAA GGATTACAGAAACTGATGCCAAGGGGTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAAAATGAAGAGGAAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT
WI-7718d	31	G A ---	---	ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAA GGATTACAGAAACTGATGCCAAGGGGTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAAAATGAAGAGGAAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT

WI-7718c	91 C G ---	---	---	ATTGCACTGAAGTTTGTAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAAACTGATGCCAAGGGG[C/G]TGAAGTGAATCACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAAGAGTGAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAGTC AAAGGAACAAAAATTACAAAGAACCATGCGAGGAAGGAAAACTATGTATTAAAT
WI-7718b	248 A G ---	---	---	ATTGCACTGAAGTTTGTAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGCTGAGTGAAGTTCACTACATGTTCTGGGGCCCGGAGATAGTG ACTTTCAGATGGAAAGAGGTGAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAACCATGCGAGGAAGGAAAACTATGTATT[A/G]AT
WI-7718a	42 A T ---	---	---	ATTGCACTGAAGTTTGTAAATACCTTTGTAGTTACTCAAGC[A/C]TGTACTCCCTACACTGATGC AAGGATTACAGAAACTGATGCCAAGGGCTGAGTGAAGTTCACTACATGTTCTGGGGCCCGGAGAT AGATGACTTTGCAGATGGAAAGAGGTGAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAG TCAAAAGGAACAAAAATTACAAAGAACCATGCGAGGAAGGAAAACTATGTATTA
WI-7227d	99 G C ---	---	---	AGGGAATTGTGTTGCTCCTGGAGGAAGCCAGGCATCATTAACAAGCCAGTAGGTCACTGGCTTC CGTGGACCAATTCATCTTTAGACAAGCTTTA[G/C]AGAAATGGACTCAGGGAAGAGACTCACATGC TTGGTAGTATCTGTGTTCCGGTGGTGAATAGGGGATTAGCCCAAGAGGACTGAGCTAAACA GTGTTATTATGGAAAGGAAATGGCATTTGCTGCTTTCAACCAGCGACTAATG
WI-7227c	291 G A ---	---	---	AGGGAATTGTGTTGCTCCTGGAGGAAGCCAGGCATCATTAACAAGCCAGTAGGTCACTGGCTTC CGTGGACCAATTCATCTTTAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGCTTT GGTTAGTATCTGTGTTCCGGTGGTGAATAGGGGATTAGCCCAAGAGGACTGAGCTAAACAGTG TTATTATGGAAAGGAAATGGCATTTGCTGCTTTCAACCAGCGACTAATGCAAT
WI-7227b	93 G T ---	---	---	AGGGAATTGTGTTGCTCCTGGAGGAAGCCAGGCATCATTAACAAGCCAGTAGGTCACTGGCTTC CGTGGACCAATTCATCTTTAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTGGTTAGTATCTGTGTTCCGGTGGTGAATAGGGGATTAGCCCAAGAGGACTGAGCTAAACA GTGTTATTATGGAAAGGAAATGGCATTTGCTGCTTTCAACCAGCGACTAATG
WI-7227a	24 A G ---	---	---	AGGGAATTGTGTTGCTCCTGGAGGAAGCCAGGCATCATTAACAAGCCAGTAGGTCACTGGCTTC TTCCGTGGACCAATTCATCTTTAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTGGTTAGTATCTGTGTTCCGGTGGTGAATAGGGGATTAGCCCAAGAGGACTGAGCTAAACA GTGTTATTATGGAAAGGAAATGGCATTTGCTGCTTTCAACCAGCGACTAATG
WI-7310b	234 A C ---	---	---	CCCAATGCCTCTCCACGATGTCAAGGACTCCTGCTGCTGGAGTGGGAGACAAGGAACCTCCG AAGAGGAAGCAAGAAAGCCGCTACTGCTATGTTGATCCTTCATCGAACAACTGATGCGAAACT TGAATCTGTTACTGAAATGAGGAGAGAGGACATGTGCTATTGAACCTGAGCCAAACACACTGTAAT ATCCACAGACTCCCTCCCTGCCCCCATCCCA[A/C]ATGATCTTGAGATTTC

WI-7310a	64 T A ---	---	---	CCACAATGCCTCTOCCACGATGTCAAGGACTCCTGTCTGTCTGCTGGAGGTGGGAGACAAGGAACQTA JCCGAAGAGGAAGCAAGAAAGCCGTACTGTCTATGTGTGATCCTTCATCGAACAACCTGATGCGAA AACTTGAATCTGTTACTGAAATGAGGAGAGAGACATGTGCTATTGAACCTGAGCCAAACACACTGT AAATATCCACAGACTCCCTCCCTGCCCTGCCCATCCCAATGATCTTGAGATTTC
WI-7878b	162 A G ---	---	---	CCAGCAACACCTACACCTTGTCACTGCCTGGACTCCTATGATGGCTGTGCTGTTGATAATATCA GATCATGCCAAGACGGCCTCCTGATAATCGCTTGGGCATGATTGCAATGGAGGCAATGCGTCC CTGAGGAGAAATCTGGGAGGAGCTGAGTGTGATGAAGGTGTATGTTGGAGGGAGCACAGTGT CTGTGGGAGCCAGGAAGCTGCTACCCAAAGATTGGTGCAGGAAACTA
WI-7878a	51 C G ---	---	---	CCAGCAACACCTACACCTTGTCACTGCCTGGACTCCTATGATGGCTGTGCTGTTGATAATAA TCAGATCATGCCAAGACGGCCTCCTGATAATCGCTTGGCATGATTGCAATGGAGGCAAAATGC GTCCCTGAGGAGAAATCTGGGAGGAGCTGAGTGTGATGAAGGTGTATGTTGGAGGGAGCACAGTG TCTGTGGGAGCCAGGAAGCTGCTACCCAAAGATTGGTGCAGGAAACTA
WI-7381c	213 C T ---	---	---	CTCCACATTCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTTTCTTCTACC AGCCCTGGAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGAGGTTTCTGCTATGGTGAGATC AGATGTGCCAAGGAAAGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAGACA AAAGGCTCTCTGCTCTCAGAGCATAATCCTTGGCAGGCTCAGCAGG
WI-7381b	54 C G ---	---	---	CTCCACATTCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTTTCTTCT ACCAGCCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGAGGTTTCTGCTATGGTGAG ATCAGATGTGGCCAAAGGAGGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAAAGGGCTCCGGCTCTCAGAGCATAATCCTTGGCAGGCTCAGCAGG
WI-7381a	53 C G ---	---	---	CTCCACATTCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTTTCTTCT ACCAGCCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGAGGTTTCTGCTATGGTGAG ATCAGATGTGGCCAAAGGAGGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAAAGGGCTCCGGCTCTCAGAGCATAATCCTTGGCAGGCTCAGCAGG
WI-1017b	93 G A ---	---	---	AAATGCTCTATTCGGACCTCATATTAATAAGAGCAATGAGAGCGAGGGAATTTGAACCTCTC AGGTACTGACTGTGGACCCAGACAAG[G/A]GATGTAGATTGCACATTCAATCCTGAAACAACCTG CCAGGCAAGTCTCTTCCCATTTTACAAATAGGAGACAAAAATAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGAGGTTTGTCCC
WI-1017a	92 G A ---	---	---	AAATGCTCTATTCGGACCTCATATTAATAAGAGCAATGAGAGCGAGGGAATTTGAACCTCTC AGGTACTGACTGTGGACCCAGACAAG[G/A]GGATGTAGATTGCACATTCAATCCTGAAACAACCTG CCAGGCAAGTCTCTTCCCATTTTACAAATAGGAGACAAAAATAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGAGGTTTGTCCC



WI-1126a	97	T C ---				CTCTATTCTCTGGGCACTGCTTTCTTTGGGGCAAACTCCAGTATCACTGATACATAATAAAAA CCCTGTAAGTCTGCTTGCATTTTCAAGATT/CJCAATATATATCCAGATTGTTTTCCAGCAAGAAAA ATTTTATTTCTCAAGATAATAAAAAATAATATTTAAATTCAGTTCCCTCAAAAGGAATATGAAATTT GTTAAATGCAAAATCCAGCTGTAACTTTTGGACTTGCTTTTATTTCT
WI-11183c	124	C T ---				TAGTGCTAATTTTGGAAAAGTTTGGCTGATTTTAAAAATCTTTTAAAACTTGAAAAATTTAGAGTAC ATATAAATAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCTTGTCACATAACATTT TTTATGACATACAAATGACCAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTAAATATTGGT ATGTGGTCTAGAGTTAGTAATGGAA
WI-11183b	192	T C ---				TAGTGCTAATTTTGGAAAAGTTTGGCTGATTTTAAAAATCTTTTAAAACTTGAAAAATTTAGAGTAC ATATAAATAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCTTGTCACATAACATTT ATGACATACAAATGACCAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTAAAT/CJATTGGT ATGTGGTCTAGAGTTAGTAATGGAA
WI-11183a	118	C T ---				TAGTGCTAATTTTGGAAAAGTTTGGCTGATTTTAAAAATCTTTTAAAACTTGAAAAATTTAGAGTAC ATATAAATAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGC/CJCTTGTCACATAACA TTTATGACATACAAATGACCAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTAAATATTGGT ATGTGGTCTAGAGTTAGTAATGGAA
WI-10770b	174	G A ---				GCTTGGTTTGGCTTATGCTTATGCTCAGTCTTGAGTCTCCCTTCTGCCGCGCTTTTGATTTCA CCCATACCTCTATGCCCTGCTCAGACCATTTCTCTATCTGGAGCGCTTCTCTGTACTTTCTCCTG TTCACCAACCTTCTTTTATCTTCAGGACACTCA/GAJTTCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTTCTGTGTCCTTTCC
WI-10770a	49	G T ---				GCTTGGTTTGGCTTATGCTTATGCTCAGTCTTGAGTCTCCCTTCTGCCGCGCTTTTGATTT TCACCCATACCTCTATGCCCTGCTCAGACCATTTCTCTATCTGGAGCGCTTCTCTGTACTTTCTC CTGTTCAACCAACCTTCTTTTATCTTCAGGACACTCAGTTTCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTTCTGTGTCCTTTCC
WI-9667b	82	C T ---				GATGACAACTTCTGCTGTGACCCCTTAGTCTTGTCTCATGACACTTTTCAATCTGCTTGTATCATGG TTATCACTGGACA/CJTAGCCACCTCCCGAGCAGGCTTAGAACTCCATGAGTAAGGACCCCTGTCTA ATGTGCCGTTTCTCCTTATGGTATTACACACAGTCATAGGCGATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAACTTGCATCT
WI-9667a	68	G C ---				GATGACAACTTCTGCTGTGACCCCTTAGTCTTGTCTCATGACACTTTTCAATCTGCTTGTATCATG G/CJTTATCACTGGACACAGCCACCTCCCGAGCAGGCTTAGAACTCCATGAGTAAGGACCCCTGTCTA ATGTGCCGTTTCTCCTTATGGTATTACACACAGTCATAGGCGATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAACTTGCATCT

WI-10400d	189 A G ---			ACATTTTATTAGCAAAATCAGCAAAATAATAAATAGAAAAGTAATTGCATTTTCAGACATCTGCTG GTTAACTGTTATAAGATGTTTAGCACACATGTAAAGCAGCTTACTAACACATAATTTTATTCTAATTTT TCCTTCCCTTACCTTACTCTCCCAACCCCAAAATAACGTAAGTACCTATGTC[A/G]TGCCATGTAG TTTTTGGTTCATTTACTTGCAAATTTATCAAGGCGTTAATGCATTATG
WI-10400c	166 A C ---			ACATTTTATTAGCAAAATCAGCAAAATAATAAATAGAAAAGTAATTGCATTTTCAGACATCTGCTG GTTAACTGTTATAAGATGTTTAGCACACATGTAAAGCAGCTTACTAACACATAATTTTATTCTAATTTT TCCTTCCCTTACCTTACTCTCCCAACCCCA[A/C]JAAATAACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCATTTACTTGCAAATTTATCAAGGCGTTAATGCATTATG
WI-10400b	165 A G ---			ACATTTTATTAGCAAAATCAGCAAAATAATAAATAGAAAAGTAATTGCATTTTCAGACATCTGCTG GTTAACTGTTATAAGATGTTTAGCACACATGTAAAGCAGCTTACTAACACATAATTTTATTCTAATTTT TCCTTCCCTTACCTTACTCTCCCAACCCCA[A/G]JAAATAACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCATTTACTTGCAAATTTATCAAGGCGTTAATGCATTATG
WI-10400a	46 T C ---			ACATTTTATTAGCAAAATCAGCAAAATAATAAATAGAAAAGTAAT[C/J]TGCAATTTTCAGACATCT GCTGGTAACTGTTATAAGATGTTTAGCACACATGTAAAGCAGCTTACTAACACATAATTTTATTCTA ATTTTCCTTCCCTTACCTTACTCTCCCAACCCCAAAATAACGTAAGTACCTATGTCATGCCATGT AGTTTTTGGTTCATTTACTTGCAAATTTATCAAGGCGTTAATGCATTATG
WI-10809b	78 C T ---			AAAGGGCTACAACTAAGGCCAAAAACCATGAACGGTATAAGGAGGGTAAATGCAAGGGGAGACCC CACCTCTACCA[C/J]TTAGAAAGGGCATTTCAAGCACATTTCAATGAGGCTTCATATACTGGTTAG CAACAAATGGAATGTATTAGCCCAAGGCAGGGTATGGACCAAAAGTGCCCAAGTGATGAGGCCACA GTGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-10809a	33 C T ---			AAAGGGCTACAACTAAGGCCAAAAACCATGAAC[J/T]GGTATAAGGAGGGTAAATGCAAGGGGAGA CCCCACCTCTCACCACTTAGAAAAGGGCATTTCAAGCACATTTCAATGAGGCTTCATATACTGGTTAGC AAACAAATGGAATGTATTAGCCCAAGGCAGGGTATGGACCAAAAGTGCCCAAGTGATGAGGCCACAG TGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-7038c	266 T C ---			CGAGCTTGGGATAAGCAAGGGGACCTTGGCGCTCTCAGCTTTTCCCTGCCACATCCAGCTTGTGTCC CAATGAATACTAGATGCTGGGCTGTCTCTCCCTTCAGGAATGCTGGGCCCCAGCCTGGCCAGAC AAGAAGACTGTCAGGAAGGGTCGGAGTCTGTAAACCAGCAGCATAAGTTTGGCTTTTTCACATTGAT CATTTTATATGAAATAAAAGATCCTGCAATTTATGGTGTAGTTCTGAGTCC
WI-7038b	140 A C ---			CGAGCTTGGGATAAGCAAGGGGACCTTGGCGCTCTCAGCTTTTCCCTGCCACATCCAGCTTGTGTCC CAATGAATACTAGATGCTGGGCTGTCTCTCCCTTCAGGAATGCTGGGCCCCAGCCTGGCCAGAC AAGA[A/C]GACTGTCAGGAAGGGTCGGAGTCTGTAAACCAGCAGCATAAGTTTGGCTTTTTCACATT GATCATTTTATATGAAATAAAAGATCCTGCAATTTATGGTGTAGTTCTGA



WI-7038a	31	G A	---	---	CGAGCTTGGGATAAAGCAAGGGGACCTTGGC[G/A]CTCTCAGCTTCCCTGCCACATCCAGCTTGTTG TCCCAATGAAATAGTACTGAGATGCTGGGCTGCTCTCCCTTCCAGGAATGCTGGCCCCCAGCCTGGCCA GACAAGAAGACTGTGAGGAAGGGTCGGAGTCTGTAACACAGCATACAGTTTGGCTTTTTCACATT GATCATTTTATATGAATAAAGATCCTGCATTTATGGTGTAGTTCTGA
WI-3429b	64	G T	---	---	ATACGCTTTCTGCTGTCCACAGTGAACACAGCACCCAGGTGGCCAGGGTCCGGCTCCACACA[G/T] CCCTCAGCCCCCTTCAGCTTTGCAATGTGTCCTCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAAATACAGATCCAGTCTCCTCTCCTCGGATTTGGATCTAGCAAGACCAGACGGTCCCTAGAA TCCTGACTGTTAACAAAGCACTCCAGGCAATTTCTTAAGACCAAGCACGGAGC
WI-3429a	62	C T	---	---	ATACGCTTTCTGCTGTCCACAGTGAACACAGCACCCAGGTGGCCAGGGTCCGGCTCCACACA[C/T]AG CCCTCAGCCCCCTTCAGCTTTGCAATGTGTCCTCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAAATACAGATCCAGTCTCCTCTCCTCGGATTTGGATCTAGCAAGACCAGACGGTCCCTAGAA TCCTGACTGTTAACAAAGCACTCCAGGCAATTTCTTAAGACCAAGCACGGAGC
WI-6786c	151	G A	---	---	ATTTAGGACAGTGAAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCTTTGGCGAAAGGATAAAGAGTGAGTGACGGTGACCT GTGAGCCCCCATTC[T/G]ATGGGATAAGGTGCCATTTGTTCTTGAGGGTGAATGCCACATTC TTTTGGCAGGGGACACTCCTCTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6786b	111	A T	---	---	ATTTAGGACAGTGAAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCTTTGGCGAAAGGATAAAGAGTGAGTGACGGTGA CCTGTGAGCCCCATTCCTCTGTGGGATAAGGTGCCATTTGTTCTTGAGGGTGAATGCCACATTC TTTTGGCAGGGGACACTCCTCTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6786a	106	A T	---	---	ATTTAGGACAGTGAAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCTTTGGCGAAATGGATAAAGAGTGAGTGACGGTGA CCTGTGAGCCCCATTCCTCTGTGGGATAAGGTGCCATTTGTTCTTGAGGGTGAATGCCACATTC TTTTGGCAGGGGACACTCCTCTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6711b	226	G T	---	---	GGCTATTTGTAATGCTTGGTTATTGACTCCAAAAATGAATAAGTATTGGGAAGAAATCCCTCACCT ACTTCCAAATCCCCTTACATATCAATTTTACACAAAGCCCCCTAAACCTTCAGTTCCAATCACTGAAT TTCATATACCTCCATTATTAATTCATATCATCTGTCAGAGAGAAAGACAAACGGTGCCAACTGGGTT TGGTTGGTGCCTGCACACCCACA[G/T]TGGCAACTAAGTGAATCTCTAAA
WI-6711a	36	T C	---	---	GGCTATTTGTAATGCTTGGTTATTGACTCCAAAAATGAATAAGTATTGGGAAGAAATCCCTC ACCTACTTCCAAATCCCCTTACATATCAATTTTACACAAAGCCCCCTAAACCTTCAGTTCCAATCACTCT GAATTCATATACCTCCATTATTAATTCATATCATCTGTCAGAGAGAAAGACAAACGGTGCCAACTG GGTTTGGTGGTGCCTGCACACCCACAGTGGCAACTAAGTGAATCTCTAAA

WI-10613b	172 A C ---			---	ATTGTATGCCAAATCATAATACCCCTGCACTCTAGAAACATACAGTGTAAATAGAAATTTGAGCCATA TGGTGAAAAATTTAGAAAGTATTATCTCTATATGTATATCTACGTTTAAACATCAATGAATGTGATTT TTTGTCAACTTTTGACAAGGCCAGGCAATTTTATTGTA/CIGCCCTAGGAGGGTTACTATAATTTAGA AAGGCTCTTACCTTCCACTCTATAATTTAAGTCTGGGACTTAGGATGTAG
WI-10613a	44 G A ---			---	ATTGTATGCCAAATCATAATACCCCTGCACTCTAGAAACATACAGTGTAAATAGAAATTTGAGCC ATATGGTGAAAAATTTAGAAAGTATTATCTCTATATGTATATCTACGTTTAAACATCAATGAATGTG ATTTTGTCAACTTTTGACAAGGCCAGGCAATTTTATTGAGCCCTAGGAGGGTTACTATAATTTAG AAAGGCTCTTACCTTCCACTCTATAATTTAAGTCTGGGACTTAGGATGTAG
WI-7587c	133 A T ---			---	GCTCTAGTGGGAAACCTCAGGTAGCTCCCGAAGATCTGTGCTTTCCAACAAGTGACTACCCCTTGAAGC ACATCCCTCTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAA(A/ TJGGAATGAACCACTCCCTGCCATTTCCCTATAAGAAATATCCCAAGACCCAGGCAATTTTGCCCTCT TTCCACATGCCOCCATATGCTGAGCCAACTGCACCTGGGGCTGCCCTC
WI-7587b	81 G A ---			---	GCTCTAGTGGGAAACCTCAGGTAGCTCCCGAAGATCTGTGCTTTCCAACAAGTGACTACCCCTTGA ACATCCCTCTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAA AGGAATGAACCACTCCCTGCCATTTCCCTATAAGAAATATCCCAAGACCCAGGCAATTTTGCCCTCT TCCACATGCCOCCATATGCTGAGCCAACTGCACCTGGGGCTGCCCTC
WI-7587a	28 C T ---			---	GCTCTAGTGGGAAACCTCAGGTAGCTCCCGAAGATCTGTGCTTTCCAACAAGTGACTACCCCTTGA AGCACATCCCTCTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAA AGGAATGAACCACTCCCTGCCATTTCCCTATAAGAAATATCCCAAGACCCAGGCAATTTTGCCCTCT TCCACATGCCOCCATATGCTGAGCCAACTGCACCTGGGGCTGCCCTC
WI-10681b	103 T A ---			---	ATGACTCAGGTGACAAAAGAGCATGTCCTAGACCCCATTTAGTACGCAAACTCAATCAGCCAAACC ACAGAAAAGCTAAAGACATCCCTTTTAAAAAGCC(T/A)AAAGACAGCCATTTTAACTCTAAATTCG TAGTTTATGATTTTCTCAAAATTTCCCCACACACAGAAAGAACTTCAAGGTAGGTTCTAATGTTA CCATTGCTAACACTATTGCTTTGGAGAAGGAGGAGTGACGCTCTGTAAAAG
WI-10681a	41 A T ---			---	ATGACTCAGGTGACAAAAGAGCATGTCCTAGACCCCATTTAGTACGCAAACTCAATCAGCCAAACC ACCACAGAAAAGCTAAAGACATCCCTTTTAAAAAGCC(T/A)AAAGACAGCCATTTTAACTCTAAATTCG TAGTTTATGATTTTCTCAAAATTTCCCCACACACAGAAAGAACTTCAAGGTAGGTTCTAATGTTA CCATTGCTAACACTATTGCTTTGGAGAAGGAGGAGTGACGCTCTGTAAAAG
WI-7222c	126 G T ---			---	GCCTCTCCTCAACTGCTCGGACCCCAAGGCTAGGAAAGGGCTGCTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGTCAAGGTGTCACCCCTGTTCTCAAGTTGGGGATGGG(G/TAATAA AGGAGGGGAATCCCTTGAACAAGAAAGAACTGGGGATAGTTATATTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGGTAAAGGTTGATTTCAAGAGACTCGAATTCATTTT

WI-7222b	255	G A ---	---	---	GCCTCTCCTCAACTGTCCTGGACCCCAAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTACCCCTGTTCTCAAGTTGGGGATGGGGAATAAAGG AGGGGGAATTCCTTTGAACAAGAAGAACTGGGGATAGTTATATTTCCACCTGCCCTTGAAGCTTTAA GACAGTGATTTTGTGTAAGTTGTATTTCAAAGACTCGAATTCATTTTCTCA
WI-7222a	126	G T ---	---	---	GCCTCTCCTCAACTGTCCTGGACCCCAAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTACCCCTGTTCTCAAGTTGGGGATGGG[G/TAATAA AGGAGGGGAATTCCTTTGAACAAGAAGAACTGGGGATAGTTATATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGTAAGTTGTATTTCAAAGACTCGAATTCATTTT
WI-8054d	41	C A ---	---	---	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTTCTCTTTC[CA/ATATCTCTCTCCAGTTCAAAATG CTTGCACTTTTAATAGCCAGCATTCCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAGCA CAATCTCTTTGTAGTTTAGCCCTTTTCGGGAAATCGGCTTAGTTTGCCACCATAGCCACTCTGCT TCCTGTCATAACGCCGCTTCCCTGGCGGTACAGAGATCCTTGCCCTT
WI-8054c	237	G T ---	---	---	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTTCTCTTTC[CA/ATATCTCTCTCCAGTTCAAAATGCTT GCATCTTTTAATAGCCAGCATTCCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAGCACAA TCTTCTTTGTAGTTTAGCCCTTTTCGGGAAATCGGCTTAGTTTGCCACCATAGCCACTCTGCTTCC TGTCATAACGCCGCTTCCCTGGCGGTACAGAG[GT/AAATCCTTGCCCTT
WI-8054b	148	T C ---	---	---	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTTCTCTTTC[CA/ATATCTCTCTCCAGTTCAAAATGCTT GCATCTTTTAATAGCCAGCATTCCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAGCACAA TCTTCTTTGTAG[TC/TTTAGCCTTTTCGGGAAATCGGCTTAGTTTGCCACCATAGCCACTCTGCT TCCTGTCATAACGCCGCTTCCCTGGCGGTACAGAGATCCTTGCCCTT
WI-8054a	131	C G ---	---	---	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTTCTCTTTC[CA/ATATCTCTCTCCAGTTCAAAATGCTT GCATCTTTTAATAGCCAGCATTCCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAG[CA/GJA CAATCTTCTTTGTAGTTTAGCCTTTTCGGGAAATCGGCTTAGTTTGCCACCATAGCCACTCTGCT TCCTGTCATAACGCCGCTTCCCTGGCGGTACAGAGATCCTTGCCCTT
WI-10854b	152	G T ---	---	---	TTCCACAAAACCTTCCCTGGCCCGGGTGACTAAGATGAGAAAGTGGGAACTGGATAGTTTAAATAA ATGTTTATATTTTACTTTAAAGCGAAGTTGAAACACGACGATAGTTAACGCTGTTGTAAGTTAT ACGGTGTCGAGGCAACA[G/TTGGAGAGGTACGGGAATAGTTTACTTCTGTTTTTATTCTTG TTTTAGACACAGGGTCTGCTGTGTG
WI-10854a	102	C T ---	---	---	TTCCACAAAACCTTCCCTGGCCCGGGTGACTAAGATGAGAAAGTGGGAACTGGATAGTTTAAATAA ATGTTTATATTTTACTTTAAAGCGAAGTTGAAACA[CT/TTGAAGACGATAGTTAACGCTGTTGTAAGTT TATACGGTGTGCGAGGCAACAGGGAGAGGTACGGGAATAGTTTACTTCTGTTTTTATTCTTG TTTTAGACACAGGGTCTGCTGTGTG

WI-9826b	127 G A ---			---	AATTTATATGTGAAGGGTTAGCAAACTATGGCCACAGGCCCATTTAGCCATGCCTATTTTGTG TGCCTGATGGCTGTTTGGTGTTCACGAGTTGAGCCATTGTGACAGAGGCTGTTAT[G/A]GCCTT CAAAGCCAAAATAAAATTTACTCTCTGGCCTTGACGGGAAAGTTTGCTGATTCTAGATATTTAAA GGCAGAGAAGATCAGAAGTGTGAA
WI-9826	125 A T ---			---	AATTTATATGTGAAGGGTTAGCAAACTATGGCCACAGGCCCATTTAGCCATGCCTATTTTGTG TGCCTGATGGCTGTTTGGTGTTCACGAGTTGAGCCATTGTGACAGAGGCTGTTATTTGGCCTTC AAAGCCAAAATAAAATTTACTCTCTGGCCTTGACGGGAAAGTTTGCTGATTCTAGATATTTAAAG GCAGAGAAGATCAGAAGTGTGAA
WI-15986	60 T G GTGGTTTT	TTGTTTGTGT		TGACATTATAT AAACGTAAAA GAAAATGT	CGGACACGTGATATACAAATACAGATCGTAIGGGTTTGTGTGGGTTTTTTT[T/G]TTAC ATTTCTTTACGTTTATATAATGTCAGCATTTCAA
WI-8655	29 A G AG	AACTGCAAAAT AGGAAACCCAG		CCACCTGGGGC TCCC	TTCAGTAACTGCAATAGGAAACCAGAGIAGGGAGCCCCAGGTGGGACAAATCATGGCTACCCC TCCCAACAGAACAGGGGAGGAGTGGCCCTACACCCTTTAT
WI-8170b	259 G A ---			---	GGACTTCTCTCTGAGCAACAGGTACACTTTTTTCTCTAACATTGATCTATAACACACCAACCCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGTGTAAGGTTAG CATTTGGTGAGAGATTTACAAGGTTAAGATCATGTGTCATCAAAAGTGAATCCTATCAATCAGAA ATAAAGTAAAGGGCCCTCAATGAAATCTACGAAAAACATAACACAAGA
WI-8170a	204 T A ---			---	GCACCTCTCTCTGAGCAACAGGTACACTTTTTTCTCTAACATTGATCTATAACACACCAACCCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGTGTAAGGTTAG CATTTGGTGAGAGATTTACAAGGTTAAGATCATGTGTCATCAAAAGTGAATCCTATCAATCAGAA ATTA/AAAGGTAAAGGGCCCTCAATGAAATCTACGAAAAACATAACAC
WI-8172	136 C G GACA	CCTTTATTAA ATTGTTTTCTT		GAAGAGAAAT GTAATACCTGT AAAGGTAC	CAGGATTCCTTAAGTCATCTTCCAATACTCCAGGTCAATGGTGAAGAGTCACTGTTAAACACGAA ATCTAACCATTAACCAAGCTTTTAAATCCTTCGGTAACCTCCTTTATTAATAATGTTTTCTTGACAT A/C/GIAGTACCTTTACAGGTATTACATTTCTTCCACCGTTTACA
WI-8183	56 G A TGC	TGAAATAAAA ACAAATTTCTGT		TGTGTTGAAAT CAACCTGC	AGCAGGGTTTGAATTTGATCCCTTATTTTACATGAAATAAAACAATTTCTGTTC[G/A]GCAGGTT TGATTTCAACACAGTTGAATCTGTAAACCAAGCTCGTTTCTGATGCAGGACAAATATCCACAAT ATTTAAACTGCAAGCACCATG
WI-14149	83 C T ---			---	GCCTTATTGGGATTGCAAGGTTACAAGGTTAAAGACAAAACCAAGCATGGGATTTTGCCGGAAT ATTAGCGTTAAAGGAG[C/T]TGAGTTGAGTCAAAACACGGG
WI-8712	44 G A G	CACAGGGAAG AGGTAGTGA		CAGGAAGCCTG ACCATCTC	TCAACAATGACACTGTGTAAACAGCACAGGGAAGAGGTAGTGGAG[G/A]GAGATGGTCAGGCTTCTG TTCTTAACCCAGCAGAGCCCCAGCAACCTAGAGGGCCCTCACCTAGCCTCTTAAT

WI-8827	22 C T	TOCCCTGGGAG TCTACTAIGG	GGGATTAGGAT TTTAGTGTCA C	GGTGTCCCTGGGAGACTATGG[C/][A]GTGAACACTAAATCTAATCGCCATGCATTGGAATTATT CCGACTATTACTTCTTTAGTCTCTTATCCACCCAGCTTCT
WI-8833	51 A T	TCTTCCATGCC ATTCTCTG	CCTCACACATT ATAGGGCA	CTCCGGCCTCTTAAAGCTCTGTAGACTGTCTTCCATGCCATCTCTG[A/][T]GCCCTCTATAATGT GTGAGGGTATTACAATAGTCCCTATTCAAAGTCCCTTGTCATAAAAGGTCAGCTATGT
WI-8377	63 A G	---	---	ATTTTATGCCATGTTGGTAAAGTTCAATTTTCAGTACATGGTAAACCCAGGCCCTTCCC[A/G]T TATATCCAGGTATGCTACAAGTCTTTTAACTCTTATCAGAAATTATTTACTGTCTTCTTAGAGAG GCTACCAGGCTAAAATTCACCTTAGTTTGGTTGTCTAATGTCTCATTATTTATCCTGAAGCTCGTG
WI-8850	21 A G	GGGACTTAAC CTTTGGCCT	CAACAGCCA GGCAGG	GAGGGACTTAACCTTTGGCCT[A/G]CCTGCCTGGCTGTTGGCTCTCGCTTGGCTTGTGTTTCTT TCTCTTACTGGTCTTCTTCTTGGCTTGGCAGCCACCTATGCTGCTGT
WI-8853	79 C T	CCCGGGCATTG T AGGATA	AGTCTTCCCTGA GCCTTCCAT	ACTTTTCTTGGCTGAGCAACCTCATCTCTTACTGCTCTGGTTGATAACGCTGGTTAATCCCGGG CATTGAGGATA[C/][A]TGGAAAGGCTCAGGAAGACTTTCATTCTCAA
WI-8865b	52 A G	---	---	AGGGTGAAGTGAATCACAGGCACAGACTGAGGAAGACAGTATGGTGAACA[A/G]JACAACATGCT TCGGACTTACCAAAGGAGAGTCGAGCTTCCATATAA
WI-8865a	42 T C	CACAGACTGA GGAAGACAGT CA	GGTAAGTCCGA AGCATGTTG	AGGGTGAAGTGAATCACAGGCACAGACTGAGGAAGACAGTAT[C/][G]GTGCAACAACAACATGCT TCGGACTTACCAAAGGAGAGTCGAGCTTCCATATAA
WI-8895	32 A C	---	---	GTGCCAACAACCTGGACACCAACCAACAGAAT[C/][C]TCCCGTCTTTGAAATTTCCATTAAAGACA CAATGGGGTAATTATACAGGGATGCTCCAATCGCTCTTC
WI-8456	93 G C	---	---	CCTTTAAAGTCAAGTCAACTCGACTGTGGACTGATATATTGTGAAATATAATAAACTCTTTTCC AAGGCTCCCATGCTTGGATGTCACA[G/C]TTATGTCAAGTTAATAAACAATTTCTAAGTGTCTCACTC TCAACTTCTGTGTTATCTTGCCATGGTCCAGTAACAGTTCAACGCGCAGACCACAAGTTGTGTAGCAC TGGCATAGACGAGGGCTTCTCAAACCTCCGCTCTGCGTCTCAGTCAACCCAC
WI-8496b	157 A G	---	---	TTTCATCATCAAAAGTTTCTTCCATAGAAGATGGTAATGTTGTATCAGTGCATATTCTATGGAAA ATTCATATCTCAAGTAAGTACCTAGAAATCAGAGACAGCAGTATGTCAAGCTAGTATACAAGGTCA AAGACACAATGCTGCCAATGCA[A/G]TTAGTATATAGAAATAATACGCAGCTGTTAGAAAAAGTCT GTGGCCAAGTGGGATAAAACAGTAGCAGTGCAC
WI-8496	41 G A	---	---	TTTCATCATCAAAAGTTTCTTCCATAGAAGATGGTAATGTTGTATCAGTGCATATTCTATGG AAAAATTCATATCTCAAGTAAGTACCTAGAAATCAGAGACAGCAGTATGTCAAGCTAGTATACAAG GTCAAAGACACAATGCTGCCAATGCAATTTAGTATATAGAAATAATACGCAGCTGTTAGAAAAAGTC TGTGGCCAAGTGGGATAAAACAGTAGCAGTGCAC
WI-14153	28 A G	GTGCAGGAAG GCCAGC	AACGGCAGGA GGGGA	CTGCAGGTCTATGTGCAGGAAGGCCAG[C/][G]TCCCTCTCTGCCGTTGTACCCACATCCACAGAGCA GCOCTAGTGCAGGTGACGCAGTCCACCCACGGCACACGGGAACAGGACCCATGCTGC

WI-12108	40	C T A T A	TGAAAAGGG TTAAACTCAA ATTTC	TTGACCTGGTA TAATGAAAGT ATTTC	TCATGTATTACTTTCTGGAAAAGGGTTAAACTCAAATATC/TJGAAATACITTCATTATACCAGGT CAAGAAAAATGCCACAGCCAGAAAAATTTATTTAA
WI-5989	29	G A C A G G C A	CCACAAAGGT CACAGGCA	GGGTATAACAG AACCGTATGTA CG	CAGGCAACAGTCCACAAAGGTCACAGGCA/GJCGTACATACGGTTCTGTATACCCCATATATTAC CCCTTCATGTCTAAAGAAGACATTTCTTAGAGATTTTCATTTAGTGATCTTTAAAAAAAAT CTTGTGTTAACTTGCCTCCATCTTTCTTGGGTGAGGACACG
WI-12201	61	C T C T G C A T G	CCCACTGATCA CCTGCAATG	CCGACCACATA CCTGGC	ATAGTCTTTTAGCCTTTTCTCGAGTGTATATGTCCTCCAGCCACTGATCACCTGCATG/CJGGCA GGTATGTGGTGGGGGTGATGGAGTGGGTTTGCAGCCCTCCACTGCTCGATAAAGGC
WI-12018	31	A T T C T G A C T T	GGCAGCCAGC TCTGACTT	GGAGAGATGAC AGAAACAGAG AG	TTTTATCTGTGAGGCGCAGCTCTGACTT/JTCTCTGTCTGTCTCTCTCCCCACATACCA ACTTCTTACCATGATGATTATACCAATAATACAGTTCCTTATAGGGGCTCTGGAAAAATTAGAC AGTGAAGCATGTTGCAG
WI-14162	57	A G C T C	TGGCCTCGCTG CCTC	AGGGATCAA GAGAAAGGC	TTTTTCGTTTGTATATGATCCGAATGCTTGAGAAGAAACCCCTGGCCTCGCTGCCTC/A/GJGCCITTT CTCTTTGATCCCTGAGTTGCTGAGATTAAAGATGAGGTCCCAATGAGAGCTACCAAGATGTAGTCG AGCGG
WI-15407	92	A G T T	CATGCCCTTTA AGGATTAAGT	TCITTTCTCTTT TGGTAGTGTGG	AGCATGTAAGGAGCAGTTTTATTGATTGGTATATTCAGGTTTCTAACCCAGCTGAAAAATTCAAATA CATGCCCTTTAAGGATTAAGTTAA/JGCCACACTACCAAAAGAGAAAAAGATTTATATGATCACAT ATAAGCAATGGAATCAGCA
WI-12319	109	T C A A T T	GTTGAGTATT GTTCTGCTCAT	GGGAAGGTCTG GTACATATTGG	TCTGATGTCATTTATTGGCACAAAAATTTCTGTATACAACTGGTGTAGACATGGCTACACATTTA TACTTTGTGCATTTAGTTGAGTATTTGTTCTGCTCATAATTT/CJCCAATATGTACCAGACCTTCCC
WI-12326	25	G A C A	GACAGACTTC AAAAGCAAT	AGGTTTGAAAA TATGTATTAG TACTTTGT	CTGACAGACTTCAAAAGCAATTCAC/GJAJCTTCCAGAAATACAAAGTACTTAATACATATTTTCAAAC CTGTTTGCAATTCAAACAAAGTTAGCGTTTGTAAATCAAAATTTGATAACCCGACTAAAAAT
WI-12361	63	C T ...	...	...	TTAAATCCACACTGAAGATCTGGAGTATGGGGGGATATAGGAATTTTCAGCATATGTATTAT/CJ TGAACATAATTTACAAAAGTGGACAGTTGGAAGGTACTTATAGGTAGACCTGAGGGTCTGTTACC
WI-11305	87	C T A T C A C A C C A	CAGACACAGC TATCACACCA	GACCCCTCCGT GGGC	ATACTGGTTTAAATCCATGTCAAATGTAGTTTACAAAGGAAAGGACAAAGTACCTTTGTATAGAATAT ACAGACACAGCATCACACCA/CJTAGGGCCCAAGGGAGGGTGGGGAGACGACACTTTTCCCTGGG AAAGG
WI-11321	67	A G T T T T	GGAGGAAAA TCCAATAAAT	CATTGGGGAAT AGCTAAACCTT	ATTTTATATGAAGGTTTCTGGTGAATCTTTAAGCAGGGAGGAAAAATCCAATAATTTTTTAAJ A/GJAAGGTTTAGCTATCCCCAATGCTATTAAATACAAATGAGGTAGGACGTTAAGTCTTATCAGA CTGTGACTGGAGCCCCG
WI-11324	40	C G T G T G C C C C A	GGATAAATCA TGTGCCCCA	ATCAAGCTTTG GGGCTCT	AGCATACTGCATCTCCTTTATGGATAAATCATGTGCCCCA/CJGJAGAGCCCCAAAGCTTGATGACAT TCTGTAAAGTTACACAAATGTATCTGAAGAAGTTAICITGTTCTGCCC

WI-11352a	69	T C G	AGCAGCAGC ATAGTGGAAA	GACCTCTCGTA GGACACTTAGC	TGACACATGGTTCTGTTTCCAGAAGGAGAGAGAGATCATCTACATAAGCAGCAGCAGCATAGTGGAA AGTTCGCTAAGTGCTCTACGAGAGGTCAGATCATATCCATAGAAAACAGCTCTCTTTTACTTGCA CACITTA
WI-11371	84	C T G	CAGCTGGAG ATTCTGATTCA	GCCCCGCTGA GCAC	TTAGCCCATGCTGTCATTTGCAATCACCTGTGAAACCTATGAAAACCTATACCTGCCAGGCTCAGCTT GGAGATTCTGATTACAGTCGTGCTCAGGGGGGCTGGACATCCATGTTTGGAAAGAGTTGGCGGGGT GATTCGATCGGTATAT
WI-11385	75	T C G	ACAGAAGACT TTCATATTCTT	GATTCTATTCT AGTCATGGTCA TATTTT	CTTAAAGCATTATAGTTGGCTGATGGTGACACAGAGACTTTCATATCTTGTGTTTTTAAAGTC TCTTCAGTCAGGAAAAAGCTACAGATTTAAAAATATGACCATGACTAGATAAGATCAGC
WI-11388	88	C A A G T T C	TGTTGAAAT ACACGTAAC AAGTTC	TGCCTTGATC CAAGTTAAAAAT T	TCATGTGGCCAGTTAGCTCAGTTGGTTAGAGTGTGGAGCTCATAAAAAATTAAGAATGAATGTTTG AAATTACACGTAACCTAAGTTC[C/A]TATAAATTTTAACTTGGATACAAGGCATTTGTTATGCTAAT
WI-11392	55	T G A T A A T A C	GGTATGTGT CTTGAACITTA	GTACATTCAG TGTTTTGTAAA AAG	TTCATCATTCCTTAAATGGGAGGTTATGTGTTCTTGAACCTTAAATAAATAC[T/G]CTTTTACA AAACAGTGAATGTACTTTTCTGTGAGAAGGGGAACACTGAGTCTCCGCTCTAGATCCATTAACTGT CATACTCCTTCCCCAGA
WI-11396	52	A T T	TTTTGTTTTG AAATGGTGT	AGCTTATTTC ATATTCAACCA TC	AAAGAATAAGATGGCATTGTTCAGTTAATTTTGTGTTTTGAAATGGTGTGTTTATGATGGGTGAATA TGAAAAAAGCTTACCTCATCCACTCTAAAAGGTAGTTGGTGAATTTTGAACCGTTGTCAAT
WI-11441	100	C A C A G C	TCCCACCAAC CAGC	TGCCAGGGCT TATTTG	CTGTAGCTTTCCCAACTAAACCGTGAGTTCAGTATGTCTGGCAGCAGCTGTCTGTTCTTGGTG TATTCCTATTACTGAATCCCAACCAACAGC[C/A]CAATAAGGCCCTGGCACAAGTAAGCTCTCC ATTTTGTAGAATGAAT
WI-11466	26	C T T T A T T T T G C A	TGAGAAGCCA	GTTTATTGTTA TAAAAATGAC CTACAACIT	ACTTTGAGAAGCCATTTATTTTGCAG[C/T]CTTCAGTCCAAAAAAGTCAACATTTTCAGAAATTTTT TATATAAGTTGTAGTGATTTTATAACAATAAACTTTCTATTATCTATTATCTCTCACATACATTT CATGTATCCTG
WI-13364	35	A G ...	...	...	TTTTCTTTTGTGCTCTTTTTTTAGTAGAAGC[A/G]GGAACAGTTGTCAATACTACCTTCTGTTGG TCCCCTGTTAGACAACATACCTTTCTTTGAAATGTAAATGTCA
WI-11276	41	A G A C A G A C	GCAGCCAGG AGCAGAC	TGTACTGAGGA GCGGTG	AGGCAACACTGCTTTATTAGCCGGGAGCCAGGAGCAGAC[A/G]CACCCGGCTCCTCAGTACACATT CCCCACCCCTGCTCGGTGCTCCCACTCAGGGCTGGGCTGGAGGGGCGAGCTAGGCTGGAA
WI-12210	76	A G A	ACTGGGAAA CAACTATTGC	TGCTAGTTGC ATATGTTTTCC	ATTGGAAACAACCTTAATAATTTGCATCTCTACATATAGAAAAGCTGCTTTGAATAACTGGGAAAAACA CTATTGCAT[A/G]GGAAAAACATATGCAAACTAGCATCATTTGCTCTAGA
WI-14186b	88	A G ...	...	...	AATGGTCTGTTTTATTGAGAAGCTGTTGGTCATTGATGGAAAGACACATACGGGTACAAAAATTACA GGTGGTTAGTTCATTACATG[A/G]TACAAATCATTAGAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT

WI-14186a	52	C T A	GGTCATTGAT GGAAAGACAC	AACAAACCA CCTGTAATTT GTAAC	AATGGTCTGGTTTATTGAGAAGCTGTTGGTCATTTGATGGAAGACACATA[C/T]GGTACAAAATT ACAGGTGGTTTAGTTTCATTACATGATACAAATCATTAGAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT
WI-12234	66	A G GTGGGCTT	GAGAACACTT TCCATGTTTGA	GGACCTATCAG TCCATGTTTGA	ATTTTTTTGGCTATAGGTCAGTGGTCTTAAACTTGAGCTTGCAGAGAACACTTGTGGGCTT[A] GTTCAACATGAGCTGATAGTCCACCCAGATTCTAAGTGGTGGTGGG
WI-12345	37	C A AAAGAGAA	GTGGCAGAA TTCAGG	TTCAGAGGGG TTCAGG	GGAAACAGACCTGATCCACGTGGCAGGAAAGAGGA[C/A]CCTGAACCCCTCTGCAAGTATTCTCT TTCTTGACCAGCTGGGCTTGGCAGCTTTGTGAGATTGCAAAA
WI-13416	71	C A AAA	AAATTTTGG AAGTTTTTCAG	AGTGTATTAG TTCAATGAATA ATTTCAA	GAAAGGGCTGTAATTTTATTTCAAATTTTGGAGTTTTTCAAGAAAAATAAAATGACAAGAACAA CATA[C/A]AAATATTGAAATTTATTCATTGAACTATAACACTTAGCAGAGGAAGGACTTTTGAT
WI-12310	46	G A AAAAGC	TTATTCOCAAG TATAATTTTA	TGTTTAAATAT GTTTGGGTCT AAA	TTTGAAAGATGCTGAATTTATCCCAAGTATAATTTTAAAGCT[G/A]TTTAGGACCCCAACATA TTTAAACATCTCTTACACATACAGAAATTCAGTTTACAAATATCCAGAAGGCAATTTTCTTAAGCAG T
WI-12086	72	C T TGGATT	CCGGGAAAC TTCGATT	GGAGTCTGG GTCITGG	GAACCGAGCTTTATTGGAGCAAGAGTGTGGACACTGTTTACAACAAACGTTTCCGGGAAACCTTG GATTTC[C/A]CAGACCCGAGACTCTCCAAAGTTCTCACTGTTAGTAAGGTCAATTTGGGGGCAGA ACAGGAACATGCTTAGCT
WI-11549	102	T G TTTATG	GGCATAAAGT TCATAATATTTC	GGAAAGTCTGT ACAAATCCCC	ATGTCTTCACAGGTTGTAATTTTGAAGAGTTTGCTATCTAAATTTTCATAATTTATTTGGCATAAAGT TCATAATATCTTTTATGATCTTTTAAATATCTG[U/G]GGGATTGTACAGACTTTCTCTC
WI-11585	79	T C AAACAAA	TGGGTTTGCAA AAACAAA	CCATGCTTCAC TGATACTCC	TTAGAAAGGAAAGAAATAAACACCGTAAATGGGAAATCAGTTCAAGGTAAGGAAGCTGGGT TGCAAAAACAAAATTC[G]GGAAGTATCAGTGAAGCATGGCCTAGAAAGTCCCAAGAGCGGGTAGAGT TT
WI-11604	68	G C ---		---	TTAGTTGGTTCTGAAACCTTTATGCTGTTTATTTTAAACCAATAGGATGTTCCAGTTACCAGCATTT G/CJAGAACTAGGAGCTTTTCCATGAAATAATTAAGAGCTAAGGAATTCIGACGCTCACCATTCTTC TTTGTTACTCTGCAGTT
WI-11614c	108	C A ---		---	CAAAATCAAAAATTGAGGAGGCAAGAACAGAGTAATAATCCAGAACTCAGCTGCTTGAGGCAT GTTCCACCCCTGGACTTGCCAACTTCAGTGTGAAACTGCA[C/A]ATATTAAGTATTCGTGAGCTAC GGACTTCGT
WI-11614a	60	A G CAGCTGCTTG	CCAGAAGACT CAGCTGCTTG	AGGTGGAAC ATGCC	CAAAATCAAAAATTGAGGAGGCAAGAACAGAGTAATAATCCAGAACTCAGCTGCTTG[A/G]GG CATGTTCCACCCCTGGACTTGCCAACTTTCAGTGTGAAACTGCAACATATAAGTATTCGTGAGCTAC GGACTTCGT
WI-11626b	83	T C ---		---	TTGATTTACTAAGGCTTCCACTGGAACATGAAGGTAGGGATAAGTGTACAGGATAATATACTCAG ATATTTTAAATAAAATTCJTTACTTAATAATAAGAAATTAGCCATACCACATTTGTTCCATTGCTAC AAGAACAAATTGGCAATGA



WI-11626a	39	G A G	TCCACTGGAA CATGAAGGTA	GTGGTATGGCT AATTTCTTATT ATTAAGT	TTGATTTTACTAAGGTCTCCACTGGAACATGAAGGTAG[G/A]GATAAGTGTACAGGATAATATACT CAGATATTTTAAATAAATTAATTAATAAAGAAATTAGCCATACCACATTGTTCCATTGCTAC AAGAACAATGGCAATGA
WI-11627	23	T C	CCTTCCCTCC CATGCTCTC	CATTTGCAACC CATCTCAAG	ACCCCTTCTCCTCCATTGTCTCT[C/C]CTTGAGATGGGTGCAATGGGAAGTAAAGCAAAAAAGGG AGATGAGAAATACTGATGCCCTTTTGTCTGGCTTACTTCCATTGCGATGTCAAGTCCATCCATG
WI-11636	61	A G T C C T	GGACTTAAAA AGATCTGCTTA	AGAAACTTGCT AAATATTTTAT GTAACACT	TCAGAAATGTTGCAAGCAAAATACTATTGTAAAGGTGGACTTAAAAAGATCTGCTTATCCTT[A/G]TA TATCCACATAACTCTAGTGTACATAAAATATTTAGCAAGTTTCTGTGACAGGTGCTCAGTAAACAC TTTGACTCCCTTTTGGTA
WI-11537	119	C G T	ATTGCTCATCT TACTCTGACCA	GACCCAGCAA AAAGAATGAT T	GTACCATTTCTTATGGTGGCAATAAGCAAACTGTGAGTAAACGAGGGCAGCTGAATAAATTTACAG TATACAATATTAGAGAAATATTATGTTGCAATTGCTCATCTTACTCTGACCATT[C/G]ATAATCATTTCTT TTTGCTGGGTCCAGGAOC
WI-11654	37	G C T G	GCCAAAAGAC TATTCAGCAA	GGCTCTCCAG GACAGTTT	AGTAGAACATCAGTGCCTCCAAAAGACTATTAGCAACTGT[C/G]AAACTGTCTGGGAGGCCACTCCAG AGCTATTTCTAAGACTTTCTGTGGTGTTCATCTACTCAGAGTTCACACTCATATTTTCATATTTTT ATTTTGGGTGTTGGGT
WI-11656	28	G A A A	ATTGATTTTAG AAGGAACGTC	CAAGGCTTTGT CCTCAAGTAAA	ACCTGATTGATTTTAGAAGGAACTGCAA[G/A]CTTACTTGAGGACAAAAGCCTTGCCCTGCAGTTGTTT AAAATGCTCTGAAACAATCAGATCCCAGCCTGGAT
WI-11680	55	T C ...		---	ACAGATACTTTCCACGGCAACATTTCTGAAATGAAAGCTTTGATTCTCCCTTTT[C/J]TTCATAAA GGCTGGGAAGGTGGTTGGCCAGACCGTACATCTTTT
WI-11696	47	T C	TTATCACAGC AGGGGACAG	GGCATTAGAGA AGCCAACCTT	GTCCAAGAACAAGATACITTTGACATCTTTATCACAGCAGGGGACAGT[C/J]AAGGTTGGCTTCTCTA ATGCCCAACATCTTGTTTTCAGAACTCTTCCACTTCGCC
WI-11702	69	C T C A G C A G	GAATAATACT GAAATAACCA	AGAACAACTT AAGCAAATTTAT ACTGAAA	TTACATGTGGTCAATGGTGACATACITTTCAATAATTAATAATCGAATAATACTGAAATAACCCACAGC AG[C/T]TTTTCAGTATAATTTTGCTTAAGTTGTTCTAGAAAACACTGCTAATTTTGTCTGCAGA
WI-11706	60	C T T C T C T C T	TGGCTGGAATT TTCCTCTCT	ATCACCAAAG AACAAATCCA	TGCTGATTCATCGCTTCTACCATCTGGCTGGAATTTTCTCTCTGTACAATTTATTTGG[C/T]GGCTG GAATTTGTTCTTTGGGATTTGCCCCCTTGCTGCT
WI-11709	105	T A T T C A G T T T G C	AGAAGCTTGC TTCAGTTTGC	TCATTTCTTCT AATTTACGGG A	AATATCATCTCATATCAGGATGTTTATAAAAATGAGAGATTATGTCCTTTTGGCATACTTCATC TTCTTCAGGACACAGAGAGAGCTTGCTTCAGTTTGCTT[A/G]TCCCCGTAAAATTAGAAAGAAATGAAT GGCCAGATGGATGGAATA
WI-11710	103	C A C A G T C T T C A	GCACCTAGCCT CAGTCTTCA	GTGTGGAGGAG GGAGGAG	TTATTACCATCAACCTGTCCCCAGCTTTCCAGCACAACAGCCAGCCACACTCTAGACAGCCTTCAC TCCAGTCCATTCTGGCACCTAGCCTCAGTCTTCA[C/A]CTCCTCCCTCCTCCACACTCCTTC

WI-11715b	123 C T	AGGCTGGCTGC AGCTT	TCCCATCTCTG TGGCT	AGAATGGAGCTGTGGGAGGGACATGCACACAATGTAAACAGACAAAATGCATTACAACCTGTGG TGTAATGTGGCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTC/TJAGCCAC AGGATGGGACTGGGAAGA
WI-11715a	49 A C AAA	AACAATCCTT AAAACAACATA TCAACA	CATTACACCAC AGTTGTAATGC A	AGAATGGAGCTGTGGGAGGGACATGCACACAATGTAAACAGACAAAATGCATTACAACCTG TGGTGAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTCAGCCAC AGGATGGGACTGGGAAGA
WI-11727	43 G C	AACAATCCTT AAAACAACATA TCAACA	CCTGTGGTTTG TGTTGCAG	CTGGATTTCTATACCTAACAATCCTTAAACAACATAATCAACA[G/C]CTGCAACACAAAACACAGGC AAATGAAAACAGATGCCCCAGACAGACACCCACCACATGGCACACAC
WI-11728	16 C G ...	ATCTGTGGTTT TCGCCTG	---	TTTTATTATCAAACT[C/G]CAATTCATTTCCAAATGTAAAGTTATCATCAGCTCCCCATCCACTTT CTCCCATCTTCTATCTCTTTCCACCCCTACACTTTCTCTCCCTACAAACCCGGGTCCAAA
WI-11758	61 A G	GCCTCACAAA GTATTTCTAA AATATAA	TGAITGGCCCT GTGGTCTA	TTTTCTCTTTTATTAAAGTCGGCTACTACTAGAGGAGAACTCTGTGTTTTCGCCTG[G/A]GTAG ACCACAGGGCCAATCACCACAGCTTCTGTAGAGAACATGGAGAGTGCCAAAGATCACCATCA
WI-11295	37 A G	GCCTCACAAA GTATTTCTAA AATATAA	AAAAGTGTCTCA TCTGTGAACCTC T	COGGCTCACAAAAGTATTTTCTAAATATAATTTGCT[G]TAGAGTTACAGATGAGCACTTTTCA CATTAGTGATATGCAACAATACTACTATTGGCTCAGCAGGAACAGACTTTT
WI-11773	93 T C ...	GGCTCAGAGA GCAAGGGAA	---	AGCATGATATCTGCCTGGAGTTTCTGTGAGCTCAGCAACAGCAGAGTCAGAGATTAAGAATT ATTATTGCCTCTTTTTCCTCCCT[C/G]GTGATTGTTAATTAGGAGTCAAGGCCAAGTTATC
WI-11282	42 C G	GCCTCAGAGA GCAAGGGAA	AAACTCAGA CTGTAAATTTT GTGTG	CATGACAACCTCTTTATTTAATGGCTCAGAGAGCAAGGGAA[C/G]CACACAAAATTTACAGTCTGA GTTTTGCGCGCAGAGACCCCTCTCCACCTTTTCATGCTGTGTGTACACACACTGTCCAAAGCCTC AGA
WI-11790	28 A G	CCCAACTTACC AAACCTCTG	CGGTAGGCGAG GCTAAGC	TAATTCACCCCAACTTACCAACCTCTGT[G]GCTTAGCCTCGCCTACCGTACACATGCTCAGAGCAC TTACATTAACTACAAATGGGCAAAATCATCTAACACAAAAGC
WI-11879	61 C A	TCATCTAATCT GTGAGGTAATTT AGTATACA	GATAGTTGAAC CTCTTCACTTT ATAAAAA	TTTTAATTCCTCAAGCTTACAACCATCTTTTCATCTAATCTGTGAGGTATTTAGTATACAG[C/A]AGT GATTTCTCTCTTCTCTTTTATAAAGTGAAGAGGTTCAACTATCCAGACAGTCCCATCTA
WI-12469b	91 C T	GTITTTAATGT GGTATTAGAA AAGTTTAA	CAATTTTCAGA TTGTCTATAGC AAAC	TTTACTAATTTTCCATTTCTCCCTTTTATAGTTTAAATGTGTTATTAGAAAAGTTTAAATACAT ATGTGGCTTATATTCTATTTCTA[C/T]TGACAGCAGAGTCTTCAAAGTTTGTATAGACAATCTGA AAATGGGTCTGTAAC
WI-11906	52 A G	TGTTATAACAT CAAAGAAAGA GATCTGAA	TTAATTTCTGC AGTCCCTCA	ACATTTGAGTAGGAATGACTTTGTGTTATAACATCAAGAAAGAATCTGAAT[G]TGAGGGAACCTG CAGAAATTAACCTTCAGTCTAATTTCTCAGAAATGCCAGAGTAAGATGAACCCCTTTACAG

WI-11909	78 A	TTTGTTGGG TGGTCAAG	CCTCCTCTGAG ATTTTCTGAAT AG	GCAGTTCTCTGAAGACAAATGGATTGTGGAGCATACTGAAGACTATTCTCTAAATGGCTATTGTGTTG GGTGGTCAAG/GJCTATTAGAAATCTCAGAGGAGGACAAATGATAGTGCAGCTGCAGCCAGCTCG GACTGGCTTGAAGAGTC
WI-11806	60 T	CATGAAGAGT GGGCAGTCA	TCCTGTAAAGC CAATTTTATAT ACTAATAA	AAAAATACCATTTAGCATCAATTTGCCCAAGTTTGGCAGGCATGAAGAGTGGGCAGTTCA/T/GJTT TTATTAGTATATAAAATTTGGCTTTACAGGAAGCATTATGG
WI-11946	31 C A	---	---	CCCTAGTGAATACAACTTTGTCTCTGGAGAC/CJA/CAGAGTAGTCTAAGAAAACTTCTAGGCTGAG CTCTCTGGGAATCTAAGATAAAGAACTGAGATCCTGGGAAGAGGGAA
WI-11965	65 T	TGAAGATCAG ATCTCTGGTT GATT	CAGCTGTGGTG AATGTTGAT	ACAAAAATTCACAAAGTACAACTGCTTATTTTCTGCTTGAAGATCAGATCTCTGGTTTATTTAA/T/ GJATCAACATTTCCACAGCTGAAGGAAATTAACCTGAACCT
WI-11027	90 T A	TGCCCTACTAC GCTTTTAAAA A	TGAGGAAATGT GTTACAGTATT TTTATT	ACCTATTTTGAAGTGCAGAAAGGGCAGGACAAAAACAATCACTTCATAGATTTTCTGGGAAATAT TGCCCTACTACGCTTTTAAAAAA/T/AJAATAAAAAATCTGTAAACATTTCTCTATTTCTACGA ATACTTCTTTTGTATTTGCAATTTCTATGGCATACACAGAGGCACCTCTCAATGCCCTG
WI-11049	95 C T	---	---	TTCTGCTGAAGATCAGAAAAACAATTTCAACCTCTGTGGTTCAAAATAATTTAAGGATCTTGACCTTT GTGTTTATTTCTGTTTCACTAAGGAC/TJAGACTTCAGAGGCATAGCTTCCCTTGTAACGTTTTT AAACATCTTTTCAATTTGTAGGAAGGAACATTTCAAAAGCCCAA
WI-15488	69 C T AC	AAAAGGACAG CCAGATATCA AC	TTTCCATCTTA TTTCATTTCTG TAAC	CAACATTTATCAACATGGTAGGAAAAAGTTCTCACTCTGCACATATAAAAAAGGACAGCCAGATATCA AC/C/TJGTTACAGAAATGAATAAGATGGAAAAATTTTAAACAAATTG
WI-13654	49 A G	AACAGTTAAT GAAACACATC CGT	GGCTGGTGAAA TGATGTCAT	TGCTCAATTTAATGTGATAATCTCCAACAGTTAATGAACACATCCGTA/GJGTATGACATCATTT CACCAGCCAGCTACTTTCATGTGGCAGAAAGGTAACTTTTCCCATTTTACAGACAAAACCCAGT
WI-11070b	135 C T	---	---	ATGAGACCTGCTTTGAACGTTAAACGTTTGGAAATAATGGAAGAGGAGCTAGGACAATTTCTTGCTT TCAAGTAAATTTGTGACTGAGCAGAAAAATCAGCCAGCTATCTT/GTJGGTGCAGAGAGGTACTCCAA C/C/TJGTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAAACAGAGGGAA
WI-11070a	110 G T	CAGAAAAATCA GCCAGCTATCT	TTGGAGTACCT CTCTGCACC	ATGAGACCTGCTTTGAACGTTAAACGTTTGGAAATAATGGAAGAGGAGCTAGGACAATTTCTTGCTT TCAAGTAAATTTGTGACTGAGCAGAAAAATCAGCCAGCTATCTT/GTJGGTGCAGAGAGGTACTCCAA GTACCGTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAAACAGAGGGAA
WI-12020	121 T C	---	---	AATCTTTTATATTTCCAGCTTTGAGACAGTATTTTGGGGCTGATGTTACCTCTAGCGGGGAAACC AGAGCCAGCTATTAAAGCAGCCAGAAAGCTACAGTAATTGAATACATGACCA/TT/CJCTCTTTTAGC ACGTTCTTTGTTCTCTC

WI-11076b	142 G A ---			---	CATGGTTCTGCCAGCTTACAGGAAGCATGGTGTGGCATCGGCTTATCTTCTGGGAGGCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGGAGCAGGCATGTGCATACCCAGAGCAGGAGAGAG AAAGAGAG[G/A]AAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTCAT G
WI-11076a	106 T C AGGCA	AAGGGGGAGC	TCCTGCTCTGG GTATGTGAC	GGTTATTCAAA AATTAGTATGG GACA	CATGGTTCTGCCAGCTTACAGGAAGCATGGTGTGGCATCGGCTTATCTTCTGGGAGGCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGGAGCAGGCATGTGCATACCCAGAGCAGGAGAGA GAGAAAGAGAGGAAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTCAT G
WI-14263	49 T C GGCATATTCA	CGCAGAAAA GGCATATTCA			ACCTTTAAAGTTTCTCCCACTACTCCCGCAGAAAAAGGCATATTCAAT[C/T]GTCCCATACTAATT TTTGAATAACCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTTCTTTTGGCTACAAGTAACA AATTATGCTGAAATTAGGAAGGGAGCAT[C/T]GAAATGGGAAGGGGAGGTTAGAGAAGACAGAG ATTTAAAGAAGCAAGTACCATTTTCCAAAGTATAAACTCGTA
WI-14267	28 T C ---	CTTTTCATTT TGCTTTTAA		---	GATTTGTTTATTTCATCTCGCTTTTCATTTTGTCTTTTAAATAGAACA[G/A]CTTTGATTTTAGTA TATGACATCATCATGAAATTTTCTCTTACTTTGTATTTAGGCTCCACCTCAGTAGTTTGACAA AGGTAGAATGAGTTCA
WI-13892	50 G A TAGAAC	CATGAGAGGA TTCCCTCTCTC	AAAAGCTTCTT TCCCTTGGGA	ATCAAAAG	ACCTCTTCTGATGACACTGTACCTGTAAAGGGTCTAGAGAGAAAGAGTAGTAGCTCTACTTTTGC TACAAATCAGGATGCAGGGCATGAGAGGATTCCCTCTCTC[G/C]TCCAAAGGAAAGAGCTTTTGGC AATAAATGGAAGAAGGAGTGAACAAAGTAATGAACAAACAGACCCAGATCAGAGGAAGAGATG GCTTTCTTGTTAATTTCTGGAGCA[G/C]ATTCAAGCAGCAAAATATTTACTGAACACTTGCTATGCTG G
WI-13951b	88 G C ---	GGAGTGAACA AAGTAATGAA		---	AATAAATGGAAGAAGGAGTGAACAAAGTAATGAACAAA[C/T]AGACCCCGAGATCAGAGGAAGAG ATGGCTTTCTTGTTAATTCTGGAGCAGATTCAAGCAGCAAAATATTACTGAACACTTGCTATGCTG G
WI-13951a	39 C T CAAAA	AAAAAGGCTC TTGCCAT	GGAGGGAGAG ACGGGAATA	TTCCTCTGATC TGGGGTCT	GAGACCAAAAAGGCTCTTGCCCAT[G/A]ATTCCCGTCTCTCCCTCCTGACTGACCCAGTGTCTT ACAATGAACATCCCTCAGCCCCCATGGCATGGTGATCCCTTCTCTTGGGATCTGTGAATATAACCA ACTGCTTGTCAATGGC
WI-13264	25 G A TTGCCAT	AGCAAAAGGA AGTTAAATAC	CATGAAAGGA CAAATTTGCAT C		TTATTTGTCATTAGCAAAAGGAGTTAAATACTGATAG[A/C]GATGCAAAATTTGCTCTTCATGCA TTTGTGGAGCAAAAGTACTAACTTGTTCACTGTCATTTCCCTCACAAGGAGTTGAGCCCTAGATGAC
WI-13960	39 A C TGATAGA	ATCTTATAACC AAGAAGCCTT			AACCTTTATTGTTTAGCTAGCCCCAGTGACTTTTATGCATCTTATAACCAAGAAGCCTTCAG[C/T]AG AGCAAGTCTGAGCCAGAGGTTTATACACTTTTGCTCAGGGTCCACAGGAACCCAGGCTTGGCT
WI-15843	62 C T CAG				

WI-13983	52	G A	TCTCCCACT CCTTAAACCT	CAATACCTCT TAGCCAGTGG	TTGTGATCTGATTTCCGAAACATAGAAATCTCTCTCCCACTCCTTAAACCTTGA/JCCACTGGGCTAA GAGAGTATTGTACAGAAATATGCACTCACTGACTAACAGAAATTAGAACATCCAGGCACCTCACTGAGA
WI-13850	51	A G T T	AATCTCAGGG TCACAGCTTTA	TGTTCCCTGAC AATGTTTGTAA	CATGAATCTCAGGGTCACAGCTTTATTTATAGATTTTAAACACAGCCATG/JTTTACAAAACATTGT CAGGGAACATTTACAGAAATAAATAAGATGGACTTGCAGGTGTAAAAGATTACACTTCA
WI-15295	27	G C A	TGTCAGTTGA ATGTATTCCTG	TGAATAGTTGG CAAAGGAAAA	AGATGTCAGTTTGAATGTATTCCTGATG/CJTITTCCTTTGCCAACTATTCAATTATGACCATCTTTTC CTCGTCAAGTGACCTGCCATCATCACAAGAAAAAGGCCCGAAAAATATGAGTGAGACTCA
WI-14284	55	C T	---	---	ATTTCAAAACAATCCAGAACAGGTTCTCACACTTTGAGCCCTTTAGTGCAAAAACA/CJTJATGCCAT GCGGGAATAAAATGCTTATCCAGTGGAGCGCTCCCTGATGCATTGA
WI-14288	85	G C	CCGCTGCTATT CCCAGAT	GGTCTCTTCC ACCAATCTT	ATGACCAGACCAGAACGCCCTGTTCTATATGAAGACAAACAGGTGCCCATACTTTGGGTGGAGGGATA CCGCTGCTATTCCTCAGATG/CJJAAGATTGGTGAAGGAGACCATTGACAGATGACAAACGG
WI-13522	33	C T	TGATGTAGTTA CCCCACTAAT	CATAATATTG AAGTCAGTGGT	TTTATTTGATGTAGTTACCCCACTAATACAAC/CJTJGAGAACCACTGACTTCAAATATTATGAGAG AAATTAATCTCCAGGGAATTTTGCAGAGAAGATAATA
WI-13529	42	T C	CACAAACATT TATTGAACAG	TCATACACTT CTCACTCTCT	AAATATGATTCCTATCCACAACATTTATTGAACAGTTACCA/CJJAAGCAAGAGAGTGAGAAGTGT ATAGAGGTGATTTAAGAGTGGTCCCTGCTCAGGGGTTTATAGTCTAACAGGGGAACAACCTCTC A
WI-13859	84	G A	---	---	TTATTTGTCAGAAATTTCCAGAAATCAGAGTCTCTACTGGGCAAGTAGAAAAATAGAAAAAGTTTACTAC TTTGAAAAAGGAAACTATG/AJACAAACAAGTATATATTCAGGAAAGGGACTCCTAGAACTTGAGCA ACA
WI-13536	29	T C	---	---	TGAAAGGATACAGAAAAAACTCAGCGAAGT/CJGAAAAAGTGGATAGCGTGGAGTAGAGGAGAAAT TAAGCACCAGCTCCAGTTGCTCTCTCCAGTGCCATTACATGGAGTACACTTAATTTTCTCAGCA
WI-13373	52	G A	---	---	TTTATTGTTGGTAGAAAAACAGGCTCTTTAACACTGAATAAACATCTCACG/AJAACCTGTCGCTC CTAGATTACAAAAAGTCAAAACCAATTTCCCTTTGACCGCGGCCCTTGAATCTGACATTCAAGTCAC CGTAATAGAACCAAGAGCT
WI-13477b	61	A G	---	---	TTGGTTTTTAATACCTCTTGTGGATAAAAGGAG/CJG/CATTGTTTTTTCATTAGCTTGTCTTCAAA/A/GJGAC AGAGAAATAAGATAAATTACCTTAAAGAAATTAATAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT
WI-13477a	32	A G AAG	TTAATACCTCT TGTTGGATAA	GAAGACAAGC TAATGAAAAA CAATG	TTGGTTTTTAATACCTCTTGTGGATAAAAGGAG/CJG/CATTGTTTTTTCATTAGCTTGTCTTCAAAAGAC AGAGAAATAAGATAAATTACCTTAAAGAAATTAATAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT

WI-14297	86 A T G	AATGTTGGGT ACTTTTCCAA	TGTGCACATTC AGAAACATTTT	CTGACTTTATTTAGCATGCAATGCAATTTATCTGGCAATAAAATTAATATGTGCAGTTATAAAAAAT GTTGGGTACTTTTCCAAAGATJAAATGTTTCTGAATGTGCACACTAGAATATATGCAGAAATCCTTTT AAACAGTCGACT
WI-12229	89 T G AAA	CATGTGCACA AAAAAGAGTAA	ACATGTGAATT GTCCCAAAAA	TCCATGTAAATATTCTCAACAGAGAACACTATCTTTAAATGAAGGATTTACCATTAAGAAAAATCAACA TGTGCACAAAAAGAGTAAAAATJGACCAAAAATTAAGATTTTTTGGGACAAATTCACATGTTT AAAAAT
WI-13582	43 C A	TGCAATCTAG AGACTGGGA	TCTGCGCAGTT AGATTCCA	AAGGCTGCCCCCTACTGGACCAATGCAATCTAGAGACTGGGA[C]ATGGAAATCTAACTGCGCAGAG AAATCAAGAGCCGATGGTGAATCTGGGGCAGCTTCAAAATTTCTGCCTCCTAAAAACATTTTCAC CCAATTTTTCATTATTGCC
WI-13857	28 A G ---		---	TCTGAGTTGATAAAATGCTTTTCTGAAC[A/G]TACATTTTAGGTATCTGGCACAAATTAACCAAATGT CTGCCCATTTTGTGTAGCTTTTCATACAGTACAGATTTTCATTGATGTCGCTCCACATCTG
WI-15809	77 T G	TGGTTTCTGT TGTAATGCC	TAAGGTAGCTA ATTCAATGTTT GTAA	GTTTAAAGTTGCAGAGATGTGAATGGTTTACAAATCTGAAGCTGAAGTTCAATCTTTGGTTTCTGTT GTAATGCCJTGJTTACAAACATTGAATTAGCTACCTTAAGTATTGAAGAGCTTCCATT
WI-15892	123 A T ---		---	TAAATCAGTCTGTGTCAAGAAGAAACAGGACTTGATCAAGCTCCAGCCCTCACCACCTATATCAGCA TAGCAATTTTAAAGGATCAGAGCTTTGTTTACATTTGCTCTAAACCAAGAGAGGAAJATJGGAATCA ACTCCACAGATCAACATGT
WI-15801b	81 T G AA	CATACTCCACT CTAGCTGCAGT	AGAAGAGTGG ATGGGATGC	TCITTTATTTCCAAAGATGGGAAGCGCATTTTCATTGGCTTGAATGAGAAAGCTTCTACTCCACTCTA GCTGCAGTAAATACJTGJGCATCCCATCCACTCTCTCTCTCTTTTGTACTGAAACTCTTCAAAGAACT GCTGAATGTCCTCTCTC
WI-15801a	24 G A	TTTATTCCAAG AATGGGAAGC	TCATTCAAGCC AATGAAAAATG	TCITTTATTTCCAAAGATGGGAAGCG[A/C]CATTTTTCATTGGCTTGAATGAGAAAGCTTCTACTCCACT GCTCGTAATGAGACAGAACGCTACAATCTGTTCAACACTGGCTGGACACTGCAGTGAJTCJAGGG GCAGGTGTGGGGCAGGTGGGGCTCTGAGCCGAGGACAATGTCCATGGCAGAGCTTCCAGAA
WI-13763	59 T C	GGCTGGACACT GCAGTGAT	CCCACACCTGC CCCT	TTTTTTTTTGGTGAGTGTGCTTCAATAAAGAGCAGAAAGAAACCTT[A]JAGACAAAAAGATGTT CTTACACACTGAGCTTTACACAGTCAACCAACATTGATATTTGCTTTTCCCGAGGGCAAAAAAGA GAGCTTCCCAGAAACCTC
WI-13578	48 T A ACC	TCAATAAAGA GCAGAAAGAA	CAGTGTGTAAG AACATCTTTT GTC	TCCAAGGAAAAAGAAAGAAACCAATCAGTGAGAAAACTCAAGAAATGGATGGCTGAGGGAG[G/A] GAACAGAGGAAGCGCACTGGGGCTGGGACTGAATATGGACAGTGGATGGTAGGGTCTCTCACTCTCTT GAGTCCCT
WI-13789	62 G A	TGATGGCTG AGGGAG	CAGTGGCTTC CTCTGTTT	AATAACAAGTTTAAAGTCGAGCTGCAATGTTGGCAATGCAGGTTTTTAAACAGATCACAAAAAGCJ G[A]JTGACAAAAAGTACTGGCGCAAGGACAAAAATATGCTAAGAAATTAGGCCAAACAGCTGC
WI-13594	66 G A AGC	TTTTTAACACA GATCACAAA	CCTTTGGCCA GTACTTTT	

WI-15625	40 C T ---	---	GTCTCCCCACCTACTCCCGCAGAAAAAGGCATATTCAA[C/T]TGCCCATACTAATTTTGAATAA CCTAACTCTOOCCTTTGTTTCTACTAAGAGAGGTTTCTTTTGGCTACAAGTAACA
WI-13367	84 C G A	TOCCACCCCA COCT	GTCTCAGTTTCTGTAGGCTGTAATTTTTCAGTTTAAACAAGTTTCTTATGTGATTTGTGGCCACACT GAAGACTCACCAGAA[C/G]AGGGTGGGTGGGAATACTTAATCAATAATTTGTGGAATTTACCCGAT GAAATCCAGTTATTCCT
WI-13600	26 G T AAGCATCCAT	CATATTGAAAA TTGTTACTAGA TGATGG	CTCAGTTTAAATGAGCCAGCATCCAT[G/T]CCATCATCTAGTAACAATTTTCAATATGCACATTATAT TATACTGGAACAAGAAATACGGATTGTAGGGAAGAGCATAGAGGACCACCATCAGCAACCCCTCT TGATTCCTTCTCTACCC
WI-13602	89 G T GACAACACA	GCATACCTCAT GACAATATTTA ATATTAAT	GATAGGAAAAAGAAATGAAGTCAATAGTCTTTTAGCAAGCCAACTAGCTCAAGGAATAGACAGCCC CTTTCATTTCTGGAGACAACACA[G/T]AAATCTATTAAATATTGTCATGAGGTATGCACCT GCOCA
WI-13650	76 A T TTTAAAC	CAGGCTAGGAT ATGAAGAGTA GTTTT	GCATTAAACATTTAAAAATCTGAGGGATATTGATGAGAACTATGATGAAAGATTTCACAATATTTCAC TTTTAAAC[C/A/T]TAAAAAACTACTCTTCATATCCTAGCCCTGATGACTTAAAAAGTTACCGG
WI-14319	83 C T A	CCAAATCATCT ATATTGTTGCA TG	TGTTTTGATTGAAGAAACATCTCTAAAAATACCATCTGAGTGCAGAGATAAAAAAGGAAATAGCAATT CAAGGCACAAAGCTAAG[C/T]ACATGCAACAATATAGATGATTTGGGGTGGGACAGTACAGAAATT
WI-13528	80 A G AAAA	CATGATACCAC AGTTTCTCTG AA	ATTGGATACATGCTTTTAAAAATGGTAGCTTTTAACTGTAACTAATACATTTTGCAATTTTCTTAAAA AAAGAAAGACATTT[A/G]TTCAGAGAAAACTGGTATCATCGAGGAAAGCAGAAAAAATTT
WI-13909c	93 A T ---	---	ACTTAACTGGCTTATCTTCACGGTAATCTATCTGTATTTCCAGTGAAGTTTCATCTTCTCACACT CTCTTCAAACCTCGAATATCTTTTTC[A/T]GAGATGCTAGTACCCACTGCAACATCTCTCAA
WI-13909b	80 G A C	GCAGTGGGTAC TAGCTAGACAT CTC	ACTTAACTGGCTTATCTTCACGGTAATCTATCTGTATTTCCAGTGAAGTTTCATCTTCTCACACT CTCTTCAAACCT[C/G/A]AATATCTTTTTCAGAGATGCTAGTAGTACCCACTGCAACATCTCTCAA
WI-14323b	86 C A ---	---	TTTTTATTGAATTCCAAATGTAGCAAAATCATTTAAACAATTTATAAAGGGACAGAAAAATTAAG AATCAAAACATCATTTCTGGAC[C/A]ATGGGAACCTTTGAAAAGGCATGGCAGTGGAGACCAGTAACCTA
WI-14323a	78 T C ACATCA	GCCTTTCAAG GTTCCCAT	TTTTTATTGAATTCCAAATGTAGCAAAATCATTTAAACAATTTATAAAGGGACAGAAAAATTAAG AATCAAAACATCAT[C/T]CTGGACCATGGGAACCTTTGAAAAGGCATGGCAGTGGAGACCAGTAACCTA
WI-15389b	104 G A AAA	GATGAGGTGAT TCCACACTT	AAAAATTGACAAATCAACTAGCTTGTCTTTTGTGCTTTGGGAAGACTACCATTTTCAAAATTTATTATGT AATACACTCATCCAGATAATGAAACATCTGCGAAAAA[G/A]AAGTGTGGGAATCACCTCATCTGTGC

WI-15389a	33 G A TC	AATCAACTAG CTTGCTTTTGG	TTTGAATAATG GTAGCTTCCA AA	AAAAATGACAAATCAACTAGCTTGCTTTTGTGTCG/AJTTTGGAAAGACTACCAATTATTCAAATTTATT ATGTAATACACTCATCCAGATAATGAACATCTCGAAAGAAAGTGTGGAAATCAACCTCATCTGTGC
WI-15747	88 T C AGTGTT	TGCTTCATTT AAACTAATTT	CATAATTCACC AAAGTTTCATA TAATTT	TGTAATCTGCTTACAGTCTTTGCAAAGACAGACATATGTTTTGCATAAAGATATAAATTGCTTCAT TTTAAACTAATTTAGTGTTTTC/JTTTAAATATATGAACCTTTTGGTGAATTTGAACGTGTACCAAAC C
WI-13752b	117 C T ---		---	AAGAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTTCGTAAAGTCTGGATATACTTGGCTTGCAC/CJGGACACCTTTTACG GAGGGATCCGGACAACT
WI-13752a	106 T C AGTGCTGA	CCCTCTCGTTA AGTGCTGA	CCCTCCGTAA AGGTGTC	AAGAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTTCGTAAAGTCTGGATATACTTC/JGGCTTGCACCGGACACCTTTTACG GAGGGATCCGGACAACT
WI-14339	102 T G TTAC	CCCAATCAA CAGTACATGA	TCCAGATTTCT GGAAACCG	AATCATTTAATGAATGTTCCAAACACACACCCTTCACTGGCTACAGGTAAATTTCACTGGGATGGAAG CAGATGAACCAACCAATCAACACAGTACATGATTAC/TJGGGTTCCAGAAATCTGGATAC
WI-13744	115 C T AAAACTGAA	TGGTGCTGAAC GATAAGCACA	AATCAGGAAA GATAAGCACA GC	TGGATGATGGATGAGGCCACCTGTGTTCAACAAAACACAGTAAATGGAACTTCATGCAGCTTTAGAT TTCCCTTGCCAGCTAGGAGCTTGTTGATGGTCTGAACAAAACCTGAA/CJTGCTGTGCTTATCTTTC CTGATTCT
WI-14061	68 C T ---		---	CCCTTGACTATATTGTTTTTCCAAAATAGGACTATGTGTAGAAAGAGAGCCCCGTACATACCTTAT C/JAACCAATTCATCCACCATTGTGAAAATCTCATCTTCTGGGCTGGATACCTCAAAAACAGAT
WI-15719	69 A C CATTGAGC	ACCTTTTCATC CATTGAGC	TGACTTGGC AAGAGTTTTAA ATT	TTACAGTTGGATTAACTACCACTACCACTGAATATATACTGAATTAACCTTCAACCCCTTTCATCCATTGAG C/A/CJAATTTAAAACCTCTTGCCAAGTATCATGAACCTACGAAGAGGAGATAAGAGATCTGATC
WI-13810	106 T C AACTT	CTCTAAATCG ATACATCCAA	GAACTGATGCT TGCTGCTAACT	TAATCCATCAATCTAAAATCACACATACATAGATCAAAACAGAAGTACCACAGTATGCTTTATTTTGCA GGTATTAATTGGTTCTCTAAATCGATACATCCAAAACCTTTC/JAGTTAGCAGCAAGCATCAGTTCTTC
WI-15736a	27 G T CACA	ATTTTATTCAC ATTAAACTTG	GTCTTTTGATA TGTGGCTTAGT TTT	GGATTTTATTCACATTAACTTGACACAG/JTTJAGCAAAAAAATCAAAAACATAAAAATAAGCCACA TATCAAGAACAATATACAATAGAGATTGAAATTTCTCAATAGCATTTGGAAGGTATTTCCATAAATA
WI-13785d	72 G A ---		---	TCAAACTGCACACTATAAAAGTGTCTTTAAAATGCAGCAGCAGGAGATGTGAAGACACAAATGAAC AAGTGC/JATTAGTGACACATAGCTGTCAACACACAGTG
WI-13785c	56 A C ---		---	TCAAACTGCACACTATAAAAGTGTCTTTAAAATGCAGCAGCAGGAGATGTGAAGAC/JC/JCAAATG AACAAAGTCGTAGTGACACATAGCTGTCAACACACAGTG



WI-13785b	40	C G ---	---	TGTTGTGACAG CTATGTGTAC T	TCAAACTGCACACTATAAAAGTGCCTTTAAATGCAGCAG[C/G]AGGAGATGTGAAGACACAAATG AACAAAGTCGTAGTGACACATAGCTGTCAACAACACAGTG
WI-13785a	27	T C TGCTT	---	AAACTGCAC ACTATAAAG	TCAAACTGCACACTATAAAAGTGCCTT[C/J]AAATGCAGCAGCAGGAGATGTGAAGACACAAATG AACAAAGTCGTAGTGACACATAGCTGTCAACAACACAGTG
WI-13793	88	C G ATAGG	GGGCGAGGGA TTTGTTACT	GGATTTTACAT TCAGCCTAGAT	AGAAACCAAGTATATCATAGGCAATAAAATAGTTTTTACCCCAATTGATACAACATAAGGGATTT TACATTGAGCCTAGATATAGG[C/G]AGTAACAAATCCTCTGCCATAAATCTATGACTTG
WI-13794	52	A G TTCTTTCTC	AGAATGGGCTC TTAACCTTGA	TTCTCAACCCT TTCTTTCTC	TAGTCTCTACAAATTCCTTCAATCCATTTCTTCTCACCCCTTTCTTCTC[C/G]TACAAGGTTAAGA GCCCAATTCCTTCAACAACAAACAAACATAGAGCAAT
WI-15729	35	A G GTGTAGACTGC	CTCAGCTTCTT TCTAAAGTGCC	CTTTGAACCAT GTGTAGACTGC	TCATTTAAGTGCACCTTTGAACCATGTGTAGACTGC[C/J]GGCAGCTTTAGAAAGAGCTGAGACTGAA AAGTCTGTCTGACTTCCAAAGGAAGGTAAAGTCCCTGTTTGCAGCCCGGGCCTGCTCATTTGTTA
WI-13424	66	G A C	TGAGGTTTTTC ACCTATTCTT	TGAGGTTTTTC ACCTATTCTT	GTCCCTTGCACAAAGTCTCCCAACTGGTTGGAGTTTCCCTTCTGAGGTTTTTACCCCTATTTCTT[C/G] JTAGACCTGGGGAGAAACACATGTGTAAAGTGCTCAGGACATGAGGCAGGCCGTTTCAACAAGAT GCTGGCTAAGCGGCTTC
WI-14065	29	T C AAT	TCTTATAAAA GGTCAGAGGC	TCTTATAAAA GGTCAGAGGC	AACTGTCTTATAAAAGGTGAGGCAATTT[C/J]GAGATCCCAGATTCAGCTTGTCTCATAAAAAGAT TCAACTTCAAGTAGCACAATTTCTGTCTGCTTTTAACTCCTGAACATCTTGAAGCACGAA
WI-13446	22	G C TCACTCATCA	AAGGGAATCA AAATCAGAAG	AAGGGAATCA AAATCAGAAG	TGCCATGTTCTTCACTCATCA[C/G]CCTTCTGATTTTGATTCCTTCTGCTCTGTAATTTTTTCTTC TTCCCTTTTAGGGCCTAGTCTGTTAGAAATTCCTGGTTTTTGAGAGTAGTGAGCCCTTTTACTTTTTT CTGACTGCCTAAT
WI-13725	56	A C TGGGTGOC	GCCATGTTCTT TGAGCACATA	GCCATGTTCTT TGAGCACATA	TCACACAAAGGCAATTTGAAATGTCACCTTACACATGGTGAGCACATATGGGTGCC[C/J]GCCCGAG ACAGCAGGATAAGTTTACAAACCTTGACCAGGCAGGTTAGAAGCAAGGCATGGTTTCAAGATG
WI-15702d	107	T C ---	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAACCCTGTAAACATACTAA[C/J]GGGTTCTTTGAACAAATAGTTT TGA
WI-15702c	101	T C ---	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAAC[C/J]CTGTAAACAATACTAATGGGTTCTTTGAACAAATAGTTT TGA
WI-15702b	90	C T ---	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAAC[C/J]CTGTAAACAATACTAATGGGTTCTTTGAACAAATAGTTT TGA

WI-15702a	48 G C A A G	A C A A A A T A A A G G C T T T C A A	C C T C A C C C C T T T A C C C C	C A A T G T T T A T G A A G A G A C T C C G A C A A A A T A A A G G C T T T C A A A A G [G/C] G G G T A A A G G G T G A G G A A G C A T G T G A G A A A C T G T A C C C T G T A A C A A T A C T A A T G G G T T C T T T G A A C A A A T A G T T T T G A
WI-13831b	113 T C ---		---	T T T T T T T T A T G A T G C A C T G T T A C A T G T T A T T A G C G A A G G T G A C T T G G A A A G G A G A T T C A C A T A C T T C C A C T G T A C T C C G G G T A A G T T T C C T C T C T G T A G A T [G/C] G T C T C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
WI-13831a	56 G C ---		---	T T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A G C G A A G G T G A C T T G G A A A A [G/C] G A G A T T C A C A T A C T C C A C T G T A T C C T C C G G T A A G T T T C C T C T C T T G T A G A T G T C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
WI-13806	62 G A ---		---	T G A T T G A G C T T A G A A G G A A G T C A T G T T G A A A T C A G A G A G A G C C A A A A C T A G G C C T C A G G T [G/A] C C C A T T A A G C A T G C T G T G A A T G C A A G G A A A A G C T T A A A A A A T T T T T A A G G G T G A C T C C A G T A A A C A T
WI-14372	86 A G ---		---	C A C A T T T C A G C A A C A A A T C G A G G T G C A A C A G G G T T A T T T C A C A T T A A T A T A T A A C T G G A T T T T T T G C A A A T A A A T A G G G A [A/G] T T C T C T T T A A A T A A C C A T C T C C T C A C T T C A T G C C A G T A G G C T G T T T T G A G G C C T G A G G A C C C A A C A C A T G A C A C G T A A G A C T G T A A C C A T G T C A T G T G A G T T A T G A G C T A G G A A C C C T G G A C A A A C C A [A/G] C A C A T A T A C A A T C A T C T C C A C C T C C A A C G C C T T T A C T T C A C A G C C T C T G C A
WI-14078	61 C T G C A A G A	A A A G A A G T A A A T T A G G A A G A	T G T G T G C A T G T C T C T A A A C T A C C T C T T A C T G C	A G A A C C G A G A A C T C A A A G A A C C A C A C A T G G T G T A T C A A A G A A G T A A A T T A G G A A G A G C A A G A [C/T] G C A G T A A G A G A C A T G C A C A C A A A T C G A A A C A A G G G C A T G G A G A A G G A C T T T A G A T G G T C A C G
WI-14083	47 C T A C A C T	A G A C T T G A G A G C T T A A A A C A	G C C T A C T G G A C C T C T A A A C T A C T G A	T T G C T A C A T A A C A C A T T A C T C C A G A C T T G A G A G C T T A A A A C A A C A C T [C/T] A T T T G T T A T T T C A C A G C T C A G T A G T T A G A G G T C C A G T A G G C T T G G C T G A G T T G T T G C T T A A G G T C T T A C A A G G C C A A
WI-14085	31 A G A G A A A A	C A T T A T T T T C A T G T G T A A G A	C A G T C A T G T T C A C G T G C T A G T T	T G C A T T T A T T T C A T G T G T A A G A A G A A A A A C [A/G] T A A C T A G C A C G T G A A C A T G A C T G C A T G G A T A C A C G G C T C A G C A C G A G G C T A A A G T C A G A A G T G A G T G A A A A C A A A A T A G C A T G T T G A T T A A G T G A A A T A A C A G A A C A G G A G G C C T T T
WI-12169	121 G C T T G C T T	A A T A A A A C T T C C T A T T T T C T T	G G G T C T G A G G T G A A A G A A A A A	G T C A A A G G T G G C A A A T T T A T T T C C A C T T A T C A A G A A C T T A C A A A A T A T T T T G T T T C A T T T C T A A A T T T C A C C T T A T T G C T A A G T T A T A A A A T A A A A C T C C T A T T T C T T T G C T T [G/C] T T T T T C T T T C A C C T C A G A A C C C C T T A
WI-15705	50 A G A T C	G G A G G A G A T T T T A G A C T G A	A G C T G T A G T C G T C A A A T A C T C T A G A A	T T G T T T T A T T T G G G G A G A A T G A A G G A G G G A G A T T T A G A C T G A A T C [A/G] T T C T A G A G A T T T G A C G A C T A C A G C T C T C T C T T T G T A C T A C G G A G A C C C T G C T T A T A G C C C C A C A G G A A A T C C T C A T C T G C G G T T G C C A G A C A G

WI-14379	102 C T	TCTATTAACA GGGTATGTCA CAAC	ATCATCTGTT TGAGGTGACA	TTTATGCTGTTGTTTCTACTGGTGGTCTGGCTCACTAATATCAATCCTAGTATGATTTTCTTT TACTTGIGTCTATTACAGGGTTATGTCACACC[C/T]GTCAACCTCAAAACAGATGATACT TAAATAAAACAAAGAGAAA[C/A]CCACCACTTAAAGAGGACACTGCAGAGGCTTATGTACA ACACGTGTCGCCGAGGCTGGCGCAGGACTGCCACTCACTCCAAAATTTCTTTGGAGCAGAG
WI-14102	22 C A	...	...	ACCGCAGAGCTGCTGTATTTAAA[A/V]JACAAAGCTGTGGATCTCTGCAGGGCTGGGACCAGCTGC AGTGGGGCTCCGGCACTGCTCTCTCCAGGACTCTTCCACCAOCCC
WI-15937	24 A G A	CGCAGAGCTG CTGTATTTAAA	GCAGAGATCCA GACGCTTGT	TGAAACTGAAACGTATTTCTCTCA[A/C]JACACCGTAGAACTTAAAGGCCGCAAAAGACTCACACCC ACCACCTAGCGCGAAAAGGAAGTTTCAGGTGATACAAGATGCTCTGCCATCACACCTGAAGGAT GGTT
WI-15944	24 A C A	AAACTGAAAC GTATTTCTCTC	GGCCTTTAAGT TTCTACGGTG	ATGTTTATGATCAATCCAAACATACAGTACAGGGAAGGTGAAATGAGTAAGAAAAAATCAT ATTTAAGTCCCGTTAACACTAAGCC[A/G]TATTATTCAAAATGTGTTTCAAAATACTCAGCCAGAT CACCAAAGCTCAGTCACTAC
WI-14124	92 A G	...	...	GACAAAGAGGCAGTTTCTGTAGTTCACAGGGCCAGAGCAGTATCAGAACGGTGTGTTGACCT GCATAGATTTTGTGACGACT[C/T]GTGGCCATGCCATTCTGTAGTGAAATTAATGAACA
WI-14125	88 C T	GGTTGACCTG CATAGATTTT	GGATGGCATG GCCAC	GTTTATTTCTCACAGTCTGGAGTTAGAACTGTGAGATGAGGATATCACCAGCATGTTAGGTTCT GGTGAGGACTCTCTGGCTTACAGCTGGCTGTTCTCACCATGTTTCAAT[G/A]GCCCAAAGAGAC AGAACAAAGCTCTCTGGT
WI-14136	120 G A	GCITTCTCACC ATGCTTTCACA	CTTGTTCTGTC TCTTTGGGC	TTGTTGTTGGCACCAGAAAAGCT[C/T]ATGTTCTATGTTATGTCACCTGTACATACTGTAAACAAGACT GCATTAATATTGTTTCTTATGATTTGTTTCAATG
WI-14138	23 C T	TGTTGGCACCA GAAAAGCT	CAGTATGTACA GTGACATAACA TAGAACA	GGCAGGTTTATTCATAATTTTCAAACTTGGAAAGCAACCAAGATGTCCTTCAGTAGTATATTCA GACAATC[G/A]AATATTACTTAGCACTAAAGAAATGAGCTATCAAGTCATGAAAAGACATGCAGG AACCTTAAATGGATATTACT
WI-13551	74 G A	GACAATC	TAATATT	TTTTTAAAGAGTGCTTCACATCATTTATTTGATTGTCACACAAAACTTTTTAACTC[C/T]GTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGTCTTTTGAGATAGAAGCCCTTCTTCAGAAATCA CCTCC
WI-15953b	59 C T	...	...	TTTTTAAAGAGTGCTTCACATCATTTGTTATTTGATTGTCACACAAAACTTTTTAACTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGTCTTTTGAGATAGAAGCCCTTCTTCAGAAATCA CCTCC
WI-15953a	26 T G A T	TTTAAAGAGTG TCCTTCACATC	TCATCTGTTCT TGTTGTTTTTG A	TTTTTAAAGAGTGCTTCACATCATTTGTTATTTGATTGTCACACAAAACTTTTTAACTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGTCTTTTGAGATAGAAGCCCTTCTTCAGAAATCA CCTCC

WI-14631	82	G A ---	---	---	TGAATCAATGGACAGTTTGCCTCTGTTTAGTGAACCCCTACAAGCACTCTGCATAGTCGCTTT CTGTCTTCTTTAACTG/AJTGCTGGTCCCTCTGCCAAACTTTTAGGATTGGGCTCTCTCAGGGCCTT GTCTGA
WI-6053	24	A G ---	---	---	ATCACCACCGTGTCTAAGAACAAC/AJGTCCTCATGTCCAACATCATCCCCGGGACTTTGTCAACTG CAGTACACTTCTGCAATGAACCTGGCTTCTGGAGGAAGCCTCTAGAGCCAGGTAAGGGGTGC AGCAGTGAAGGGGTATATCTGGGCTGGCCAGTTGGAACACGGAG
WI-15964	99	T A CTGGAGGTA	GACTTCTCCAC CCTCTTGC	---	CAGAACTCTTCTGTGTTAATAGCTGATGCTAAAGTCAGAGCAGTCCAAAGCAGGAGGCTGCCTT GGGAGGTAGTAAGCTCTCTGCTCCCTGGAGGTAT/AJGCAAGAGGGTGGAGAAGTCTTGGCAAG
WI-12075	103	G A GGCAC	AGCAGCTGGG TCTTCTTC	CCCCTTCTTC TCTTCTTC	CAGCTAAAGGATCACTGCAGCTAAATACAGATAGAGAAGCAACAAGCCAGGCAAAATACCCATCAG AGACAGTGACAAGAGCAGCTGGGGCACGGGGAGGC/G/AJGAAGGAAGAGAAGGGGAGGAG CCT
WI-12179	96	G A TGGAGGTCA	GGAGGTACGG TGTAGATGC	TGGAATGACCC TGTAGATGC	TAATTTAAAAACACGCCCTTCCACATAGTGCCTGAGGCATCTGCACATTTCTCTAGAAGGACATGA ATAGTGATGTGGAGGTACGGTGGAGGTCA/G/AJGCATCTACAGGGTCACTCGAGGAGGAACAG
WI-14651	49	C G ATTGT	CAAGAATCAT TCTCATTTAAA	GGAGATATTGA TCTTTTCTGA	CACAAATAGTGAATTTATCTGAGCAAGAATCATTTCTCATTTAAAAATTGT/C/GJAAATAAGTCAGAA AAAGATCAATATCTCCCTGCTTCAAAAAATGACACTCCCAATTTTACAGGTAACTGTTA
WI-14666	105	T A ---	---	---	AATGGGACTTTCAACAAGGGTTTAAACTAATCTAATAACAATCTCTACAACACATTTCCAGAGCAT TATAACAAGAATTTATACAGGCAGCTAATGTATTAAAT/AJAAACCATGAAAAAGAAAAAACTTG ATCTAGATGTCAGCAATGGGCTGAGACTGT/C/JTGCTGGTAGAGTGCAGTGTGTGTATGTTTCTAC TCTATTACAAAAATTAACAGAAATATGGCTTCGCTTTGTGCAAAATGTTTATATACAGTC
WI-13967	103	A C AAATAAAAA	AAAAGACTAC AGATACAAGG TG	TTGTGTTTCA TCTCCTAAAAG	AATTTAATAGCAGCTCTGTGTGTGATTTTAAAGAAAGATAAAATATGTCAATTCAGCAGTCATTT AAAAAATAAAGACTACAGATACAAGGAAATAAAAAA/AJCACTTTTAGGAGATGAAAAACACAAA
WI-14408	60	T A G	GCAGACACAC TATTACAGGCT	TTAATTGTGA AAACTCATTTG TTACTTT	TTAATATTTAGCAAAAGTTATTGCAACAGGTTGAAAAATGCAGACACACTATTACAGGCTGT/AJAA GTAACAAATGAGTTTACACAATTAATAATTAAACACATACTATTATGGGATTTGTTGAATGA
WI-13683	47	C G ---	---	---	TTTTGTGTTAAGAACAGCATTTTGAATAAACCCTATCTGCCCATG/C/GJTTTACAGCCTTTTAAAT TTGTAATATTATATAGTCGTTTATGGTACATATTGATTGIC
WI-13910b	63	C T CGTCT	CACCATGGCA CAC	CATTGAGATAA AGCACACTTAT CAC	TTAGAAAACTGATAAAAGCAACAACACTTTTGGGAAAGCACCATTGGCAGCTCCTTTGTGCTA/C/TJ GTGATAAGTGTCTTTATCTCAATGAAGCAACCCCA
WI-14635	22	G A ---	---	---	ACATGGCAGATACAGAGCTGT/C/GJCTTGAAGACCACCACCTGACCAGGAATGCCACTTTTACAA AATCATCCCCCTTTTTCATGATTGGAACAGTTTCTCGACCGTCTGGGAGCGTTGAAGGGGTGACCAGC ACATTTGCACATGCAAAA

WI-16002	59 T	GATAACATAA AATGATCATG C AGAATTC	GCCATCTCTC TTTGACTTTT	CCAACATTTAAACCTATGACTGGTCATTGATAACATAAAATGATCATGAGAAATTTCA[T/C]GTTA AAAGTCAAAGAGGAGATGGCTAATGCATGCTGGGCT
WI-15361b	101 A G A	CCCACTTGAAC TCAAGTCATC	AAACTAAAAC CTTTGTGCCTA AAA	GTGGAATTTTAAAGCCATAAAATTTCTTCACACTCAATACTACTGTTGAACAACAAGATAACACAT CTTCTTGCTCATCCCACTTGAACCTCAAGTCATCA[A/G]TTTAGGCACAAAGTTTAGTTTCTCGG GAAATCAAGTTTAAACCA
WI-14759	73 T C	GGGTTTGACTT GTGGGG	TCCACACTGC OCCC	TGAGTTACAACAATGAGCAACAAGTTAGAAAAATTTGGTTTATTCAAACCTTCTAGCGTTTGACTT GTGCGG[T/C]GTACTCAAATGGGGGCGAGTGTGGGACGGGAGGATTCACACAGATTCATACTG CAA
WI-12535	50 A T T A T	CTAGGAGGGTT GAGGTGTAGA	GCTCCACGAGA AGAGAGGAA	TCCCTAACATTTATTCAGGTGGTGACTAGGAGGGTTGAGGTGTAGATAT[A/T]CTTCTCTCTTCTC GTGGAGCCTTACTGAAGACAGGATCGCCGTTCTTGTGTTATCAGCTGAGAAGGGCAGTCTCGCCATC TTAAGACCTGCCCC
WI-13805a	112 G A G G G G A A	AAAGGCACAC GGGGAA	CTCAGCCTGCC TTGACC	TTCCATTCAATTATGCTTGGCTTTACCAATTTTATAGCTATTGGGAGGCGAAAGGGAAATTTTGGC COCAGAAACCATGAGATTTGGGTGAGAAAGGCACACGGGAA[G/A]GGGTCAAGGCAGGCTGAG AGTCACATTTCCAGACCTC
WI-12340	18 T C	---	---	ACACAATAATATCCATT[T/C]CGAGTGATTAAACCTATTTGTTGTTAGAACCAACAAAACTAG AAGAAAAACATTTTCAAAACCTTTTTCAGGCTGA
WI-14808	52 T A C T A C C C T G T	ACCCACCACA CTACCCGT	GAGGATCACA ATGTTAAGATT TT	CTTTGAAACACTTTAAGCAACACAGTTAAAAAGTACCCACACACTACCTGTT[A]AAAACTTTAAC ATTGTGATGCCTCTGCATCAATTTTAGAAAAACAAGAAAAACACAACTGAAGGCCCATGTA AGTTAAAAAAATCGAGTCAGCATTTATTT[A]AAAACTGGACACGCTTCTATATTGCAAGCTCAT TCAAATGCATTTATTTGTATCCCAAGCCCTGAAACATGAAAAAATATTTACTAAAGGAATGTTG ATTACCAGCTACGACTTTC
WI-14816	29 A T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG[G/T]TAGGTGATTGATACAAATACGATCCATAA
WI-12542c	71 G T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC AT[G/T]TAGGTGATTGATACAAATACGATCCATAA
WI-12542b	70 G T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC AT[G/T]TAGGTGATTGATACAAATACGATCCATAA
WI-12542a	45 C T	GCTATTAGGC AAACTGAACA TTTAAA	TCTAGAGCCCT CACATGGAT	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAG ATCATGGTAGGTGATTGATACAAATACGATCCATAA
WI-12173	57 C T C A A A A A	GGATACAGCA GTAAAGAATA	CCACCTCTAGA ATGTATGCTCT ATAA	CACCTAAATCATTTCTAGAAAACCTGGGATACAGCAGTAAAGAATACAAAAATCCTGC[C/T]CTTATA GAGCATACATTTCTAGAGGTGGGAAAGAGGCAATAAATA

WI-14836	28 T C ...		...	TC TTG GAGG GATAGAGGACAGAGTGTT/CJGTTGATTTTCGTTTCGTTTCAGTTTGGTTGTCATT GGTTTTTGTTTTTGCTAATTTTGCCCCACCCTATAAAAAGCAGTGCACCCACAGGCGAG
WI-14856	60 A T A A	TGGTGACAG GAAATACTT	TTTGTTTGCTA CTTTTACAAA CTTT	ACATTTCCCTTATGATAGCAACAACATAAATATGATGGATGGTGACACGGGAAAATACTTAAT/ATTTAA AGTTTGTA AAAAGTAGCAACAACAAAATTGAGTATATACTATAAGTGATAGAGGATGTATATGAAAAA GGCTATAAAAAGCTCCAAA
WI-14863	61 G A ...		...	ATGGCAATTTACTTTATAGCAATGAACAATAATTTGTCAAAGGGCAAAATATTTTGTCTG/G/AJAG TTAATAAGTTAATATCTTTTACCACAAAGCTAGAGGTCAACAGTACCACCTATTATTGATTGCCACT ACCTGGC
WI-14867	46 T C A	GACATTCCAA GGCTCTTAAC	TGGGGCTGCAG ACACTC	TTTTAATTAAACGTAAAAAGGCAGGACATTCCAAGGCTCTCTAACAT/CJGAGTGTCTGCAGCCCCA TTGGCTTTGAGATGTGAATGTGTTAACCCAGGGTGGA
WI-14733	98 G A A	CCAAATTGAC AGATAATTCTGC	GATGAGGTCAG GCCATTATT	ACGGAGTCGTCTCTGATGATTTCTTTGTCAA AAAAATGTTTGGCTGATTTCTAATCATGAAAGAACAAATT AGAAAAATCCAAATTGACAGATAATTCTGCA/G/AJAATAAAATGGCCTGACCTCATCAAAAAACATCA ATGTCATGAAAAACACAAAA
WI-14898b	79 A C ...		...	TTTTGTACCTATTCCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCAT/CJAGGTGCCACTAAGGAAA ACTTCTCCAT/CJAAGCTGCTGTGTGCACGTTGCCCTGGGCTTTGCTAACCCCTGGTGTGCATCT GCCGTGTTCTGCTT
WI-14898a	50 A C C A	CATGTACAGG AAGAGTTGTCT	AAGTTTTCCTT AGTGGCACCT	TTTTGTACCTATTCCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCAT/CJAGGTGCCACTAAGG AAAACCTTCTCCATAAAGCTGCCGTGCTGTGCACGTTGCCCTGGGCTTTGCTAACCCCTGGTGTGCATC TGCCTGTGTTCTGCTT
WI-14907	48 G A	GGCACACATT GGACTCTGAC	TCTGCTGCAAG GGGAAT	TGGTATTTATTTCCGACATTACTGTAGAGGCACACATTGGACTCTGAC/G/AJATTTCCCTTGCAGCAG ACATTTGTGAAGCTGCTGTGGCGCACACCCCATCAATCAGTGACTCTGCTGACAGAGGGGCGCACATG CACGATGCTCAGGTG
WI-14911	52 G A C	CCAATACATT CAGTTCTGTT	CAAAACCAGGA AAAGGACCTT	CTAGAATCTGGGAAGTCCAAAGCTCAGTGCACCAATACATTTCAGTTCTGCTG/G/AJAGGTCTTTTC CTGGTTTGCAGACAGATACCTTGTCTGTATCTCCTACATGGCAGAGAAAGAGAGGAAATATCT
WI-14913	88 C A ...		...	CTGATGCTTTGACATCTGGGGCATTGCTGTCTCTAGAGAGACTACTTCTCTGGGACCGCAATTTTC TAGTGATAGTAGAGGACTCA/C/AJCTGACGCTGCACCTTTTCATATACAGATCAACCAATCCAAAAC CTACACCTCCACACCT
WI-14914	66 G C A	CTGGACACAG TTTCTCTAGC	CAAGCCCAGGA CAATAAATTC	ATTTCTTGATTGGCTGTGTAAGCCCTGTGAAGTCAATGCACATCTGGACACAGTTTCTCTAGCA/G/ CJGAATTTATTTGCTGGCTTGATGGCTTTCACAGC
WI-14926	49 T C ...		...	GTTTATTTCAAATGACACATCCAGATTGAAATGGGCACTTAGCGAAT/CJACTTGTGGACCACA AGACTTGTCTGAGAACATGTTCAAGACAGTTTTCAAAATAAAAAATTTTCCITTAATCAGGTCCA

WI-16083	89 C T	ATGTTTAAACA CAAAACATATC AAGGAT	TGGAAAAGATT CCAGCCC	GCATCTTTATTACCACAGAAACTCATTTATGTCTTAATCATTTGTTTAATAATAATATAAGCATGTT TAACACAAACATATCAAGGAT[C/T]GGGCTGGAATCTTTTCCATTCTATAGAAAAGCACTAACCATC CATTAAAGCAG
WI-14930	55 C T	GGAGGAGTCC CTCATGGAT	CACAACCAACC AATACCGC	CAGTTCTGTGTTCTGGAACAGCTCTCTTTTCCACAGGAGGAGTCCCTCATGGAT[C/T]GCGGTATTG GTGGTTGTGTGATTGGGGAGCACGAGGGAGAGCAA
WI-14946	47 T C	---	---	TCAATACTGAAGGTGTCAAAGTGGTCTATTTGCCCCACAGACATAACA[C/T]CTCTAAATCATCTCTTA GATCAGGGAGTCATAAGGACCATTAAGGCTCATACACACAGTACTTTATGGAAGGATT
WI-15987b	80 A G	---	---	ACATTAAACAGACACAATTAAAGGGTCCCAACGAGTTGGTAGTGCTTCCACTATGTGAGGACAC TAAGAAGATGGT[C/A/G]TCTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
WI-15987a	32 C T	CACAATTAAA GGGGTCCAA	GGAAGGCACATA CCAACCTC	ACATTAAACAGACACAATTAAAGGGTCCCA[C/T]GAGGTTGGTAGTGCTTCCACTATGTGAGGA CACTAAGAAGATGGTCACTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
WI-14948	56 T C	AGGGAACGTG CTAACTTGCA G	GATGATCTTAC ATCAGTTGTTG GA	GAATAAAGTTCTATTGCCGTCTCTCAGGGAACAGGGAAACTGCTAACTTGTCAAGT[C/T]TCCAACA ACTGATGTAAGATCATCTCTGACCATAGCGAACCTGTAAAGGCTTGTCTTCCCTCCAGCTGA
WI-16100	52 A G	CAAAAAGCTA TTTCTCTACAC TTGA	ACAGGAATGTC AGAAAACAGT ATATTAC	TTGTGTTAAATTCATCAAGGAATTGACAAAAAGCTATTTTCTCTACACTTGAC[A/G]GTAATATATACTG TTTTCTGACATTCCTGTTATCAACTCTCTGAAAATC
WI-14958	83 A G	AATAATTTAT CTCTTCTTTT CAAGGG	AATGCATTAT TTGGGTTTT	GTGATTGATCTGTAATTATTGGGATTATTTATCAACTCTAAAATCCAAAGATGAAAAATATTTATCT CTTCTTTTCAAGGG[A/G]AAAAACCCAAATGAATGCATTTTTCAGTTTCTCCAGGCTTTGAACTGC AGCAGAAAAATCAAGGA
WI-14976	35 C T	GTTGATTGCT TCGTTCAAAG AGC	TCAAACTAAAT CTTCCATTCTA AGC	TATTTTAAATTGTTGTTGTTGCTTCGTTCAAAG[C/T]GCTTAGAATGGAAGATTTAGTTTGAGGAG GGGCAGGTTTGGGGTAGGCTCAGCGGGCATAGTGGCCACAAAGAGATGCCCATCTCACACCTGGAG ACGTCCATGAGCACCTCG
WI-14981	31 G T	TCAGTGGTGT TATTGGATTT T	CACCTCTGACA TAATACCTAGC ATAAA	TAATTGATTCAGTGGTGTATTGGATTTT[G/T]TTATGCTAAGTATTATGTCAGAGGTGGAGAAT AAAGAGGAAAAAGAAACAAGTGTGGCTCTCGCATCAACGACCTGATCTTGTACAGGAAGTTTITGA GAGCTCACAAA
WI-14992	80 C T	TGCATTAAAT GAAGCTGCAG	GCTATGTGCTC AGCTTTCTCT	TGATTACATTTTAAATCATGCCTACCAGCCCATCTAAGCCAAATCAAAACACCACCTCTGCATTA AATGAAGCTGCAG[C/T]AGGAAAGCTGAGCACATAGCACCCTGATCGGAAAGAAACGTA
WI-15002	72 T A	---	---	AAATCTCTTCTTTCACACACAGATGAACCTTTAATAAATTACAAATGCACCTGAAAAATGCCTTCTTGA TTTCCCT[A/T]TTCAGTTTAGGCTCAAATGGGCTCTCTCTCAAGGCTGGACCTCAAAGGCCAGTT
WI-15000	90 G A	GACAGAAAAA GACTCAGACT GTCTAA	GTTTCTAGTTC TGCACAAACTT CA	TCAAGCCAAATATCTGCAACAATAACATGATTGAAAGGTATAGAAATAAACAGATGGATAGACAG AAAAAGACTCAGACTGCTAAGTA[G/A]TGAAGTTTGTGAGAACTAGAAACAAAAATCCACCT

WI-12323	68	G A	CACAATACTT CATGTACCTAT	CACTGGACATA TTCCCTACCTG	ATTTTGTGATGTTGGTAAATCTTATCTCTTTTATACACAATACTTCTATGACCTATGAAATAA G/AJACAGGTAGGGAATATGTCAGTGCAAAACAGAGGACTCACACCTGTGCATAGACAGCAC
WI-14683	91	A T A A A C A	AAGGGACGAT TTAGTATCTAA	GGCATGTCCCA GTGTTTTT	CATAAGTTGCATTTATTCACGTCCACGCCATCTAAAGCTACTGTGTACAGTAATCAGGACTGGAGAA GGGACGATTAGTATCTAAACA/A/TJCAAAAAAACACTGGGACATGCCCTGAATTGCAAGT TGGAGTTCGTAAGAACTCTAC
WI-13470	100	C A T	CCTGCCCTTTAT ATTGGAATTC	GGGAGACCATG GGTCTCT	ATTTTGTGTTTATTTAGCACCTGAAATTTAGGCAAGAGAGAAACATTTCTACCTGAAGACTCCATGCAGT CAAAATTCCTGCCCTTATATTGGAATTTCTA/C/AJAGAGACCCCATGGTCTCCCCAAGTGAGGAAGCC AGGGCACTCAGCCCTTC
WI-14712	38	T A C A	TGAATGCTTCC AAGTACAAAT	TGAAAGTATGT TGTATATGTA	TTTGGTGCTACTTTGTGAATGCTTCCAAGTACAAATCA/T/AJCTCACAATACCATATACAACATACT TTCAATCACAACCTCAATATAAAATAACCTACAAAATCACATTGC
WI-13712	40	A C T C T A T T G	TTTACTTTGT GTCAATTTTAT	CCATAAGGTCT CACACTTTTCT	TGGGATACCCCTTTACTTTGTGTCAATTTTATTTCTATTG/A/CJATTATAAGAAAAGTGTGAGACCTT ATGGCTCTCTGCTTATTGGCAATATGCAATATAATATTGTGTGTTGTTAAATTTATGCAAT
WI-16163	35	C T A	TCTGGTGATGC AATTGAAATA	GCTGCCAATTA CATTAACTTAC	TCTAAGATTTTACTCTGGTGATGCAATTTGAAATAA/C/JATTGTAGTTAATGTAATTTGGCAGCATT GCCAAAAGTTTAAAGGAGACTATTTCTTTAAACAAAAGACAGTGTCTGACATTTATTTTCAGGT
WI-13453	88	T A T C	AATGCACAAA ATCTTGTCTCT	TCAGATTTTAA CATCTCTTTCT	TTTTTTTATTGCAATTTGAGTGCCTTTATTATATTGGGAATTCAGTGATATTAAACATTTGTACAAAT GCACAAAATCTGTCTCTCT/C/JTGTAGAAAAGAGATGTAAAAATCTGACCTAGTTGAACAGTCTT AATGAACCTCATTGICCAT
WI-16167	58	T C G A T T T T T	CGCACTCTAA ATTAGAGATA	TGCTDGTGGTG AATAAGATG	CGGATATAATTATGTACCGCACTCTAAATTAGAGATAGATTTTTTCTGATATACATTT/CJCATCTT ATTCACCACGAGCACACCACACGACAGTAGAACAGTTCACACCTGATAAATTCACAAGATG
WI-14482	17	G A ---	---	---	GCAGAACCAATTAATAA/G/AJAATCTGCAAGTTTCCCCAAGAACTCTGGAACCATAGTGCCTAAT GCCCTTTAAATCGATACTAAAGGAGAGAGAAATAAAGGACTGCTTGATGTGACAGTCACCTGGT
WI-15069	81	T C ---	---	---	TGTAGTCTTCAAAAGACATGTTGGCAGATAGCCAGGCCATACTATGTGTATTCOCAGTATCATGTAC GCACTAAAAAAAT/CJGTGTGCTTGTCTGCTGTGAGTGAACCATTTGCTTAAGATAAA
WI-16156	97	A C C C A G A T C G C	TGAAGATTAA CCAGAGTCGC	AATGTGTGCA TTTTGAAGAGA	ATCTGGTATTGTGTATCCCAACAAGTATACAGATACTCTATAAAACCAACCCCAACCTTCAATA TTACACTAATGAAGATTAAACCCAGAGTCGC/CJCTCTCTTCAAAATGCACACAATTAAGACG
WI-15012	59	G T A T G T	GCAGCAAGAT TACATCAGTA	CTCCAAATAGC CTAGAGTATAG	CATGGCAGCAAGATTACATCAGTAATGTAATATAATACAGCTTTTTTTCATTGAAGCTTTT[G/T]TACCT TACTATCTCTAGGCTATTGGAGTGTTCCCCAC



WI-15100	74	G A	---				TCTATTACAGCCAAAGAAAAATACCCAAATATTTCCAAATAAGCAAAAAATTTGGAACAGACTGGA GTGAGAAC[G/A]GGTCCACCCAAAGCCCTCAAGACAAGATGGACACGGCAGCTGGTTCTGGGGT GCATTCTAGTGGACTTTAT
WI-14492	92	A T	AATTACT			GTCACCATGTT ATATTTCTTT TAAGAC	TGGTACAGAAATGTTTAAATTACAGCAGGCGAGTGATTCAGTTAAATAAAATTTAAACCTTTATTTT CCCAAAATATAAAATTAATAAATTA[A/T]GTCTTAAAGAAATATAACATGGTGACAGCTTT TCTTTAAATTTATCGGAATCCAGGACACAACAAGAAAAACCCCAAAACCCACATGGAGACAGAAG ACGAGACACAACCTCTCCCCAC[T/C]GCCCTCCCTGCTCTAGAGTGGGACAAAAGTGGGGTGAGAC AG
WI-12002c	89	T C	---			---	TCTTTAAATTTATCGGAATCCAGGACACAACAAGAAAAACCCCAAAACCCACATGGAGACAGAAG AC[G/A]AGACACAACCTCTCCCCACTGCCCTCCCTGCTCTAGAGTGGGACAAAAGTGGGGTGAGAC AG
WI-12002b	68	G A	---			---	TCTTTAAATTTATCGGAATCCAGGACACAACAAGAAAAACCCCAAAACCCACATGGAGACAG AAGACGAGACACAACCTCTCCCCACTGCCCTCCCTGCTCTAGAGTGGGACAAAAGTGGGGTGAGAC AG
WI-12002a	30	C G	GGACAAA			TGGTATTTGGG TGTTTTCTT	TCTTTAAATTTATCGGAATCCAGGACACAACAAGAAAAACCCCAAAACCCACATGGAGACAG AAGACGAGACACAACCTCTCCCCACTGCCCTCCCTGCTCTAGAGTGGGACAAAAGTGGGGTGAGAC AG
WI-15116	96	C T	GTTGCAGTAA			CCTGAATATGC AATTATTTAT ATGACA	TTTTCAATTTATTTCCAGAAAAAGAAATCACATTTTCAGTAACAACATTACATATAGAAATTAACCTTTG TTCTGGAATGGGAGCCCTAGTTGCAGTAA[C/T]GTGTCATAATAATAAATTGCATATTCAGGATTTTG TGAAATAGGTGATTGGGA
WI-12578	37	C T	AATGGGAA			TCAAGCGACCA CCAACAC	GCAAAAGCAAAGCTATGGAGGCTAAAGGAATGGAA[C/T]GTGTTGGTGCGCTTGATACCTTGGT GCTTGTTGATGGAGCAGAGTCTTCTGCTCCATGCAGGGGCGTCACATATTTAACTGCACATAAT TTGGCAAACTGTCATTC
WI-15153	40	A G	GCATTGCA			AACCTCAGATA AGTGCAGTGT T	ATTTACGTTGGCAAGATCTCCCTTATGTTGGCATTCGA/GAAGACACTGCACCTTATCTGAGGTTA GAAAAAATGTAGTCTTAATAGCCCTCTTAATGTGTAGCAAGGCAAAATTACCATTTCTAA
WI-15215	84	G C	TCAAATGGG			CCAACAGGGGA AAAAGTCA	CCTTTGCTCTCTGAACCTGGGACCAGGATGTGAATAAATTTTGAATCTGATGCAGGTGAGGTATGGC TTTAGAATCAAATGGG[G/C]TGACTTTTTTCCCTGTTGGTGAAAACTCTGTGAGGGTTTGCA
WI-15225	80	C T	CTGAGGACCT AGAAAGCAAA T C			TTGATTGGCA TAATCACTCC	AGGAAAGAGTGGTAAAGCAAAAGGCGATCATTTGGATGGAATGATTATGTGTCACGAGCACTTGAGGAC CTAGAAAGCAAA[C/T]GGAGTGATTATGCCAATCAAAATGCAAGGTTGGAGATATGCTAAAA AATTTGCTAGTGCAAATGGACCCAGAAATTTGGAAGGCTATGTAACACACAG[G/A]TATGCACACCAG AGCCATGTCAGTGCACAGATCCTCTTTGTCATTCAGCTTTCTTAAAAACACATCAAAAGGCTGCA
WI-15152	51	G A	---			---	
WI-15123	55	C T	TAGGATG			TGTTAGTGACA GACAGATAAA CAACAGAC	TGACTGTATACCAAAATGCTGTGCTTAATGTTAGTGACAGACAGATAAATAGGATG[C/T]GTCTGTTT GCCCTTAAGCAATTTACAACTCACTGGGGAAGAAACAGACATGCAACACAGAGATAAACACAAAT

WI-15182	49	C A	GCACAACCAG GGCAAAATA	GCATGGGTTAA TCCAGCA	GAGACTGCCCTGTGACACAACACTAGCTAGCTGCACAACCCAGGGCAAAATAC/AJTGCTGGATTAAACCC ATGCTAATGGTTACCTTTATTTAGTAATCATGGTCCCTCATAGCATGGTCCAGATCCG
WI-15198	38	T C	GGGOCCTGGC ACTATG	ACTTATCCGTC AGGCAGAGTAG	GTGGACCTCTACAAGTACCATGGGCCCTTGGCACTATGTC/CJCTACTCTGCTGACGGATAAGTTGGC ATATGGTTCAGATTGCTGTCTACACAGTCCAGTTCCCTAGAGACTAGTCCGACTCTCTT
WI-12601	42	T C	CATTATTGAG TATTCTTGCTT	GTGTAGTCTT ACATGCTTACG	TCAAGTGGTAATAGCCATTTATTGAGTATCTTGCTTTGATTC/CJGCTACGTAAAGCATGTAAGACT ACAACATTACGCCCATCTCTTCAAGAGGAAGTCTGGTATTATGGAATAACATTTTGTGCTTCCAGAT T
WI-14510	104	A T	TGGCAAAATA TGCATAACAA	TTGAAAATGGT TAACTGGCA	ATGTTGAGAGTAATAATGCCCTACATATTTAGTGAAGTACACCCCAAGATATTTTGGGGAAGAG TTGTTTGCCTTTTGTGGCAAAATATGCATAACAAATATTTGCCAGTTTAAACCATTTTCAAGAGT
WI-15239	57	T C	CATTTGCAAT AAACACCATC	GGACCTTATCT GTGGACTCAGG	CAGTGTGATGACATTTCAATGGGAAAAGATTGTGCATTTTGCATTAACAAACCATCATTC/CJCTGAG TCCACAGATAAGTCCCGGAGAAAGGGCTTCCCTCCTTCTCGCTGGGTGACGTTCCCAAGCGAGT GAAGCCTTTTCTGGAATG
WI-12634	52	T C	GCATCATATG AACTGTCTAGC	GGACAAATTTGT AAACATAGCT	ATGAGTTTATAAACTGGAGACAGCGCATCATATGAACCTGTCTAGCAGTATTATTC/CJGCTATTAGCTA TGTTTACAATTTGCTCTGAAGGGTCTAGATGTACACCCCAAGAGTGGTATTCCCTGA
WI-15249	34	T C	GGGCTTGACAC AAAGTTCTAA	GGAAAGCCAG AGATTTTAAAC	TTTGCTTGAAGGGCTTGACACAAAGTCTAACTTT/CJTTGTTAAATCTCTGGCTTCTCGCTGGCTGG TGAGGAGGCACAGGCTGGGGTCTTCAGGTATCCACTGGTGGCCCGCATCTGTTCCCTCCACTCCCCAG CCACATTTCTGGCTCT
WI-12159	28	C T	AAGACCCGT GCAAATGC	CCCTCTCCTCA GTGCACCTT	CTGTCCGGGGAAGACACCCGTCGCAATGC/CJAAAGTGCAGTGGAGAGGGGAGGGTCTGTGACTC CCAAACCCCTCGAATATTTATGAATCTAAGAGTCCAGACGAGTTCATCCACGGAGATCTGC
WI-12648	41	A G	CCTAGTGGCAT TAAGGATGC	TTGCTACTAAA AGTGGACATCC	TCCCAGATTGTATGGAATGCCTAGTGGCATTAAAGGATGC/CJGTAGGATGTCCACTTTTAGTAGC AACCAGATTAAATCACTACTCCATGTTAGGTGCTTTACTTGGATTATCTCACTTAAACACACA
WI-12684	64	G T	CATGCTGTAA ACAGCTGTGC	GGAACAACAA AGCCTAAATGG	ATGAGAGGTAAGTGTCAACAGTAGGCTTAAATATTCAAGTAAACCATGCTGTAAACAGCTGTGC/CJ TJCCATTTAGGCTTTGTTTCCATTTAGAGAGCACAGGAGAGGAAATTTAGCATAAATCTT
WI-15260	75	G A	AAAGGATGAA GCTAATCATG	TCTCTCCAGGG AGCTTGC	TTTATAAGCTGAATGAAAGAGGTCGACACAGCGGACACTGTCTAAGTGGAAACAAGGATGAAGCT AATCATGGA/CJGCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGATGAGCTGGAGAAATTA TCTG
WI-15325	39	T C	CATGTGGCTGG GAGGC	CCTTCCACCAT GATTGTGA	AAGGTTAATGGACTCACAGTTCCATGTGGCTGGAGGGT/CJTCACAATCATGGTGGAGGCAAAA GGCACATCTTACATGGTGGCAGTCAAGAGAGATGAGAGC
WI-13936	123	C T	AGTTGGCATT AATAGCCTAT	TGAAACTCCCA CATGGAGTT	TATTTGAGTATTTTCATCCATGGGCTTCTCACTCCCTATACATTTCCAGGGTTGAGGTAGTCTACCC CCATAGGTTTCAAGAACCTATGACCTGTATCTTCAGTTGGCATTCATAGCCTATC/CJTAACCTCCATGT GGGAGTTTTCATAATAA

WI-14528	62	T G T A A A T	TTTAACTTTT TCTGGATGGTA	CTCGATTAGCA CTTATTATAAA AATTAAAA	TATGCTTTATTGAAGAGAATAGGCTATTAAATATATTTTAACTTTTCTGGATGGTATAAATTT/GJTT GAATTATAAATTTTAAATTTTATAATAAGTGCTAATCGAGACATCAGTGGGTATAATTGA TATTTCTTCGGTTTCGGATGCAAAACAAAAATTTTAAAGAAAAATGTGACTTCAAAGGAAAAAGA ACAAATTTTC/CAAAGACTTGGGGGAGTGAAGGCAGAGCCTGGTGCAGATGGACGAGTCTGCAGA GG
WI-15347	74	C T A A T T	GACTTCAAAG GAAAAGAACAA	TCACTCCCCCA AGTCTTIG	GTATTTTCTGATGCTTTGACATCTGGGCGATTGCTGTCTAGAGAGACTACTTCTCTGGGACCAGC CAATTTCTAGTAGTAGAGGACTCA/C/AJCTGCAGTGCACCTTTCATATACAGATCA TTTATTGGCTGTCTCTGTAATACAATGTGGTGAACAC/G/AJCTTAAATTCAGGACATCTTCCACCTTG TTTGGCTTCCAGTTGTAAGTCAAGACCAAGTGTCAAGGCACATAGGCTGATTATCAGTGG AGAAATTTTCTCTTTTAAACAGGACAAGTAACAGATTACATCAAACTTTCAGAACTTCTCAAATAC CTAGTTATTATACACATCCCATCTGTCTTGA/C/AJGGAGGGATCTTGGTCGGCTTAAACA CCAGCTGGAGGTGGAATAAATGCGGCAACCAAGAAAAACACACAGCTACACACAGGCTTGCATT TGGCTTAT/CJGTGCTGAAAAAGAGGGCCGACCTCTTGATAAAGAATGTCT AAGTAGAACACAAATAGAAATGGCTCAAAATATCAGAATGCACACTACGCACATCAGAGTAAATACTG TTTGGTAAACCTTGTTCAGTTAAATATGTAT/CJGTGTCGTCATGTCATGATTAAATATCCTTCT TACCACAGTCAACCTAAAGAACCAAGCTTAGGACTAGGACACACACCATGCAGAAAGAGCAGGGA GACCAGACACTCTGGGTTGAGATGATGATTTTAAATGCCGACGCGACACCCACA AAGTAGAACACAAATAGAAATGGCTCAAAATATCAGAATGCACACTACGCACATCAGAGTAAATACTG TTTGGTAAACCTTGTTCAGTTT/CJAAATATGTATGTGTCGTCATGTCATGATTAAATATCCTTCT TACCACAGTCAACCTAAAGAACCAAGCTTAGGACTAGGACACACACCATGCAGAAAGAGCAGGGA GACCAGACACTCTGGGTTGAGATGATGATTTTAAATGCCGACGCGACACCCACA CACAACATTCAGAAAGTTTCTGCATTGTCTCTGTGATGTCTAAAAAGATTGAGCTTTGACTAT ACGATTTCACACACTGAACGCTTCAAGGTTTCTCC/C/AJAGTATGGATTCTCTGATGATTAATA AGCCCCGAATCTGGCTAAAGGCTTCCACATTCAGACATTTGTAAGGTTTTTCTCCAGTGTGGAC TCTCTGGTGTGCACAAAGATGGAACCTCGGCTGAATGCTTCCACACT
WI-8039b	97	T C ---	---	---	CTTACTACATGGGAACATCAATGCAACAAGTA/G/AJAATTTGTAACTCAAGCCACAACTTAGTTA ATAATCATGGTTAAGGGACATTGCCAAAGAGCAACTGATGCCCTCAGTGAA TATTAGATAAAACCCCTTGTCCCGATTCCAGGATGTTTAAATTTGCTTCTTTAAACTCTGTGACTTTT CCTGGTTCAAAGGACAGTT/AJGATGGACAGCAGAGGAGTGGGGTCTGAAAAATGTAATCTTT GTGTCAAGGCACCTCTGTGGCTCACAACCTGCCCTGTGAGGGGATGCTGCCCTCCAGCCCTAAAG ACACTAGGGCTTTTCAATGGACGGGTGTTGAAGCAGCCAGATGTTAAGG
WI-8039a	87	T C ---	---	---	TTTGTGGCTTG AGTTTACAAAT T
WI-8044	107	C A ---	GGGAACATCA ATGCAACAAG	---	---
WI-8550	32	G A A T G C A A C A A G	---	---	---
WI-8057	87	T A ---	---	---	---

[illegible]

WI-6375	28 A G A A	GGTTATTGCA TATGGAAATC	AATGTGAGATC TTTATTCTAAC CTTTTT	AAGGTTATTGCATATGGAAATCAATAG/GJATATCTTTTACAAAAAAGGTTAGAATAAAGATCTC ACATTTGTAAAGGCACATATGAACATTTTATAGCAAGCACAAGGGAGTGAGACATCAACAA TTGTGCTCAACAGATGAAATTCATAACCTTGTTTCTGATAAGACAAATTCAAACATACAAAATCAAT TACAACAATGTGCTTATCAGCTCCCTCCACCCCTATATTTAA/T/A/GCAACTGACAGTTTGAAG GACACCAAGACAATAGGGCT
WI-6409b	112 T A ---		---	TTGTGCTCAACAGATGAAATTCATAACCTTGTTTCTGATAAGACAATTCAAACATACAAAATCAAT TACAAC/A/TATGTGCTTATCAGCTCCCTCCACCCCTATATTTTAAATGCAACTGACAGTTTGAAG GACACCAAGACAATAGGGCT
WI-6409a	73 A T ---		---	CTAATAATCCTGGGCACATGGATTCCAAAGAGAGATTTTGACGAGATTTTCATTATAGTTACTTAA CAGCTAAATAATAAGGGTGATTTAACTTACTTACAGAGTCACTAAATAATGGAGGGGAAAGGAAA GAGTAGGGCTAATCCAGTAGAGACTGAAGCTG/G/TJATCAACCTTCCCTAAGCATCTGTCTGGTCCG CAGC
WI-6523	165 G T GCTG	GCTAATCCAGT AGAGACTGAA	AGATGCTTAGG GAAGGTTGATA	TCTCTAGCCCTATTAGGCTACACTGTAGTCACCTTCTATGAGAGCAAGGAAACAGAGATGGGC TCCTGGAGTCCAAACAGGATGTGGACGTCCTGGTAGTCTCTCTTTTACACAACCTTTCCCTGAGA ACTGTCCAGTCAGGTGGACCTTCAACAACACACGACGCTAAACTCTGAGAGAAAAC/GJCTG ACTTTCAGAAAACATAAAGCTGAGAAAAA
WI-6554	195 C G ---		---	ATTGTAATTAATAATTTACATGGGCCCTATTATTAAAGGACATTTGTGTAATGTTCCACTTTGTTTTAA /C/TJATTAACAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAAGTTTGAAAAATGGCG
WI-6558b	68 C T ---		---	ATTGTAATTAATAATTTACATGGGCCCTATTATTAAAGGACATTTG/GJGTAATGTTTCCACTTTGTTTT AAACAATTAACAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAAGTTTGAAAAATGGCG
WI-6558a	42 G C ---		---	AACCAACAAAACCTAAGAAATGGGAAAAAGAAATGGCAGGTGAAGAACTCTTTTTCAGAGAAATAA AGTTGTCATAT/CJAGCAATGGATGCTGTGTCAGAACATCTGCCAATAAATTTAAGAAAAAAGGA ACTCAATGAAGTTACTGTTATATAAAACAGGAGCTCACAGCAGGATGTAAAGATTAATGGAAGAT ATCGTGAGCCAAAAC
WI-6629	75 T C GTCATA	TCTTTTCAGAG AATAAAAGTT	TGACACAGCAT CCATTGCT	CTGCCCTGAACCAATCAGATTTAGTTAAATCAATCAATCAAACTCCAGCTGTTTCTTGTCTTT TTACTTAGCAAGGAAAACTTTAGTGAATGCTACTTGACAAGAAAGAAAGTCAATTTCTCAAGCACA/ T/CJACCCAAACTTGAAGGTGATTGAACCCAAAATAATGGGTGGGAAACACCAAAATGAGGTGGAGGA ATGAGAAAGATGTGTGGGCCAAAGCTATCTGTTTATTTTGTATTTGTTGCCAAT
WI-6644	134 T C ---		---	TGCTAAACACCACCATTTAATGAAGGAGAGTACTAGGAAAAACTACCAACACAGCATGTGAACAGT TGCGCACGGTGGTAAAGGGCACAGACTCTGGAGCCACAGC/CJGGCTAATACACTGCAATATTTTA TGTTAGCAAAATTATAGCTGGTCTGTGTATAACCAAGAGCGGTATCTGG
WI-6690b	106 C T AGCCACAGC	CAGACTCTGG	ACATAAAATA TTGCAGTGTAT TAGCC	

WI-6690a	28	T C	AAACACC ATTATTAAGG AGAG	GCTGTGTTGG TAGTTTTCT	TGCTAAACACCACCATTAATTAAGGAGATTCJACTAGGAAAAAACTACCAACACAGCATGTGAAAC AGTTGGGACGGTGAAGGACAGACTCTGGAGCCACAGCCGGCTAATACACTGCAATATTTTA TGTTAGCAAAATTAAGCTGGTCTGTGTATAACCAAGAGCGGTATCTGG
WI-6770	53	A G	CAAAACCCAA AACATCACA	GCTTTGGAGT GTATAATAGTA TGAATAA	GATGTTAATGACACAGATCTTCCAAAGTAATCCAAACCCCAACATCACA[A/G]AATTATTGAT ACTATTATACACTCCAAAGCAAAATACITCAACTGCAATCC
WI-6886	151	A G A	GCATTCITCCA AAAACAAAGA	CCTTGTAAGTG ACTATTCCAAT GIT	ATTCTAGGCAAGGTCAGCAAAATCAGCTAGCTAGTAACTCTTGACCAAAATGGTGAGTCAGCCTCA TCACAGAGATTTTTTTTAAATTTAGATGAAATTTACATTTTAAACATGTTAACTCCAAAGCATCT TCCAAAAACAAAGAAT[A/G]AACATTGGAATAGTCACITACAAGGAC
WI-6761	32	C A G	GATCTAACAG CTGCAGAATG	AAAGCTGGG AAGGAAGAAG	CCTGAGAGGCAGATCTAACAGCTGCAGATGG[C/A]CTCTTCCCTCCAGCTTTTGTGAACAAAAC AATCTCTAAGGCATCAGAAAGCACTAGTGCAAAATGGTTGTCAGGTACAAGGTCTC
WI-6844	225	T C ---		---	TAAATACTGCCAACTAGCATACGTCCTCTTGTCATCATTAAACAAAGGGTATTTCCCTCCTTG GTATTTTCAATGATGATTAACAATAACGAAAGTTAGAACTTAAATGCACCTGATTAAATATG TAACTGGTAATTTGTTTTAAAGCATAATAATTTGGTCTCTTCTCATAAATGGAATTTAAA TATTTCTGTAGTCTTGAGGTT[C/J]ATCAITATGAGTAGTGCAAGGTG
WI-6824	112	A G ---		---	CGGTTTGTCTACACTTAATGGTTTTTTTAAAGGATTTTTTTCAGGCTTTGTCAGCAACATCAA ACAAAAGGTACTGAGTACTCCACAGGTACAGAGTGCTGCCAA[A/G]CACCTTTAGAAAAATTACAT GACACGGAGAAAATGCGCTCTTGCTTGAAGAGCTTACAGCTAGGGATTTGACAACTCACAGT CTTAGGAACTGGGCAAGTAAGGCAAAATCTTCATCCCTAGAGCTATTGTG
WI-6889	139	T C AATTC	GAAAAATGAG ATGCAGTTAA	TCACTTTGTGG CTTTTAATTAT TCT	GTACAAAAAAGCTGAGAAGAGCCCAACATGGAAGTGTCAGAAACATTTCTGATAGGTACGGACAA AAGAGCTCCTTCAATCAAAAGGAGTTACATATTAGTTCTCACCATGCTAGAAAAATGAGATGCAGTTA AAATTCT[C/J]AGAATAATTAAAGCCACAAAGTGAAGTAACTGTTGTTCTGGGGCCCTATGTTGTAGATT CTCT
WI-6911	216	T C ---		---	TCCCCAGCTCATATTTATTTGGCACAGAGTGGGCACTCAAAATATCTGATGAACITTGATGAACGTAA AAGAGGTCTCCTTAAACAAGATATCATCTCCGGAAGAGAGAGTCCCAACCATATATAAATGTATGAT CAAGTCCCAAGAAACTTGGCTTCCCAAGGAATGTTTCTAAATTTGGTTTCAAAAGCACACTGGTTCC CACITTTACCACCTT[C/J]CATGACATTGGACAATAGTACTACTCTTTTCTAC
WI-9413	112	G C ---		---	GCCAGTCTCTAGTAAGTCTCTAGGGACATGACAGACCAGAGCCCTGTTCTATATGAAGACAAAC AGGTGGCCATACCTTGGGTGGAGGATACCGCTGCTATTTCCAGATG[C/J]AAGATTTGGTGAAGGAG ACCATGACAGATGACAAACGGAACAGTTTCTCAAAACAGAGGTATGA
WI-9557	74	C T ---		---	AAAAGCTTTAAAAAAGGTGGTGTCTATCTTTAGAAACACTTTTACGAAGATCAAGTAGCCCCAGCT ACAGCCT[C/J]GGTGCACTTAACCCCTCTCCTTTT

WI-9617	37	G T ---				TGCTCTTTTATTTACAGTTTCAACAACACACGCCGTG/GTJGGCACAGTCTACCAAAGTGCCCGCAG CGCCACGCTTGGCCGGAAGGCTCATCTGTTGCTCTATGGACTGATTGAATTTGGGATGGCCAG CTOCAGAATGTTCCACGTGGGGCACTCTGTGGGCAGAGAGGCTGAGCCCTTGCCACACTGGCACCA AAGAGGTTGCACGATGAGCTTGCAGTGGTCCAAAGCGGGTGTGCTGTG
WI-9657	121	T G ---				AATGCTGGAGAAACATCAACATTGAGTTGACATTTGTTTGTCTGAAGTATAGCTACCATCCACTAT CATGAATTTTGTTCATTACAAATGATAGAAAGCCAGATTCTCAAAATAAAGT/GJATAATTCCTT TGTTAAATAAATGTTTATAAATGTTTATGAAGCTCATTAACATTATCTTTTAAAAAAGTAAAAA TTTTAGAACATATGACGCTTTTCATAATTAATGCTTTTGTATATAGATTGAGG
WI-13119b	114	G C GCTGGGA			AAAAATTAAAC CAGGTGTGGTG T	CAGGGTCTGCTCTGCTCCAGGCTAGAGTGAGGTGACACAATCAAGACTCACAGTAGCCTCAACCT CCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTG/CJACACCACACACCTGGTTAA TTTTTTAAATTTTGTAAAGATAGGGTCTCACTATGTTGCCCGTCTCAAAAAACAACCAACTAAC CAGGGTCTGCTCTGCTCTCCAGGCTAGAGTGAGGTGACACAATCAAGACT/CJGJACAGTAGCCTCA ACCTCCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTGACACCACACCTGGTTA ATTTTTTAATTTTGTAAAGATAGGGTCTCACTATGTTGCCCGTCTCAAAAAACAACCAACTAA C
WI-13119a	51	C G ---				ACAGGAATCTGAAAGTTACCAAGGCAATTTCCCTTTTAGGATCATAAAGACTACAGACTTAAGCTT TTTT/CJCTTTTCCATATAATACACAAAATTTCTAAATATCCTTAAAAAGAAAAATATAAATAGT TTCAGTATGTTATGTAGAGTCACATACCTATGTCGCAAAAATATTTTATTAATTGAGGGAATAGGCCAAT TT
WI-13112	71	C T AGCTTTT			TTAGAAATTTT GTGATTATAT GGAAAAAG	TGTTAACATTTTATTGGTACGTGCTCTCAGTACAA/CJAJAACAGCATCAGTAGTGACACTTTGAT AAAAAGGAATTTTAGCTTAGTAAAAAGAAAGCCCAAGGTCAGAAGTATAATGAATATGTACAT CTTTATGGAAGTGTGTTGTGTGACCATCTTATCTCCCTGTGGATGAGATGTGCACACACAAGT AAA
WI-12988	36	C A CTCAGTACAA			CAAAGTGACAA CTACTGATGCT GTTT	TGCTATTCATGACAGACACGTGAGACAAATATCTTATTTTACAGATGGAATAGACCCAGACATTA TTCAGTACTTTAACCACTAATAGTGAACCCCTGAGACTTTA/GJAJATCTGCAAAAGGGTTTAAATAT GCAAAATACACATATATTTCCATTTTAAACACCATAATTAAGTTTCCATTTCTTAATAGAAAAATGA TAAAAATGTTTTCCCAATAT
WI-13020a	108	G A CTTT			CATTATTAAC CCCTTGCAGA	TGTATAAAAAATCCAACTGTTCCACAAGTACATATGTCCTATGATTTTATGCATACATCCATATAC ATATATCAAGGTAAAGTCCAA/GJTACAAAAAACAGCATTTCCCTATGGCCAGTGTCTACAGAAGT AAGACTGTGCAAACTTTATCGTATAGTCAAAATGAGATTGCACACTAAGGCAGGATGAGGCAGAAAGCA AGTTGTGTC
WI-12837	87	A G AAAGTCCA			GCCATAGGAA ATATCAAGGT ATGCTGTTTT	

L42611b	50 G C ---			GTCTCAGGCCCTCTCTGGCTGCAGAGCCGTCTTCTCAGGTTGCCTGTCGTCGTCCTGCGCTCTAG TCCTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCTCACTTCTCTCTGCTATACCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTTACATCATATGTTATTCACCA CTGGAGCTTCACCTTTGTTAC
L42611	34 T C ---			GTCTCAGGCCCTCTCTGGCTGCAGAGCCGTCTTCTCAGGTTGCCTGTCGTCCTGCGCTCTAG TCCTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCTCACTTCTCTCTGCTATACCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTTACATCATATGTTATTCACCA CTGGAGCTTCACCTTTGTTAC
WI-1172b	179 C T A	TGAAGAAATG GCTGATACCA	ATGTGCATTTT TCACTGCAG	TGAACGTGTGGTTAAACTAGGCAATTGGTTAAAAATCAATTTAAAAACAGGCCCTAGAAAAACAGTG ACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAATACCATTTTCTGCTTTC AAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAG[C/T]CTGCAGTGAAAAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1172a	17 C A ---			TGAACGTGTGGTTAAAC[C/A]TAGGCAATTGGTTAAAAATCAATTTAAAAACAGGCCCTAGAAAA GTGACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAATACCATTTTCTGCT TTCAAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAGCCTGCAGTGAAAAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1177	35 G C A	GCAGATTGGA AGTGTGAAAA	CACCTACATTT CTGAATATTTA GACTCTTT	AGAGGCAGATTGGAAGTGTGAAAAATGAAAGAA[C/G]AAGAAAAAGAGTCTAAATATTTCAG AAATGTAAGTGTGCTGCCCTCAACTGTTCTTTACCCCACTTAATTTCTGCAATTTTGAAGAACTAGATTGAAT TCCTTTGCAAAACCCCTTGCCATCATGGATACCCGAGTTAAACCCGTTAATTAAGAGACATTAAACATGG CCTGGTG
WI-1231b	141 G A ---			TCCATGGTTTGGTTGCTACTGACTTGTAGCCTTACTGCCCACTATGCATTGGAACATTCCCATATTC CAACTAAGCAGGAGTGTTCACAATAAACAACATAGGCTCTTTATTCCTCTCTTTCATTAAATTTCTT TCAC[G/A]TTATTCCCTCACCCCTGAACGCCCTTCTTCTCGTAGTGACATTTTAAAAATCCACCTTAC ACATTGGGACC
WI-1231a	126 T C A	GGCTCTTTAT CTCCTTCTTTC	CGTTCAGGGTG AGGGAATAA	TCCATGGTTTGGTTGCTACTGACTTGTAGCCTTACTGCCCACTATGCATTGGAACATTCCCATATTC CAACTAAGCAGGAGTGTTCACAATAAACAACATAGGCTCTTTATTCCTCTCTTTCATTAAATTTT CTTTCACGTTATCCCTCACCCCTGAACGCCCTTCTTCTCGTAGTGACATTTTAAAAATCCACCTTACA CATTCGGACC
WI-472	114 G C ACAGAAAAG	ACATACATAT CCATTATACA	GACCTTTCTTT TCCAGGOC	GAAGGCAGGACTGTGTTTGGAGGACAAAAGTAAATCTTTTATATCTTTTATTTTAAATTTTATT TTTTTTCAGGCATATAGACATACATATCCATTATACAACAGAAAAAG[C/G]GGGCTGAAAAAGAAAG GTCAAGTGAGATTTCAGATATCTTAAATGCAAGGCTGACAAATTTGGGCTTGATT



WI-478	46 C T	GCATGCTGTG T TACTCTATTT TGTTCT	AAATGCCACAG GTGGCT	AAACCACTGCAACCTTCAAGCATGTCTGTGTACTCTATTTTGTTC[CT]AGCCACCTGTGGCATTTC CAAAATATGATAATCTCTGCCACCATACTGCTTTAAACACAAATAGAATCTGGCAGCAAAATATAGC ATAAGCTTACTTCTAAATCAAAGGCTACCATCAGTACCTTAGCACATTTAAAAAATAAAAAACCAAC ACTGCCCA
WI-533	29 T C	ATCACAGCAG AGTACCTTTCT AACT	CCITCGAACCT CTACACAATCT T	AGCCATCACAGCAGAGTACCTTTCTAACT[CT]ATAAGATTGTGTAGAGGTTGGAAGGAGGACAGGA CTGTTCTGTTGGIATATATGACCCTGTGTCCAGTTAATCCA
WI-601b	112 T A	---	---	TCACCTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGAAATGATCAATTTCAAATAAAGATGG TAGTGAGGCGAACAGAGAGGTTTCAATTGACTCTAACTGAGTAC[CT]A/CAAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-601a	74 C T	---	---	TCACCTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGAAATGATCAATTTCAAATAAAGATGG TAGTGAG[CT]GAACAGAGAGGTTTCAATTGACTCTAACTGAGTACTCAAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-863	107 A G	CTCCTTCACAA CCTCACCA	CTCCCGGTAA GCCAAGT	AACAAAAACAGACACCCCTGGCTTCTCTCACCCAGTCCACATGGTGCCAAACATCCACATTCCCT ACATCCTCCCACTGGGCTGCCCTTTCACAACTCACA[CT]A/AGIACCTGGCTTACCGGGAAGCATAAA GCCAAAGCATTTAGTCTTTTATGCAACATGGTCTGGCTGCAATAC
WI-919	36 G A C	ACTGCTTGCTT GTTGATTTAAT	TTATCTAATC CCACATGACAG C	ACTCACTGCTGCTGTTGATTTAATCAACCTAGCC[CT]A/GCTGTCATGTGGGATTAGAATAAAATA AACACAAAAATGAAAAACACACGATTGCTAACAAAGCAGATTCTTTTCAAGGCACACACGTAAAGAT ATAACTTCAA
WI-991	37 A T	---	---	TGCATTCATTATGCACCAATAATAACTTCTGTACAT[CT]CATTATTGTTTTCATTATCACAAAAAT TATGAGTGAGGGATGATTGTTATCCCTATTTTACAGATGAGAACACTGAGACTTAGAAGAAAGTATCT TTCCCAAAGTCACAAAGTTAGTGACAGAGCCGGGATTCGAATCCATCAACTTGAATCCAGAGAAAAAT GTTCTGCATCACTGTACAACACTGACTCTCTTTTCTCCTTTGAAAAACAAGGC
WI-1011	70 G C C A	CAGTATCTGA AGTTTTGCTCT CCA	AGGAACACCTA CAAAATGACTT CT	CTTCTGACCTGTTTGCAGTGGATCTGTTTGAAGGCTCTGCTCAGTATCTGAAGTTTGTCTCC A[CT]GAGAAAGTCAATTTGTAGGTGTTCTCTGGGCTTTTGTCTAGCTTTCCATTTTCTTAATACACTGC CGTCTTAAGGGAGGCTTGCAGAGCATTTATCAGATGGCTGTTTGTGCTGCACTTCTGTGCACTGAAG
WI-5381	178 A T	---	---	TTCATGCAGAGGTCCATGAGTTTACAGAACTCAAGGAAGAAAGGCCCTAGAGATGACACCAGAA ATGAGAGTGGCTTGTCTCATGAAATTTGGACAGCATGTTCCAAAGCAGAGGGAACAGCATGGAGAAGA AAAAATCATCTCTATCCACGTGCAGAACTGGCAATTAGTTTGT[CT]A/TTTACTAAAAACACAAATGT TTAACTTGGGGTCCACAAACAAAGGATATGTTGGCAATGGTATTTCTGIGATG
WI-5791b	76 G A	---	---	CTATGTTATCCATCTAGCAAAAGCAAGACTATTTGGATAAGTTTCAAAAGATGAGAACAGGTCCTA GAACCTCAG[CT]ATCGAAAGGAAAGTTTCACTAGTCCATAGACCCCTATCTCACTGACCCCAAAAGGTA AAAAATAAAATAAAGTAAAGAACTTACATCAGATTGTGCACTTTCTTATTTTGCCACCCTGTTTGT TAGGAA

WI-5791a	44	C G ---			CTATGTATTCCATCTAGCAAAAGCAAGACTATTGGATAAGTTTC/G/ACAAAGATGAGAACAGGTC CTAGAACTCAGGATCGAAAGGAAGTTTCATCTAGTCCATAGACCCCTATCTCACTGACCCAAAAGGTA AAAAATAAAATAAAGTAAGAACTTACATCAGATTGTGCATTTCTTATTTTGCCACCCCTGTTGT TAGGAA
WI-5406c	120	C T ---			CACCTGCTGTTGTCCATGGTGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC/C/TTATGAGCCAC ACTTCTCATTTCCTTAGAAATTTCTTGACTCTGTGAAGAGGAAGGAAAGGAAAAAGAGAGGCAA GG
WI-5406b	118	C A A	CCAGGATGTC AAGGTGAGAA	AATGAGAAGT GTGGGCTCAT	CACCTGCTGTTGTCCATGGTGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC/C/TTATGAGCCAC ACTTCTCATTTCCTTAGAAATTTCTTGACTCTGTGAAGAGGAAGGAAAGGAAAAAGAGAGGCAA GG
WI-5406a	42	A G ---			CACCTGCTGTTGTCCATGGTGCCACAGACTCTTCCAGAAG/G/GCCACTTCCACAGATGCAACAG GCCCTTTGAAGGAGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCCCTATGAGCCAC ACTTCTCATTTCCTTAGAAATTTCTTGACTCTGTGAAGAGGAAGGAAAGGAAAAAGAGAGGCAA GG
WI-5798	48	G C T G	TTATTCCTCC TTGTTTCCTT	ACTGTTAGAAA ACCAGTATTTT TCAAT	CCATTCCTCTCTCCCTCTCCCTTTATTCCTCCCTGTTTCTTTTG/G/C/JATTGAAAAATACTGGTT TTCTAACAGTGTGCTGGTATGGATCTATGTTATAACATGCATAGTTCTATATGGGTATCA
WI-5415	54	T A TTT	TCATCTTTTCAG TTT	GGACTAATTCA TGATCCGATCT	CCTGCTAATAATAATTAAGCAGGATTTGCTTCATGAATTCATCTTTCAGTTT/A/JTAGATCGGAT CATGAATTAGTCCAGGCTTTAGTTGTAATCGAAATTGGA
WI-5437	41	C T G	TCCAGAGAA AAATCCAAAG	AGTTTCTAAAC ACAAAATATG GTTTAAG	TGTTTTAACCCAGGCAGACCTCCAGAGAGAAAAATCCAAAGAG/C/TJCTTAAACCATATTTTGTGTTTA GAAACTCCTGTGCGCAACCACTCTTGATGTGAGTGAC
WI-5481b	131	A G CTGCACTG	TGTCATTTATG CTGCACTG	TTACTCCAGG CTCCAAGTATT	AAGCCAAATTCACATTAGTTGATGAATTTG/A/JAATTTTACAGTATCTAATGCATGGGCATCTGTTTC TCTGTTTTTCAAGAGGTAGTATATGCTGAAAAATCTATTTGTCAATTTATGCTGCAGTCG/A/GJA ATACTGGAGCCTGGAAGTAAAGACTTGGCTATTTTCAACAATTA
WI-5481a	29	G A AATTT	CCAAATTCAG ATTAGTTGATG	CCCATGCATTA GATACTGTAAA ATT	AAGCCAAATTCACATTAGTTGATGAATTTG/A/JAATTTTACAGTATCTAATGCATGGGCATCTGTTTC AACTCTCTGTTTTTCAAGAGGTAGTATATGCTGAAAAATCTATTTGTCAATTTATGCTGCAGTCGAA ATACTGGAGCCTGGAAGTAAAGACTTGGCTATTTTCAACAATTA
WI-5492	38	T C ---			TCATGAGTCTTTCTTCAAGATGCTTGTAAAGTCCCA/T/CJCAAGAAAGGATCCCATGGCCTAAT GAAGATGTACCTCCACCTTAGGATAATTTGCAGACCAA

WI-5826	134	T C	---	---	TATTTTTTTTTCTCAATTCCTGGAGCACACCATGCTCTTTCTATTTTCATGCTTCACATTTATTTTTT TTTCACCTAGTTAAATGCTTTTCCCTTGATCTAGCAATGGCCAGTTTATACATATTCTTTAGT[C] TTTCAAAATTAATGCCACCATAGAAATAATTTTCTAACCAACGAGCCAAACAGCCTCACTCTTCCTT CCTTGGTGCAATTACTCTTTACAC
WI-5546	40	C T A	CCCAATACITTT TTCAGGTGAA	CCTGTATTTTA GCAAAACATGGG	CCTTATAACCCCAATACITTTTTCAGGTGAAAAAGGGAAAA[C]TACCCATGTTTGCTAAAAATACAGG AGTATAACAGCATGACATGTTAAAGGGAATTACAAATGCTTGAGTGTAATTCGTATGTGGGAAATAT TAGAAATTAAGCGAGAGAGGCA
WI-5552	97	C T	GGCACCAGCCT TTTTAGAGT	TGCACAAATTG CCCAGG	TGTTTGTCTGCACCTCCCAACAAGTGGTCAATGAGCCTCAAGGGTTTGTATTGAGCGGTATGGGT GGGGCTATCGGCACCAAGCCTTTTAGAGT[C]TCTGGGCAATTTGTGCACTAGTGTGAGA
WI-5836b	161	C T	---	---	TAA GTTGA TTTAAACACTCTGTGCCTCAATTTCTCACCTATAAAATAAGATAATAGTATCTAAAA AAAAAGAGAGAGAA TTAAGTGGATAGACATGAATAACTCTGATGATACTGGTTGTATCCCTGAA TCCTGCAATATACACATGATCAATGAT[C]TJCCA TTTTGA AAAATTAAGCTTTTGAATGTTTTCCTCA ATG
WI-5573	58	C T	GTTCAATAGG AGGTGGGA	TGAACAGTTGG AGAGTAATGTG TC	TCGGGTATTAGGATGCGTTACCCCTCGATGATGCGGTTCATAAGGAGGTGGGA[C]TJGACAC ATTACTCTCCAACGTTCATCAGAACACTTCAACAGCG
WI-5850b	134	G A	---	---	CAGGACCTTGGAGCCTTTGCTGTTTGCTTCCACCCCTCACTCTTTCTCTGCTGCCCATGGGTGGAGC CTCTCTCAGGCTTCTCTATGCAACGCGTCTATCTCTATATGGGCAATATCCAATGTCCCATTC[G/A] TTTTGCCATTTCTGTATATCAACAGAGAGAGGAGGGTGG
WI-5850a	92	C T	---	---	CAGGACCTTGGAGCCTTTGCTGTTTGCTTCCACCCCTCACTCTTTCTCTGCTGCCCATGGGTGGAGC CTCTCTCAGGCTTCTCTATGCA[C]TJGCGTCTATCTCTATATGGGCAATATCCAATGTCCCATTCG TTTTGCCATTTCTGTATATCAACAGAGAGAGGAGGGTGG
WI-5612b	125	A T	CTATTAATGA GCATCGTGTCA TTC	TTCTCTTGAGA AACCTAAAAC ACTG	TGCTGTATTGACACATAGTTATCTGACAGTAATCATCTAACATCTAACATCAAAATATCTTTCTGCCTG TCACACTAATTTGCAAGCATTCATTAATTGACTATTAAATGAGCATCGTGTCAAT[C]A/TJGAGTGT TTAGGTTTCTCAAGAGAAATATGCTGTTCTTCTCTGTAACCTCAAGTA
WI-5612a	44	T A	---	---	TGCTGTATTGACACATAGTTATCTGACAGTAATCATCTAACATCTAACATCAAAATATCTTTCTGCTG CTGTACACTAATTTGCAAGCATTCATTAATTGACTATTAAATGAGCATCGTGTCAATTCACAGTGT TTAGGTTTCTCAAGAGAAATATGCTGTTCTTCTCTGTAACCTCAAGTA
WI-5636	26	A C	GCCAAATTTTAT CCGCAATAAA	CATCGAGGACT TTGGGAA	TGAGAGCCAAATTTTATCCGCAATAAA[C]TJTTCCCAAGTCTCGATGGAGGCAATTCAGAAATCGGG GCAGGGGAGGCAGAGGTGAGACAGATGTGAAGAAC

WI-5865c	103 C G ---	---	---	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTTAAGAATCTTTTTTCAATTTATGCATTC ACTGACTCACTCACTGCTCTATCAAAAATTTAAAC[G]AAATATTAAATTTTATTTACAGAGGAA CTCAGAAAGCCAGAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCTTCA GAGAAGACAGACAACATAAATAATTCACAG
WI-5865b	99 T A ---	---	---	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTTAAGAATCTTTTTTCAATTTATGCATTC ACTGACTCACTCACTGCTCTATCAAAAATTTAAACAAATATTAAATTTTATTTACAGAGGAA CTCAGAAAGCCAGAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCTTCA GAGAAGACAGACAACATAAATAATTCACAG
WI-5865	165 T A ---	---	---	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTTAAGAATCTTTTTTCAATTTATGCATTC ACTGACTCACTCACTGCTCTATCAAAAATTTAAACAAATATTAAATTTTATTTACAGAGGAACTC AGAAAGCCAGAAAAATGACCAAGACACAGTTAAACAGTCTCCATCTTCAAAAGGTCACAGTCTTCC AGAGAAGACAGACAACATAAATAATTCACAG
WI-5874	76 T G ACAGAAAA	CATAGCATGG ATAATATTAT	CCTAGTAAGTT TCAGTCATTTG ATATGT	CTCAGACATTCATTTTCATTAGTTGTTAAATTTTGTGTTATTTCAAGCATGGATAATATTACAGAA AAAAAATTTTGTACATATCAAAATGACTGAAACCTTACTAGGTAGCAATTTGTTTGTCAATTTGCT CATGGAGCCGACGTTGAGCCTCTCAGTTTTCATC[A]TTTTTTCATAATTTACTCTCTTTTCTGTC ACAAATGTTCTGCTTCTGTTTCAACTCTCATTGCTGATTGGATGGTAGTCATAAAATATGGGTGATTC AGAAAAATAAGTAAATG
WI-5752	36 A T TTTTCCATC	CAGCCTCTCAG AGAGTAAAT	GACAGAAAAAG AGAGTAAAT	TTAGCAGAAACAACAAAAATGTCACAACACTGCAGTAAAGAGTGTTCCTCCGATAAATA[G]GJC CATTAGGTATTAGATAAGCATCCCATAAACATTTGTTGAAAAACGAGCCGAGTTTCGATTACACACA GTTGCTGTTTAAACCTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCGTCCACGAAA CATTGTTGAAAAACGAGCCACGTTTCCGATTACACAGTTAGTTGCTGTT
WI-5760b	61 C G ---	---	---	TTAGCAGAAACAACAAAAATGTCACAACACTGCAGTAAAGAGTGTTCCTCCGATAAATAACCCAT TAGGTATTAGATAAGCATCCCATAAACATTTGTTGAAAAACGAGCCGAGTTTCGATTACACAGTT GTTGTTTAAACCTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCG[G]ATCCCCACGAA ACATTGTTGAAAAACGAGCCACGTTTCCGATTACACAGTTAGTTGCTGTT
WI-5760	187 G A ---	---	---	TTAGCAGAAACAACAAAAATGTCACAACACTGCAGTAAAGAGTGTTCCTCCGATAAATAACCCAT TAGGTATTAGATAAGCATCCCATAAACATTTGTTGAAAAACGAGCCGAGTTTCGATTACACAGTT GTTGTTTAAACCTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCG[G]ATCCCCACGAA ACATTGTTGAAAAACGAGCCACGTTTCCGATTACACAGTTAGTTGCTGTT
WI-5944	52 A G GGAATCTTG	TTCTCACCATG AACCTTGA	GGGTGGGATCT AACTTGA	AATATCTGGCCTTTTCTCTTAGGAGGAGATTTCTCACCATGGGAATCTTG[A]GTGCAAGTTAGAT CCCCCTCACTATTGAGAAGCTAAAGGTAAAGACTACTCATTCTCAGTCTTCTGCTG
WI-5967b	148 C T ---	---	---	GAGTTTAATGAATCCTGTTCCCTCTCTAAAAACCTCCTGTTCCCCAACCTCAGATTCAGCAGATATT CTTTCATGGGTTATTTGGCCAAAGTCATGAGGAGATGATGTAATTTGATCATTTCAAGAGTGTGAG TAATGCTTGGTA[C]TTTGTCTGTGCCGTATCTGCTCCAAATCACCATTCCACTTTATTTCTTATTAT GCTGAATGAAACGGTTATATTACAG

WI-5967	165	C T ---		---	GAGTTAATGAATCCTGTTCCCTCCTCTAAACCTCCTGTTCCCCCACTTCACATTACAGCAGATATT CTTTCATGGGTTATTTGCCCAAGTCATGAGGAGATGCATGTAATTGTGATCATTTCAAGAGTGTGAG TAATGCTTGGTACTTGTCTGTGCGGTATC/TGTGCTCAATCACCCATCCACTTTATTTCCCTATTAT GCTGAATGAACGGTTATATTACAG
WI-6093	53	G C ---		---	GGTAAAGTCCAGAGCCACAGGTGAACCTGCGCGTATTGAAGTCTTTGGGCCA/GC/GTCTGTAATG ATCTGACTTCTCCAGAACCCCTCTCTCTGGAAGTCCAACTGTGCACCTGAGCCCATTTGTAGGGA GCATTGAACCAAAACCCAGCGACACTGCTGACATTTGACITTCAGCAACCTTGTATTGACGGTGAC ACACCATGCTTCGAGAAGGAATGAGG
WI-6141	80	T C AGGTACTT	CTTCTTAATTA AGCATCTACA	TGAAAACCCCA GAACAGTG	GACTCTGTCTCAAGAAAAAAATTTGAAATTTGAATAATTATTAGCACITTCCTTAATTAAAGCAT CTACAAGGTACTTAT/CJCACTGTTCTGGGGTTTCAATCCTCTTCACCTTTTAGACTTCAGGAAAT CAGAAAAATGCATGAAACAGGATTGTTACATGCAGAGAAATAGGGGAGATAAAAATTTGTCTTTT CTC
WI-6450	45	T G TGCACA	CCAATGACTT ATTCTATATCT	TTGTTTGAAT GTGTGGTACTT CT	ATAGGACAGTTTTTCTCCAAATGACTTATTCTATATCTTGTCAAT/GIAGAAGTACCACACATTTCA AACAAAGCCAGGCTATGCCAGGGTGGGATTTTTCACGGTCATGTAATATGCATGTAAGACTA TTTTACTGGCCTTCTTTTATGCATAAAACAAGGATTGGTCTATTCAACAACATGTGTCAATACAG CAGTTGTCATGTCCTCTGGTACTAGAATATAGTCTTTATAGAATATGTGTTTAGAATAAAGCCACA AATTATTCTATAAACCAACA/CJTAAGGAACGAGGCTCAAAAGTGAACAAAAACGGCCTTAGTTTC TAAGTGAAGACTAAGACGATATAGGAAATATAATCCGTGACCTCTTA
WI-6461	88	C T ---		---	GAACTATCCTTTAGTGGTCCACATTTTCTATTTCTGATTCCTTTGGTCACACAGGACTTTCTGGCT ATGAAATAGTC/TJATTCAGTGAACACTAGTTATCATAAAGACATGCAAAACCTTTTCACAGTCTT CCTGG/GJAATATCTCACAAAATTAATTATAAATGGCATGCGACTTTCTGATTTAGCCTGACAGG ATTGTTCCCTT
WI-7466c	141	G A TTTGTCCTGG	TTTTCACAGTC	AGTCGCATGOC AATTTATAATT	GAACTATCCTTTAGTGGTCCACATTTTCTATTTCTGATTCCTTTGGTCACACAGGACTTTCTGGCT ATGAAATAGTC/TJATTCAGTGAACACTAGTTATCATAAAGACATGCAAAACCTTTTCACAGTCTT TGTCCTGGGAATATCTCACAAAATTAATTATAAATGGCATGCGACTTTCTGATTTAGCCTGACAGGA TTGTTCCCTT
WI-7466b	80	T C GTC	GACTTCTGGG CTATGAAATA	ACTGAA	TGCTTTTAAAAATAACAATGACCACCACCTGACACCATAGTGTCTCTCCATTTGCCACGTCCTCTC AGTAGAATAAGACAGGACTTTGCTGGCTGCTATCT/CJATTCCTCAGAAAGGACACTTTGGCCCT CATAGGCATTCCATAGATATTTGTTGAATGAATGTGCTTTTGCATATTGATTCCTACATTTGATACA TTCTCAGGAGGGACATTTGGCCTAT
WI-9814	104	C A ---		---	CCTCTAACAGAAAACTTGACTTCTCTCAACTCAAAAAACCTTCTCTAATAATTTT/GIAGTAACCA AAATATTCCTTCAAATAAATAATCTCTTTAATTAGAAGAAGCAACAGTGTAGAGGTAGTACATTCA CCAAC
WI-9720b	55	A G ---		---	

WI-9720a	47 A G ---	---	---	CCCTAACAGAAACTTGACCTTCCCTCAACTCAAAATACCCCTTCTCT[AG]ATAATTTAAGTAACCA AAATATCCCTTCAATAAATAATCTTTTAATTAGAAGAAGCAACAGTGTAGAGGTAGTACATTCA CAACC
WI-9825	123 A T ---	---	---	CACGCTTAAGGCAGGATGGCTTATGAGATACCTTTCATTTGCTGTGTCACACCTTGAATCTGCC TGCTGGCTCCCTTACTTTACCTCTCTGTCATGTGCAGATGAAGGCTCAGGGTCT[AT]GAGGATTAG TAAGATCTCTTTCTAAAGACAGGAGAGATTATTTACAAGAAGAACTACCAGGGTTAGTTTGCAAT TAAGAAATGCCAGCTTTTGTCTGTCATCATCTTTGAACATTATCCACATG
WI-9748	74 C G ---	---	---	CCACTCAGTAATCAATTTGTAGCACCTTATTTCTAAAGATTTCTAAATTTTATATGTTTACCCCTT GTCATT[C/G]TCAGACCAAGTACATGTTTTCACACAGCCATCTTCTTTCTCTGGAATCTTTTCAGAA TACAGTTATGATGCTCTTTTATATCCCA
WI-9943	91 T C ---	---	---	TGAGGCTATGATTCAGATTTGTAGTGAATACTTATTAGCAATTTCAATGTTGTGGCACTGTT CGTTGTGTTTATATCCATCTTC[C/AT]TTTAAATTTCTACTGAGCAGAAAAAATAATGTATACATT AACCTTTGCTCCCTATTTGTACCTTTTAAATATGCAATTCACACCTTCTCTTTTGTCTATTAGGA
WI-9891	39 T C ---	---	---	AGGGCCCTTACAGATCCGTCAGCTCAACACTGCGCTCTT[C/AGT]GAGCCTGTGAACCCCAAGAC GGCTGGTCATCAGTGTCACTCTCTCTTTCCGGACAACATCTTTTAAAGAAAAAAGAGTGT CTTTGAATGTATCCATTTATCCCAAAATAATCTTGTTTAAATAATCTTTATAGGCCAAATCCCAAT GTGCTGAAATATCTGCCAAGCATGTCATTTCTACACAAAAAGGATTTGCAAA
WI-9897b	84 C T ---	---	---	CTCAGAATTATTCAGATCTTCCCAATGTATGATCTTGTCTCAACATCTCTTTTTCCTCAAAC ATTTATCTAGCCTGTAT[C/AGT]CATCCAGTGAGGCTGTTTATTCATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9897a	83 A T ---	---	---	CTCAGAATTATTCAGATCTTCCCAATGTATGATCTTGTCTCAACATCTCTTTTTCCTCAAAC ATTTATCTAGCCTGTAT[C/AGT]CATCCAGTGAGGCTGTTTATTCATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9935b	115 C A ---	---	---	AGATAACCCCTGAAAACTAGAAGAAATTAATAACGTGTGTCACACCTCACCAGAACTGGAAGGAGT CTGACTGTGTTCTTATGGGTGCTTGGACTGGCAGGGGAGTTTCAGACA[C/A]AGCCCAAGAAAAAGCC TGATATTAAAGAGGCACITGCATTAA
WI-9935a	42 C T ---	---	---	AGATAACCCCTGAAAACTAGAAGAAATTAATAACGTGTGTCACACCTCACCAGAACTGGAAGG AGTCTGACTGTGTTCTTATGGGTGCTTGGACTGGCAGGGGAGTTTCAGACACAGCCCAAGAAAAAGCC TGATATTAAAGAGGCACITGCATTAA
WI-9983	146 C T ---	---	---	CCTGTTAGGTGCCAGAGTCCATGCTCTTGGCCACAATGTTAGGCTGCTCCCATTTCTTGTCTTGA TCCCCAAACCCCAAGGTTCTACCCCAATCTGATCAATGCTGACTAGGTCATGGCTGGTCAGGGTAA AGCATTATGA[C/T]AGACACAAAGACAAAGAGGTTAAAGTTGCTGCTCAAGAGAGAGACATAA AAACAAATGGATCTGGAACTAAGTAAGGCTTCGAGGAGGAGGTGAGCAAGG

WI-10019	139	A T A T C T	T G A T G T A A T G C T A T G T A G C A A	T T G A T T A C T G T G C T T A G G G G A	A T A T C A G T G G G T T G A G T A T A C A G C A A T C T A T T T G T T A T T A T T G T G C T A T A A T C A A T C A A T G T T C T A A C A T T C A A A T A G A T C T T T T G C T C T G C T C A G A T G C T T C A A T G A T G A T A T G C T A T G T A G C A A A T C T A T A T T C C C C T A A G C A C A G T A A T C A A G G C C T T C T A C C C C A
WI-10020b	122	T A T T T	G C G A G A A A A G A A A T C A T G A C	G A C T G T T A A T T T A T T T A A T C A T T A G T C T G G	T T T A C T T C A T T G T C A T C T T G A C T C G T A T T A A A T A A T A A T A T T A A C T G G C T G A A A A G A A T T T A G G C A T G C A T A G A G A A T A G C A G T G T T T A T T G C G A G A A A A G A A A T C A T G A C T T T T T A J A A A A A T A C C A G A C T A A T G A T T A A A T A A A T T A A C A G T C C T A G G T T C C G A A G T G G C C T A A A G C A C G T A G T A G C C C T C C T T A G A
WI-10020a	39	T C A T A A A T T	T G T C A T C T T G A C T C G T A T T A A	A A A T T C T T T T C A G A G C C A G T T A A C	T T T A C T T C A T T G T C A T C T T G A C T C G T A T T A A A T A A A T A T A T T A A C T G G C T G A A A A G A A T T T A G G C A T G C A T A G A G A A T A G C A G T G T T T A T T G C G A G A A A A G A A A T C A T G A C T T T T T A A A A A T A C C A G A C T A A T G A T T A A A T A A A T T A A C A G T C C T A G G T T C C G A A G T G G C C T A A A G C A C G T A G T A G C C C T C C T T A G A
WI-10084b	170	T T T A C A T G	C C T T T A G A T A T A T T G T G A T T G T	A C C T T T C T G A A G C C A G A T T T C	T C T G A G T C T T T C T G A C A C A C T T G C C A T G T C A A G G T A G C A G G A T C A G G G A A G G C A T T A T A A T A A A T A T A A T T T G C A G A G A C A T C T C T C T A T G C A C C A G A T A T T G T G T G A C A C T C T G T T T A T C C A G T A T C C C T A C T C C T T T A G A T A T A T T G T G A T T G T T T A C A T G C T G A A A T C T G G C T T C A G A A A G G T A G G T G T T T
WI-10084a	54	C A G G G A A G G	G T A G C A G G A T C A G G G A A G G	G A G A T G C T C T G C A A A T T A T A T T T A T T A T	T C T G A G T C T T T C T G A C A C A C T T G C C A T G T C A A G G T A G C A G G A T C A G G G A A G G C A J A T T A T A A T A A A T A A A T T G C A G A G C A T C T C T C C T A T G C A C C A G A T A T T G T G T G A C A C T C T G T T T A T C C A G T A T C C C T A C T C C T T A G A T A T A T T G T G A T T G T T T A C A T G C G A A A T C T G G C T T C A G A A A G G T A G G T G T T T
WI-10289	29	T C A A A C T C T T	T C T C C T G T C C C C A A A C T C T T	A T T C T T G T T G T A T T G A A T G G A A T T A A	C C A G G G A T T C C C T G T C C C C A A A C T C T A T A T T A A T T C C A T T C A A T A C A C A A G A A T T T A T A G A A T A T G C A C C A C A T G C C A C A A A G A C A C C C T T A T A T T A G T
WI-1319	40	A T A T C T T	T G G C A C T T A G A A C A T A G T T T	G C C A C A C A C C C C T A T G G T	A A G A A A A T C C T T G T G G C A C T T A G A A C A T A G T T A T T C T T T A T A C C A T A G G G T G T G G C T T A T C T T T T A C C T G G C A T G G C T T A G G T C C T G T T A T A A T T G G T A T C T T T T G C C A C A A A G A G T C T G T T C T G A C A G T C T T A T G A T C T A T T T T A A C A T T A A C A C T G G T C A G A T G I G T T A A A A C T T G T T G A A C C T G C A G C
WI-10316	104	T C C T C T T	C T G T T G A T T T T C T A C C T C T A T T	G C T T T G G A A T G T A T C C A A A A G T T T	A G C A A C G T G T A C A A C T A G T A G G G T A A A T C A G A A G C A T C T A T A T T A T T C A C C A G T C A C C A C C C T G G A C T A T A G T C T G T G A T T T C T A C C T C T A T T C T A T T A T A T T A A A C T T T T G G A T A C A T T C C A A A G C A T C A T G G T C A C T T C C A G T A T G A A A G G A T G T T A A A A G C C C A G C C
WI-2572	61	C T ...	...	...	A G T G A G T T G C A C A A T T T G G A G A C A T T C T G T A C C C C A A C T T A A A A C A C T T C T C C C A C A C T A C A A G T T A A C A C T C A G T T A C C A G G T G A T G A T T G A G C A G A

WI-10368	31 C T	TGAAGCAACC AGGCTCTGTT	CAAGATATTAT ATTTATCTCT AAGAGGGG	GAGGAACGCGCTGAAGCAACCAAGGCTTGTTC/C/TCTACCCCTCTTAGAGAAATAATATATCTT GAGATAGGGAGGAGCAGCGCTGAGGACAGTCTGGTTTGTCTACCCCACTGGAAGCAGAATATCC TTCAAAGCTTTTCCAGTGAGTCATGTTGCTGCTAAACTATATGACCCCTGATGGATTGCCCTTCAGGG T
WI-10391	32 A G	CTGCTCAGGT ATGACTCCCA	GGAGTTAGGA GTCAAGAAGTT GA	CCTCCGTTCTCTGCTCAGGTATGACTCCCA/G/TCAACTTCTTGACTCCTCACTCCCATCTCGGTG TCTGCTCCCAAGGGAGCGCATCTGACACAGCCCTTGTCTGCTGTGACAAACAGAACATTCGAGAAG TGATGCTGGGTGACCTCCAGGATA
WI-10567c	146 A C	GTTACCCAGA GTCCTCTAATA	TGCCGCTTCCA GTAGCT	AGCGATGAAATTTATATGTTATGCTGACTAGCGGGTGCTCAATAAATATTATCTTTTTCATATT TTCCAAATTAATACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAGTTACCCAGAGCTTT CTAATAGCAA/C/JAGCTACTGGAAAGCGGCAAGAAATTTAACCCCT
WI-10567b	82 A C	GGTGCTCAAT AAATATTATT	...	AGCGATGAAATTTATATGTTATGCTGACTAGCGGGTGCTCAATAAATATTATCTTTTTCATATT TTCCAAATTAATA/C/JTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAGTTACCCAGAG TCTTCTAATAGCAAAAGCTACTGGAAAGCGGCAAGAAATTTAACCCCT
WI-10567a	60 T C	CTTTT	AAATCTGTT GGTGAAATTC TAG	AGCGATGAAATTTATATGTTATGCTGACTAGCGGGTGCTCAATAAATATTATCTTTT/C/TCTCAT ATTTTCCAAATTAATACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAGTTACCCAGAGT CTTCTAATAGCAAAAGCTACTGGAAAGCGGCAAGAAATTTAACCCCT
WI-11153b	84 C G	CAAACTCAA ATTGCTTTAAG TACTTTA	AAATCCAACA GTCAAGGCTCT C	CGTTGGGAATTTTCTATCTCACCTAAATTTATGCGTGATTAATAATACATTTTAAACAACTTCAAA TTGCTTTAAGTACTTTA/C/GJGAAGACCTTGACTGTGGATTTTGGATTTTCTTTTATTTCTTAATA AAACATGCATATTTAAGTTGTCAGCAAGATGTACTTATATGTTAATATCTGATATCAGCATCCCTT TATGTAAT
WI-11153a	33 C A	GGGAATATTC TATCTCACCTA AATTATG	GCAATTTGAAG TTTGTTAAAT GTAT	CGTTGGGAATTTTCTATCTCACCTAAATTTATG/C/AJGTGATTAATAATACATTTTAAACAACTTC AAATGCTTTAAGTACTTTACGAAGACCTTGACTGTGGATTTTGGATTTTCTTTTATTTCTTAATA AAACATGCATATTTAAGTTGTCAGCAAGATGTACTTATATGTTAATATCTGATATCAGCATCCCTT TATGTAAT
WI-2616	125 T C	CACAATGTA ACAAGAAATG ATCC	CCATGGCTGTA GTCCAGT	GTTGTAAACTCCAGTATCATTTCCCTCAAACCCGCTTAAATCACAATCACTTTTCTTTCTGTA GAGCTCAAACCTCAGCTGAATGAATTTGCTGCACAAATGTACAAGAAATGATCCTAT/C/JACTGGG ACTACAGCCATGGAGAAAAGCAATGTAGTCAGCAAAATGTTAACAG
WI-11163	58 C T	CAAGTGAATT ATGACCAAAA TGAGA	TGCTCTTTCA TTTGAGGTTTT T	TGACTCAAAGGAAACACACACAAAAAGTTTCAACCAAGTGAATTTATGACCAAAATGAGA/C/TAAAT TTGTTAAAAAAAACCTCAATGAATGAAGAGACAAATATAGTTCAAGATTCAGGTTCAATATTTGT ACCTACAAATAGGGATAGTCATGTTGGCAGACTTTCTTTCTTTTCTTTTGT/GJCTCTTA GAATCCATTTTGTCTTTTGGCCAGCAATCCCTCTCCCAATATTTTAAAGGAGAGAAATTCACCTTTTCT CTGTTGGATGATCAGGTTCTGCTCTTCCCAATCCAGAGGCGAGTACTATTCACCCCATGGGGTCAT AGAGAGGATTAAACAGGGGTGATGCCCTGCAATGGGAATATTTGAAAACC
WI-10656	59 T G	...	...	



WI-11169b	154	T G T T T T	TTAACCAAGA GTTTTTCATTC	CTAACTTAAAA ATCCTCATTTCA AAATATAA	CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAATAATTTAAGCCTAAGTAGTGCTTTTAAACCAAGAGTTTTTCATTCTTTTTT TTTAAAAAAGAGCAGACAT/GJTTCATCATGTCTGATAATTTTTTATATTTTGAATGAGGATT TTTAAGTTAGCAT
WI-11169a	95	A G T T G A A A A	AATAAGTGAA AGTAACTGAC	AAACTCTTGGT TAAAAAGCAC TACTT	CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAATAATTTAAGCCTA/GJTAAGTAGTGCTTTTAAACCAAGAGTTTTTCATTCTTT TTTTTTAAAAAAGAGCAGACATTTATCATGTGTCTGATAATTTTTTATATTTTGAATGAGGAT TTTTAAGTTAGCAT
WI-10685	25	A G ---		---	CAAGTGCTGGACCTTGGATAGGTC/GJACCGGCTGAAGTTGGACAGTTGTGGTTAGGTTGGAG ACCAAAATTCAGTCATCTGTAATATAGATCTTGTCTCTTTGGGTTTACCAGTAGGGGTCACTAAAG AGAGATGGGAGACAGTCTCAATCTTGCTAAATAATCCAAAATAGCCATGGGTTGGACAAAATAC AAGTTAGTGCTCTCTAACTTTAATGGGCATA
WI-10686	133	C T A A G G	TGCCCTGTGC AAGG	CAATCTCTAAA TTCATGTGTAG ACACA	AATAACCTGTGGCACATAAGGCAATACTGAGCCCCATACAGAGTGTTTTATGTTAATATTGAAA AAAGTCAAGAGAAACAAGATGATATAGTTCTGCTAGAACTCTGAAATCTGATGCCCTGTCCAAGG C/TJTGCTCTACACATGAATTTAGAGATTGAATGAAATGGCAAAATTCAGAAAAGGG
WI-11175	77	T A A	AAATGATTTCTT TCTGCTCAAG	CTGTTCTCACA TTCTTTTGA AA	GGTAGGATGATTTCTAGAAATGCCACTTACAGCCACTGAAATATATTCCTCCCAATGATTTCTCTG CTCAAAGAGT/JTTTTTTAAGTTATCTACTATTTATATTTCTGCTTTTTCAAAAAGAAATGTGAGA ACAGTCAAAAATGTGTTTCAGTATAGCAAAATTAATAATTAATAAGTAAGAAAAAGAGCCAAAT TGGGC
WI-10694	144	A G T A T G A G T T T C	TGCAAATGCTT TATGAGTTTTC	GGCATTTTGTA AAGGAGGAAA	TAGAGAGTCTTTCAGTTTCAGGTTGGAGGGGTGGTGAGGTGAGATTCACCTTAGAAGCACTGGC TATGTACAGAAAGATAAACTCTGAGAAAGAACTCAGTTCTAAAGTTTCAGTCTTTGCAAAATGCTTTA TGAGTTTTC/GJTTCCTCCTTTACAAAATGCCATCAATTCCTCAAGGAAAAAAAAGCTTTCT
WI-2716	23	T C C	TGAATTCATCC AGAAAAACAG	TCTCTTTCTC TCTTGTGTCA TTC	GTGAATTCATCCAGAAAAACAGT/CJGAATGACAAACAGAGAGAGAAAAAGAGATAAAGGTTTTTGT ATACGACAAGTGGCTCAAGCAATTTCTCTGTCCAGTGATGGAGCAGTG
WI-10719	115	T C G C C A T T C T A G	TGACTCTCAAG GCCATTCTAG	GCACTGCCAGC AGCC	CAGGCCCAACTCTGTGATTAAGTGTTTTGAACAGACACCTCAGTCACACAAAGTTCTCTGTATGT GCCCAACATAACAGTTACTGGAGGATGACTCTCAAGGCCATTCAGT/CJGGCTGCTGGCAGTGCTT TTCCAGCCTGCTGCCATAACTAA
WI-10721	40	A G C T T G C C A	TGGCTCTGCTA CTGCCA	GAACTCCAC ATAAATAAAT CTCA	CAACCAATTCAGATTAAATTTTGGCTCTGCTACTTGCCCA/GJATGAGATTTATTATGTTGGGAGTT TCTGAAGATTCCCATGGTAAATAGTATTCCTCTCCCTGCTTAGGTTTTGAAGAAATTGAA

WI-11204b	88 T C ---			GCACACGAAATTGATTAAATATTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAAAGGGTG AAAAAGAAAAACTTTCACCTTTT[C]JATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATTGGGAAGAGATTAGTGAATCAGAAAAATAAGTCTGAGGAAATTTATTCAGAAG GCAACATC
WI-11204a	80 T A AACTT	GTAAAAAGGG TGAAAAAGAAA	TGATCACTTAA AATGTACATAA TACCTTT	GCACACGAAATTGATTAAATATTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAAAGGGTG AAAAAGAAAAACTTT[A]CACCCTTTATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATTGGGAAGAGATTAGTGAATCAGAAAAATAAGTCTGAGGAAATTTATTCAGAAG GCAACATC
WI-10732	80 C A ATTGGTCACT	GCTGTGCTTC CTGTATGTACA	AAGAACAATG CATAACAGAA CTTTAA	ACATGTATTTCCCTTAGTGGTCAGCCCTTCCCTACCCCAAGAAATACCCCTGGTTTATTGCTGTGCTTC ATTGGTTCACCT[C]AJTTAAAGTTCTGTATGCATTGTTCTTGAGTCCACATAGGTGTTAATCATTCCA CACCACCTCTGTTAAACTGTC
WI-11206	127 A T ACTC	GGTTGTGTTT CTGTATGTACA		TAGTCTTTTCTTTGTACGAGTGCATAAAGAAATTACCACCTCTGCACATTTTGTAAAAAGATAGCACAG AGAGAAGCATTACAGGGCACAGCACAAACATGAGGTGTGTTTCTGTATGTACAACCTC[A]TCCAA CCATTAGGATTGTCACCTCATATATAGACAGAAATTCAGTGGTGATTGAAATTCACACATGGA ATAAGTCTA
WI-11215	68 C T ---		---	GAAAAAAAGTTTAAATTGGATTGCTTAGTTGCTTAAATTTGACCTACTTTCAGATTTATTTTAGT [C]TJATTTTCTCTATAATTTTCTGTAGTGATGGATTTCTATAAATTAGGAACAGATATTT ACACAGAGAAGACAGGATTGCTTGAATTAGTATAACATTCCTTTATCCAAAGCCCCATCCACCATGT TTT
WI-11219b	89 G A AGAGAAA	GAGAGAATAT TCCAAAAAGT	GGTCTCTAAT TTTCTACACT TTCT	ATGAAAAATGCATTAGAAGAAATTGGAGGATAAAATTGAGAGAATATCCAAAAAGTAGAGAAAA GAGACAAAGAGATGAAAAATAGGA[G]AJAGAAAGGTAGAAAAATTAGAGGACCATTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAAGAGGCAAGAAAAATGAAGGGGAGAAAAATCCAC AAACATCTC
WI-11219a	18 G A ---		---	ATGAAAAATGCATTAGAA[G]AJAATTGGAGGATAAAATTGAGAGAATATTCAAAAAGTAGAGAA AAAGAGACAAAGAGATGAAAAATAGGAGAGAAAGTGTAGAAAAATTAGAGGACCATTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAAGAGGCAAGAAAAATGAAGGGGAGAAAAATCCAC AAACATCTC
WI-11222b	136 G A GCGTGG	CATACCACTGC	CCTGGTAGCCA AGTTGTGA	AGCCACAGTGGAAATCATTTACACTACCGAAATCAGCAATGCTAAAAATTGGGGCTTTGGATTTTGT TTTTGTTTTTCCATAGACCCACCGTTGAACATTTGTTAAACATTTACCAGCATACCAGTGGCTG G[G]AJTCACAACCTTGGCTACCAGGAGAACCTGACACAGACTTCGTAATTGCTTTCACAGGGCTACTGG AAAGCC

WI-11222a	25 C T A	GCCACAGTGG AATCATTTAC	TTTTAGCATTT GCTGATTCG	AGCCACAGTGAATCATTTACACTA/C/TGCGAAATCAGCAAAATGCTAAAAATGGGCTTTGGATTTT TGTTTTGTTTTCCATAGACCCCGGTTGAACATTTGTTAAACATTTACCAGCATACCACCTGCGG CTGGGTCACAACTGGCTACCAGGAGAACCTGACACAGACTTCGTAATGCTTTTACAGGCTACTGGA AAGCC
WI-10775	39 C T CACTC	TTTATGCCATA TTAATTCATTA	CTAGATGTATT TGCTAAGAAA ATATGATG	TTGCAAGTTTGTATATGCCATATTAAATCATTACACTC/C/TJACATCATATTTTCTTAGCAAAATACA TCTAGACACCTGGCAGCTCAGTAAGGATATTCTGGCAGATAATCATTGTTATCATTAGACATTGCA GGAACCAACCATATGGATGATAAATGTTGTTTAAATGAAGGCAAGCAATTA
WI-11226	165 A C ---		---	TTGCATGCATTTATACGAAAGGAATAAAATATCTTCTTATAGTTGAATTTTAAAGTAAAAATAAA GTTATACATATAATACAAAAAGTTGTAAGTATAGTAACAAATGAATTAGAAAAATTGTCAGTGGTTGC TAGTACAGGAATCAAAATTTGGACTATGAACA/C/GACATAGTTGCTAAGGATATTCACACAAATTAT TTCATGA
WI-10778	62 A G G	GCAAGGGAGG AACATTTACA	CTGGTGACATC AGAGATGGAC	CAGTGGCTGGCTACTGACAAAACGTAAACATCGTGGCAGGTGGCAAGGGAGGAAACATTTACAG/A/G/G TCCATCTCTGATGTCAACAGCAGGGCCAGGAAGGTTGATCTGGAG
WI-10789	21 C T GCTCTAGACC	GGGACACACT GCTCTAGACC	TTGAGGGACCC TGGGA	TGGGACACACTGCTCTAGACC/C/TTCACAGGTCCTCAAAGGTGGGTAGAGGCCCTACTGCCCT GCCCTGGGACGCAGAGGCATCAGGGCCTTAGTCTCTCTGGGACAGTGAAGGGCCACACC
WI-10810	58 C T GCAGGAATT	CATCTTCATGG GCAGGAATT	CAACCCCTAAG AAACACAGAA ATG	ACAGAAAAATGCCTAGGTCTTGTAGCAAGAGAGGAAAGCATCTTCATGGGCAGGAATTC/C/TJCATTT CTGIGTTTCTAGGGTTTGTGGCTGGCCATCAGTTCAACTCAGCCCTGTCCCTGATCCAGCAACATT TCCGTAACCTACCCCTCTAGAAGTCATGCAAGAGAAATGATGA
WI-10828	23 T C ---		---	GGACCAACACAGAAATTAACITGGCAT/C/JAGGGTTTCTTAAACTATTTCTGCAGAACATTAGTAAAGT TTAAATAAGGATCAGGCTACCAGGAATACAGTTAGGGAACATGTGGATGAATATTTCTTTAGTAGAG GACTTCTAAAAGGCTATAATATTTGGATACATTAGGCTCATTATGAATCTCAAAAGGAGCATGTAGT AGGGCATATCTAA
WI-10832	91 G C AGGCTCTCC	CATTAATCTGC AGGCTCTCC	CCTAACTGCAG GTGACTTAGAA A	TATGCCCTCCCAACGAGCCATCCACGCTGCTTAGCACAAAAAATAAGAAATACATCATTTCTGAATG GGCACATTAATCTGCAGGCTCTCC/G/C/JTTCTAAGTCACTGCAGTAGGTCTGCAGACACTGTGTA TACCATATAAATCTGATTTCTGAGCAGGAGGAGGCAGATGAGAGAAGGGCTGCTCCGTGAATAC TAGTTCGG
WI-10834	96 C T GTGTTAAT	AGAATTTAACT GTTCAAAAAGT	TGGCCCTATAA AATTGGTATTA AG	GATTTGAGTATTATCAAAATGGCCAAAGACCATTAAACAGATTTAATAGTTAAAGCCAAAACTATA AAGAAATTAACGTGTTCAAAAGTGTGTTAAT/C/TJCTTAATACCAATTTATAGGCCACCAATTAACCTT CTGAAGAAAGGTCAGCATATGCAACTAAATTTCTAAAGTCCAGT
WI-2287	24 T C ---		---	GGATGATGTTCTGTGGTCCCTTTA/C/JAAGCCCTCTGTCATCCCAATGTTGTAATATTTTATTCT TGGTATTTCTCGCTTACCCATAGTCACCTGTCAAGTGTCCACCT

WI-2296	81 A	TGTTACTTTGA TCTTTGCTCT	GCAAATCACAC AGCTAACTGG	TGGAGGGTTAGAAATGCAGGTGGCATCTAGAAAGGCTCAGGCTTGAATAGATTGTTACTTTGA TCTTTGCTCTGAC/GGCCAGTTAGCTGTGATTGTCAGAAAGTTACATTTGTTGTTG
WI-2300	77 G	GGCAGAGAAG CCAGTCATAC	GGTTGGGTCAA TTTTAAAGCA	TTTCATCATGCTGCTTCCCTGGAAATTTCCCTTATTGAGCGGGCAGGTGGTAGGCACAGAACG CAGTCATAC/GTTGCTTTAAATGACCCCAACCATTAAGAATAGCAATTCA
WI-2371	55 G	GTCTTGTTCTT CCAGCTTCT	CAAAGATTGAC AGCCACCAC	CAATGATCCCCCAACATTTCCAGGGAAAGGCTGGTCTTGTCTTCCAGCTTCT/GTGGGGGGCT GTCAATCTTTGACATTCCTTGTCTTGCAGCTGTATAATTCATCTTGCCTCCAGCTTTACATGATGT TCTCTCGTGTCTGTG
WI-2395	122 A	GAACATATTT GTAGAAAAAT	TCACCTTTCTA TTTATTCTGAA	GGGGGCACAATTTAGCTACAGTGCATATTTAAAGATAACATAGAAATATCAATAACTTGGTTTAC TGAAATCTGAAAACTTAGGATGAGTGAACATATTTGTAGAAAAATTAATAATCCAA/A/CJCTGAATTC AGAAATAAATAGAAAGGTGAATCATCTTATATCATTAAGAAGCTAAATTTATTAGTAACAATCTTTA CATTTACACAAACCCA
WI-2437c	192 G	---	---	CACAGCCACCACCCCTACACCTCTGTGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAAATCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCTCTGCAAGAGGCAATCGACGAACATCACAGTG/GA/GCTGTG GTGCCAAGGACGCATTATG
WI-2437b	179 G	---	---	CACAGCCACCACCCCTACACCTCTGTGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAAATCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCTCTGCAAGAGGCAATCGAC/GA/JAACATCACAGTGGGCTGTG GTGCCAAGGACGCATTATG
WI-2437a	128 G	---	---	CACAGCCACCACCCCTACACCTCTGTGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAAATCCCAAT/GA/JCTC TAAATAGATGGACTCAACCCCTTCTCTCTGCAAGAGGCAATCGACGAACATCACAGTGGGCTGTG GTGCCAAGGACGCATTATG
WI-2440	71 G	GCAACCTACT GACAAATTTAA TTTTAGTT	AACAACCTCTGC TATTGGTCTCA C	CAGTAGGAAACGGGTTCTTCTTAGACCCCTCCAGAAAAATAATGCAACCTACTGACAAATTTAATTTTA GTTG/GA/JGTGAGACCAATAGCAGAGTTGTTACCTGCAGAACT
WI-1356	123 T	TGTTTAGGAA ATAATGACAA GAAAAA	TGGTTACAAC GTACCAAAACAT G	CTGTAACCTACACACATCTCTCTGTAACTCTAGGTTACTTGTATACAAAAACACAATGTAATGCT ACATAAATAATTGTACATCTATATTGTTTAGGAAATAATGACAGAAAAAAGCC/T/CJGTACAT GTTTGGTACAGTTGTAACCCAGCCATTTTCCCCCAATATTTCAATCCACAGTTGGTTTATCCACAG AAACCACGAATG
WI-2886	46 C	CAGAGTCTGG GGGAGAAGA	TTGCCATGCTT TATCTGTT	ACAGTTAAGAAAAAGGCTGCAGCCGTTGCAGAGTCTGGGGGAGAAAG/C/AJACGAGATAAAGCATG GCAAAGACCACGCTGAAAGTATCCAGGGTGTCTGTATGTGCACATAGGAAGATCACTTACCTCAGCA TAGGAGGAGGGCTAGGCAAGGAAAGGTGTCAGAGAAACAGAGGAGCGTT

WI-2906b	77 T A ---		---	CCTGAACACCTGGAGCACTTCCCTCCCTTGACACCTTCATCTGCTGGAACCTTGCCTGGAATGCTCTTCCCTCTA/GAGCTTTGCTTGGCTTACTTTTCTTTTCTTTAGGTTTTCAGCTTCAAAGTGACCTCCTTAGAGTTGGTTTCTGACCAACAAA
WI-2906a	50 A C TCTTGCTGG	GACACCTTCAT	AGAGCATTCOA GGCAAAGT	CCTGAACACCTGGAGCACTTCCCTCCCTTGACACCTTCATCTGCTGG[A/C]ACTTTGCCTGGAATGCTCTTCCCTGAGCTTGGCTTGGCTTACTTTTCTTTTCTTTAGGTTTTCAGCTTCAAAGTGACCTCCTTAGAGTTGGTTTCTGACCAACAAA
WI-1736	175 C T ---		---	TACTCCTCATTCTCCTCATGTCCCTAGACGTACTCAGATTCCATGCCCTGAAACATTTATTTCCCTAAATAGATTTCACCCACCCAGCACTATTACACAGAAACAGCATGGAGCAGTTGGAGTCTGGCTCTTAGAGAACTTACTTAAGGACAGTGTTTCCATCTGCTTCCA[G/C]TAGAGATCTAGGGTGCTTTTGGAAACCACCTTGG
WI-1851	136 G A GTGTTAAGTA	GCATTGAATT AACTATAGAT	CACTAGCAATG TTAAACTGAAG TTG	AATACCCACGTCCTAACCCATCACACTGATCATCAATCAGGTTTAAACATATTAACTCTGGGAGGACACAAACATTTAGACCATAGCATTAAGTTAAGTATAGATGTGTTAAGTAAATATATTAAACATGGTACA[G/A]JACAACTTCAGTTTAAACATTGCTAGTGATCCATGTGGATACCATGTACCTTCTTACATCATGTGA
WI-3000	62 G A AGAGACCCC	CCCAAAACAC	GCACATATAGG ATTGACTAAGA CTCA	CTGATGTTTGGGAAGCACTGCTTACATCTCTAAATGTACAGCACCCAAACACAGAGACCCC[G/A]TGAGTCTTAGTCAATCCTATAGTGGCAGTACCTGAATCAGTGCCTGGTGCTAGTAGACACT
WI-1754	177 G A TAGTC	TTTCTCCCTT CTTAAAGAGA	AAAGTCGAATT GCCTCTGG	ATGGATCTGCTCAATTATAGTCCAGATAAACAGCCCTTCTCCCCGCCACCCCGGATTATTTTACTTAAGGGTTTAGCAAAATTCACCTGACAAAGAGTTAGGTTTCAACATTGACCCCTCATAAAGTGATTTTTTCTCTTTCTGTTTGTGTTTCTCCCTTCTTAAAGAGATAGT[G/A]CCAGAGGCAATTCGACTTTCTGTAGCCACAAGATT
WI-3167	37 T A TAGATTC	AAATTC AAC ACAGATCTAT	TGTGATAGTTT TGAGATGGGTG	ACAACACAGCAAAATTC AACACACAGATCTATTAGATTC[T/A]CACCCATCTCAAACATATCACATCAAGAGCAAGGAGACATATTACTGGTGAGGAAGCCAAATTTCAA
WI-3208	140 G A AGATAAAGA	GTGGAGTGGGC	TCACCTCAAAC AGGGCTTGG	CAAGCACACATTCAGGCAGTGGGCAGGTAGGGAAGGTGGCAACTTGGCAGCAGAGAGGAGGAAGAAAGTTCAGACCGTTGGTAGGATAAGTGGATCCAAACCCCTTTGTAGGGCAGGTGGTGAGTGGGCAGATAAAGA[G/A]CCAAAGCCCTAGTTTGAGTGACACTGTGGGGATTCAAAG
WI-1775	47 C T TTTTCTCTG	CCTGCATGGTC	AGTTGAGATTT ATGACAATGAT GTAAA	ACTCCACCAACAGTTTGTGAGCCAAACCCTGCATGGTCTTTCTCTG[C/T]TTTACATCATTTGTCATAAATCTCAACTGACACATCAGTGTCTCTGCCACCCCA
WI-3402	55 G A ACAT	AGCATATTCA TTGATTTCCTT	GAGGACTTAAA AAGGAGCATTT G	CTGCCCTTTACATCCAAAGCCAGTTACTCGAGCATATTCATTGATTTCCTTACAT[G/A]CAAATGCTCTTTTAAAGTCTCAACTTTTAAAGCGGAAGTTGAGACATGCACAAAATAGATTTCCTTAGGA

WI-3416	33 C T	CCAAGTTGTA GCATTCAGAA	ACGAGCACAA CTACCTCTAAG AG	TCTGGTTCTCCTCCAAGTTGTAGCATTCAGAAGTC/C/TCTCTTAGAGGTAGTTGCTGCTCGTTAAAA TATGTTTTCAAGATAGTATCTCCCTGTTGTACATTCCTCCAAACAAGTGTACCAACAGCATTTGTTAAG GAAATGTGCAATGCTTGCTACCTCTGACGCACAACATAATTAATCCCATTTGCCCTAAAGAACCCAGG TCCTATTCTACAACAACAGAAATTTAACAAATTAAGAAATCAGCTACTCTCTTAGGCCCATCAGAG AAT/C/TJGAAGTCATGGGGAAAAATTTGATGCCATGTGAATTTGGAGAAACAGACAGGCATATATGGAG AATTACAGTTTACCAGGGACACAATCCCACTTCCAGAGCCATCTGTAAAGAC CATGCTAGGTAGATCTGATCATGAAGTTTGAACAACTTAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTTCCCTAAATTTAGCACAGTATTTAATGAGGTGGT/GA/TJGGGAGAAAAATTTGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3453	70 C T	TTCTAGGCC ATCAGAGAA	TCAATTTCCC CATGACTTC	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAACTTAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTTCCCTAAATTTAGCACAGTATTTAATGAGGTGGT/GA/TJGGGAGAAAAATTTGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3474b	109 G A	---	---	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAACTTAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTTCCCTAAATTTAGCACAGTATTTAATGAGGTGGT/GA/TJGGGAGAAAAATTTGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3474a	90 A G	AGTCAGTTTCC CTAATTTTAGC	CAACCATCAAT TTTCTCCCA	TTTGACCCCATACATGAGAAATAAAACCATAAGAAATGTTGGAAAAATAAAACGGGAGAGACCTGGG TTTCTGGATGTCT/C/TJTGAGGACAGGGTCAACCCAC
WI-3502	79 C T	CCTGGGTTTCT GGATGTCT	GGGTGACCTG TCCICA	TCACGGCAAGTTCTGCAGCAGTGTCTTGACTCTGCCTGTTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGTGAGCCACCCTAAACTCGTTTCTGCTTAAGTTATCCAGAGGTGGTTCTAACCTGGATA TAAACATCT/G/CJATGGAAGGCTGCACTGGATGAGGTACAAA
WI-3600b	146 G C	GGTTCTAACC TGGATATAAA	CCAGTGCAGCC TTCCAT	TCACGGCAAGTTCTGCAGCAGTGTCTTGACTCTGCCTGTTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGT/GJGAGCCACCCTAAACTCGTTTCTGCTTAAGTTATCCAGAGGTGGTTCTAACCTGG ATATAACATCTGATGGAAGGCTGCACTGGATGAGGTACAAA
WI-3600a	78 T G	CCATGCCCTG ATAGTTCTG	GGAAACGAGTT TAGTGGCTC	TAAATCATGCTTATTTTACAAGGTAATCCACTACAATAGGCAATTGATGTGATCTCTTTCTGTAA GAAAAAGCTCTCATGCTCTTCTGAACTTCTACTGTGCTGTATGATGCACCT/GT/CCTTTTGG ATAGATGGTTGATAGGAGATGGGTTTAAAGACACAATTTACCTTGTGTTCAGGCAGAAATAG ACTCTCTCTGTGTAATCACTGAATGAGTCCAAAAGCCTTATGCTTAC AAAGCGATGTTGAGATACCACATTCCTATGAAAAAGTAAAAACACACACAAAAATATGACATAAAA T/A/CJAAAAAATACTATAGTTTATGAAAAATGACTTCCAAAATTCAGAGAAAAAGTCACCTTAAACAGG ATTCTCAATTTCAATCCAGAAATACTCCTCTGTCAATCTTAACCTTGTACTGCACAG
WI-3678	125 G T	---	---	TCTAAATGTGAAACCAAGAAATCCTGACACGACCTAACTGCCAGTCTCAGTTATGTATCAAAATGA AAAACT/CJACACCGGTTCAATGAAAAAACAATGATTTGGTGAGCCATGTCCCCTTATTTAATGAAAA GATCTGGCAATTAACCTC
WI-3687	67 A C	CCTCAGTTATG TATCAATGA	GGCTCACCAAT CATTGTTTT	TCTAAATGTGAAACCAAGAAATCCTGACACGACCTAACTGCCAGTCTCAGTTATGTATCAAAATGA AAAACT/CJACACCGGTTCAATGAAAAAACAATGATTTGGTGAGCCATGTCCCCTTATTTAATGAAAA GATCTGGCAATTAACCTC
WI-3735	72 T C	AAAAAC	---	TCTAAATGTGAAACCAAGAAATCCTGACACGACCTAACTGCCAGTCTCAGTTATGTATCAAAATGA AAAACT/CJACACCGGTTCAATGAAAAAACAATGATTTGGTGAGCCATGTCCCCTTATTTAATGAAAA GATCTGGCAATTAACCTC

WI-1819	51	C T	---			GAAAAAGCAGGAAGCCAGGACGACAAACCTTTGAAAAAGTCTTTTCAGCAC[C/TT]TCGTGGATCCG AATTTTAGTGTGATTTGGCAGGCAATCGGGGTAAACATGTTCCAGTGTTTTAACTTGCACAGAAATTCG CAGATTAGCGATTGTTGACTTGTCCAAATTAATGAAATGTGGAAGAAAAAAGGGTGGTAACTGTT AAGCCTGCTGCAATGTTTAGACACGAGGGTGGGGTGGGAGGTGGAATACC
WI-3746	116	G A	---			GGCCTATTACATGACACTGGGCCAAGATCTTGCTTCCCTTTCTTTCAATAGATAGACTAACTAGAAA ACTGCCCTGGCCAGGAAGATGGTTGCTTCATCATCTCTGTCTCTGC[C/GA]GCCCCAGGATAAAGCA GGCA
WI-3867	49	T C	CAA	ACAGTCATTT AGTCTTCCTGA	TAAGATAACC ATACTAGGTAC ATCCG	AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCCCTGACAA[T/C]CGGATGTACCTAGT ATGGTTATCTTATCTGACAGACAAGGACACTGTGACACAGAGATTGTTACTTGAACAAAGACACAGT CATTAAGTGGAGAAGCCAGCATTTCTAATCAGGCTCAGTGATCTGCCAAACCAACCCCTTCTGCTATAG CATC
WI-3898	25	A C	G	TGACCAATGTC TTTAGAAGCA	TCGTCCGGTGC CTCTCC	CAATGACCAATGTCTTTAGAAGCAG[C/C]GGAGAGGACACCGACGAGACACACAGGAAGGAGTGAG GTGAAGATGAAGCAGTGTGACGCGAGCCACAAGGTGAGGAAGCAAGGGTGTGCGCCACT
WI-3901	114	A G	---			GGACCATTTGCCCTCAGAAGTACATTCAAGCCCTGGACGGTGTCTCCTAACACTGTGACCTCAGGCA AGTCATGTCTGCTTCTGAACTTCCCTGCTTCCCTCAGTGCACAAAGTGG[G/G]TATCATGTGCTACACTGC AGTGTTTATAATGCTGCAT
WI-3914	99	C T	CC	TGATCTTCTC AAGACTCACA		CTGAGGAGATTGATGCTACTTTACCTGAGGAACCTTTTATTACCTCCCTGAGTTTGTGCTTGCAA GACATTGCTGATTTCTTCAAGACTCACAG[C/TT]ACCATCCTTCTTCTTCTAGACCTATAACTAG ACTCAAGTCCAGCAGGCCCTTAAAGGTAAGGTAAAGGTACAAAGTGTGACCCATGGGAGGTATGTTACGCTA CAAAAGAG
WI-4019	33	G A	A	CCAAGAGGT CCTATGAATC	AACAGCAATA ACAGGAACAA ATG	CCACTCCAGGCCAAGAGCGTCTCTATGAATCAT[G/A]CATTGTTCCTGTTATTGCTGTTACAGAGT GGCAACTCTTGCAAAGGGAGGGGTACAAAGTGAATTTTAGATGCTGCAAGGAGACGAAGGGTC
WI-4091	84	A T	GTGAGTCTTA GTGATGTCATG	TTGAGTCTTA GTGATGTCATG	TGAGTTCCTAT TAAGTGACAAT ATTGTT	TAATTCACATTGCTCTGTTGTGCAATTTATTGCTTCTCTTATGTAACACAATCACCACCAATTGAGG TCTTAGTCATTGTCATG[A/TT]GTATAACAATAATTGTCACCTTAATAGGAACCAAGCATAGTTATGTGT ACATTTATTGCTAACAGCAG
WI-4160	117	A G	CAACAGAA	CCTATAATTTA GCAACAATAT	TGCAGGTAGAA TTTTCTAATAT AGCC	TCCTCTTCTGTAATAGGAAGTCTGATTAGATGCCCTTTTGGGTTAGGTTGGCTTCTAAGATGGTAAT ATCTGTCCAAGTTTGTGTTTCTTATTAATTTAGCAACAATATCAACAGAA[G/G]GGCTATATTAGAAA ATTCTACCTGTCATCCCTGGATCTGAACGTTCTTCATGATACT
WI-4168	32	A G	AAACA	GGTGAGAGTC AAATTGATAC	ATTGCCAAACA GATTTTCAGA	CGTTGCTGGTGAGAGTCAAAATTGATACAAACA[G/TT]CTGAAAAATCTGTTTGGCAATCTATTAAAGG CAATATATACCAGCAGTGGTGTCTAGCAATTTCACTGCTGGGCATTACCTTAACATAATGAT

WI-4177	68	T C	TGAATAAGCA CGTATTAAATT TACCTA	AAGGCAGCAA ATCATGATG	ATGCCTGCGATACATTTCCAAATGACTAGTATGAATAAGCAGTATTAATTTACCTATTATATTT AT/C/CATCATGATTTGCTGCTCTTTCCAAATTTACTACAAATTTGATTGTCACATGAGGCACATG ATCCCATTAACCCCAATAG
WI-4199	51	A C	CTCCCAAGTT AGTCAATATA AAAA	ATATGTTGATT AGGTATAACA ATATGTGTG	GCCATGAGCACAGAGGCTGAACCACTCCCAAGTTAGTCAATATAAAAAA/A/C/CACACATATTG TTATACCTAATCAACATATAAATGTTATAGATTAAACAGTCCACAGCAAAACAA
WI-5163	24	C T	CTGCACTGGT CTGCCTGT	AAAGGAACAC AGGAACAGAC C	TTCTGCTGCTACTGGTCTGCTG/C/CTGGTCTGCTCTCTGCTGCTCTTCAATGTTCAACTGCTTGTAT CTGTGCCACTAAGGTATCAGGTTTATATGGCCACAGGATGAGGGCTTTGTAGACCAGAGTTTCTTT GGAAATTGCAACATTTGGGCAT
WI-4250b	117	A G	---	---	TAAGTGCATTAACTGTACAAGTCCACAATACTCTTCCACCAAGTGTCTAAAGCAGTTTAAATAACA GGTTCAATATGAGTCTTGTGAACAGGGTGGGAAGGATCCTGTAAAGG/A/G/TAATATATTGTTTT CCATAATATTGAAGATGTG
WI-4250a	94	G T	TCAATATGAG TCTTGTGAAC AGG	CTTTTACAGGA TCTTCCAC G	TAAGTGCATTAACTGTACAAGTCCACAATACTCTTCCACCAAGTGTCTAAAGCAGTTTAAATAACA GGTTCAATATGAGTCTTGTGAACAGG/G/CTGGGAAGGATCCTGTAAAGGATAAATATTGTTTT CCATAATATTGAAGATGTG
WI-4255	68	G C	TGCTCCCCCAT CACCT	AGTTGTGTAAG G	TAAATGCTCTGGGAGATAATAGGAAAGTCCCATCCCTCTGATACCTTGGTTCCTCCCATCACCT IG/C/CCTTACACAACCTTGAAGTAGGCCCCATCCAAACACTGGTCAGAAGAGTAATACTGTCGAC
WI-4256	57	C T	---	---	ACAGCCTCTTCAATGGCAATCAAAAGCACCAGTAAAGCAGAGGCAAAATCTGG/C/CTCAC CATTGGAAAGTCTCTGAAGGATAAGGGAGTGAATGACTGCTAGAAGAGAAATGTTGGCCTT
WI-4325b	71	C T	---	---	AGTTCACCTGCCTAGATGAGTAGACCATGTTGCTTTGTTAAATGTACATGGGCAGGCCGGAATGG GATG/C/TTTACTATAGATAATCTTTTTTAAATGACTCTCTTGGTCTCTTCAAGATATCACCAGCCAC CCAGGACACTGCCATATCT
WI-4325a	58	C T	---	---	AGTTCACCTGCCTAGATGAGTAGACCATGTTGCTTTGTTAAATGTACATGGGCAGGAC/C/TTGGAAA TGGGATGCTACTATAGATAATCTTTTTTAAATGACTCTTCTTGGTCTCTTCAAGATATCACCAGCCAC CCAGGACACTGCCATATCT
WI-4347	158	A G	---	---	TGGGCAGAAAGTCGGGTATGGCAAGTCAGGGTGGTTAACTTGGATGCCACTTCTGCCTGTACCTTCT CTAGACTCTTGACCTGCAGGAGGATCCCTGGCCTCTGAGTTTATCATCTCCACCTCCAGCCCCAG GGCCTGTATCTGTTCAAGGCC/A/G/AAATCGTCACGGCTCACAACTGTGGGAGGTAGGAATGACGA G
WI-1936	117	T C	---	---	CCAGTCTAGGCTGCAAGGACTTCAATTTCTGGGGCAAGTCTGGTGTGTGCTAGGTCAGAGGACGG ACCTGAGGGACACACAAACCAGTGGGACACCAGGGGTACTTGTATCACCT/C/CTCCCGCAACCCCA AGCAGCACAGCTTGAGTCCAGGAAAGACTCTTACTTCCACTTGAGAAAAGGAGAGGGAAGAGA AAAGAGGACTTTGACACACAACCTTGGGA



WI-5204	54 C T ...		...	TAGATTTTGATTGATGACAAATAGGGAAGCCCTTTGTTAAATTTGGGTTTTGAAGAA[C/T]GAAGAAAA TGGAAAGGGAAGAATTGACAGAAACCAAGAGAGTGTGAGGGGAGCAAAATCCAGTTTGACTGGGA ATATAGAGTGATGTCAGGGTTG
WI-5215	70 A G C T C A A A A A	GGACCTTAAT ATTTAACAGA	AGATAATTTTG TAAAGATAGTT TTCCG	TTTCCCTTATTATTAGGAAGCAAAATGTTTCATACAGGACCTTAATATTTAACAGACTCAAAAA TAT[A/G]GCGAAAACTATCTTTACAAAATATCTCCATAGCAAGTAGACATTTTAGCACATTTTCCT GTAGTCAAGGTTTTAAAGGCCAAATGAAGTTGACTAAAGACAAT
WI-4448	112 T G A T A T A A	TTGTATCAAA GAGATGGGT	AATTAAGAA ATCTTTACATG GTCTTT	CCCTGAAATGTGCTTTGCTTCTCTCCCACTCTCTAGGGAACCTTTTCCATGTGAGGTGAAGGTTTTGA AGAGTACTTTAATTAACCTGTATCAAGAGATGGGGTATATAA[T/G]AAAGAACCATGTAAAGATTTT CTTTAATTAGTGAATTTTCATCAGGGCTCTTCCACTGTCTATCAGTAA
WI-4456	49 C T T A T A G T T C C	AGTTGAATTA TTCAGAAAAT	TTTCTGTTAT GCATGAACCTG	ACACATTTCAATTTTGCTTTAAGTTGAATTAATTCAGAAAAATTAAGTTCC[C/T]CAAGTTTCATGCATAA CAGGAACACCCAGGTTGGGCAATTGATTGAATGT
WI-4461	49 A G C C T T C C	TCACTGTTATT TTAAAATTAT	TTTGACCTTTC ACCAATTTCA	CTGAAACTAATGAGGTGCTAAATCACTGTTATTTTAAAAATTAATCTCC[A/G]TGAAATTTGGTGAAA GGTCAAGAAATGAATTCACACTTTTAGATTTCTGAAATTTTATTCGGATGATAATGCAATGGGC
WI-4465b	75 G A ...		---	CTACTGGATTTTACTTTGCTCAAGCCAGACAACACGAAAGT[A/G]TATAAAGAAAAACAGTTAGTAAT TCACCTTT[G/A]TATTCTCTTCTACCTCAGGGAATC
WI-4465a	41 A G A C A C G A A A G T	AAGCCAGACA ACACGAAAGT	GGTGAAGATT ACTAACTGTTT TCCTT	CTACTGGATTTTACTTTGCTCAAGCCAGACAACACGAAAGT[A/G]TATAAAGAAAAACAGTTAGTAAT CTTTCACCTTTGTTATTTCTCTCTACCTCAGGGAATC
WI-1949b	160 T C T A A T C	GAGTGAATAA ATGAATGCCA	TGAGAGGTGGG GACAAAAA	GGGTTAGGACCTCGAGATCTTTTTCAGAAAGCACAATTCAAACCATAATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTTCAAGGCTGCTGACATGGCTGAATATATGTTGAAGAAAT GGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTGCCCCACCTCTCACACCTTTCCCTGG CACA
WI-1949a	86 T G A T G C T C T G A G T	CAGTGGTGAG	CCATGTCAGCA GCCTTG	GGGTTAGGACCTCGAGATCTTTTTCAGAAAGCACAATTCAAACCATAATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTT[G]CAAGGCTGCTGACATGGCTGAATATATGTTGAAGAAAT AAAGGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTGCCCCACCTCTCACACCTTTCCCTGG CACA
WI-4529	64 T C A A G A T G	CCAAGTAAGT CTATCATTTCTG	TTCTAAAAATA ACACTTCCTGA AAAA	TGAGAGAGTTTTTGGATTATTCATCCTCTGCAACACTCCAAAGTAAGTCTATCTTCTGAAGATG[T/C] GAGTCTCTCTTTTATATCCTATGATTATTTTTCAGGAAGTGTTATTTTAGAATATAAACTCCTGGGT CCCATCCAGGCTAGGGTCAATGGCATCCATGGGTGGCTGGACAAGATGGGCCCTAGGATCATTTT

WI-4540	110 A G	GCACCATGTGG CATCC	GACAATGCAGC CATGCA	AGCTTTTCCTTTCTTAAAAATGGTGCCATAGTACTGGCTTCTGTGTGCATCAGGAAGCAAGCCTAT TGCTCGGTAAACAGTACTTTGCAATAAGCACCATGTGGCATCC/GJTGATGGCTGCATTGTCOCAGTC AAATGAGACAACCTTCTCTAT
WI-4582	226 T C ---		---	AGCAAGCATCTGGCAAGCCTCGGTGACCAGAACATTAAATTCACCAACACCACCTGCTCCAAATGT CCATGTTAATGCAATTATAGAGACTCCAGTAGCATTCAGAGGCCAGTTTAACTTATTCCTGTACACA ATAACTTTATGGGAGACAGCATTGTAATTCAAATCAATAAATGACTCGGTTTGGCTGTACAAGCAT AAACAGAACGCTTGCAAAATAIGGTT/CJCTCTCTGTAGAAACCATTTGAT
WI-1965	105 G C AG	GCCATTGAGG AAGTGTTTAA	GAATGGATGGG TCATCTCTCT	CAAAGGTTAGTTTAACTTGGGGGCAACACAAAGTTATGAGTACTCAATAACCTATGTTCAAGGG TAACCAACACCTTTTGGCCATTGAGGAAGTGTAAAG/GC/JAGAGAGATGACCCATCCATTCCTGG GCTTCTTATATGACACCATACTATTCCACACAGATGGGAGTCATTTATTTGGTTGGTGTATGACAGT CATGG
WI-5248b	99 C T TTG	CACTGTTTCT ATTGACCGTAG	AGAAAAGAG AAGAAGGAA AAA	TGTTTAAACCACATACAGTTTGCTGCTACGTTGTGCTACGTTGTTA/GC/JAGCAACCCAGAAAAATTAAACGCC CATTTTCACTGTTTCTATTGACCGTACTTG/CJTGCTTTGCTTTTTCCTTCTCTCTCTTTTCTG CCCTCTTTTAACTATT
WI-5248a	38 G C	AGTTTGTGCTG CTACGTTGT	TTTTAATTTTC TGGGGTGTCT	TGTTTAAACCACATACAGTTTGCTGCTACGTTGTTA/GC/JAGCAACCCAGAAAAATTAAACGCC TACCATTTTCACTGTTTCTATTGACCGTACTTGCTCTTTTTCCTTCTCTCTTTTCTG CCCTCTTTTAACTATT
WI-4596	69 T A AGCACTGTGA	TGAAGCAGAA AGCACTGTGA	CAGGAGATGGG CCTAATAATG	CATTGGTGGTGCCAACTTCTCGGTGACATTACTGTGACTTTGCTCTGAAGCAGAAAGCACTGTGA C/T/AJCAATTATTAGGCCCATCTCTGCTGAGCCCTGCTACAGCAATTTGTACATATGGCATTGGG ACATATCTCTGAGCCCATCAACTATTTGACAAGATTCCTCTTTTAAACA
WI-5252	119 A C ---		---	GAAATAGGGCAAAATTAAAGACTTCAATAATTAAAGAGTCTTGGGAAAAGGATTTGTGATGATCATTG AATCTGTTTAAATACAGAAATTAATACTGAATACCTGTGTGAATCATTTGCTTTT/A/CJTACCATGTACA TATTATGAATTAACAATGTAAAAATAGTATGACTAAGAAATATTGGGCCCT
WI-4606	61 A G CT	GCAATGCTAG AAAATTATGC	TTAGGTGCTTA AGTTGTCTACT TGG	TGCAAAAAGGAAAATGATAACCAGGACTGTTGTTCAAGCAATGCTAGAAAAATTATGCCTA/A/GJC CAAGTAGACAACCTAAGCACCTAAGGCAGAAATGAAAGTTTCTCTCTGTCATTAGTCTCTATTCA ATTACCATTTATCGGGTAAATTAACACTGGAAAGTAATGCCAGGCTAATTGTTAGATTATGATAAT TACACGTCCTTGTCTATGCT
WI-5257	77 C A GCAAGAGG	GAGGCATGAA	OCAGGGGCAGA TGAAAG	CAATGAGAAAGTTACCAGATCGGGGCAAAATTAAGCATATGAAAATACCAAGTGTGGCAGAGGCATG AAGCAAAAGAGG/CJCTTTTCATCTGCCCTGGTGGGTTTTCAGTAACCTGCAACATGTCTTTGCCCTCC CGGATGAAAAGATACCCCTTCTATGACTCAGCAATCCACTCTAGGTATGCACCCTAAACATGGGTG GCAAAAT
WI-4649	50 C T TTCCGAATG	GAGACCATTTCT TACTTACAAGA	TGTAAGGTG TACTTACAAGA AATCATC	TCACGTGTTAGAAAATTTCTTCTCCTCAGTGAGACCATTCTTCCGAATG/CJTGATGATTTCTTGTA AGTACACCTAGTACATCTATGAGCACACAAATTAACAAGTACTTGCTACCTGAATTTGTTATTTTTTAA AAAATCCTCCCAATATTG

WI-4650	148	A	G	GCACAAAGAA AGTATAAGTT G	CTGAAGTGTTA AACTGGATTG G	AACTGTGGTATGTAATTTCTGGAGAGTCAGTACTCTCACTAGATCATAAAGGG GACTTGGGAACCAAAAGTATCTCAAGACATTTAATCTAGAACGACAAAGAAAGTATAAGTTGCTCTC TTATATTGCTTTT[A/G]CCAAATCCAGTTTAACACCTTCAGTAACGTT
WI-4677	82	T	C	AA	TTTCAACAGTG TCATTATTCAA CTT	AACTCAGATTTTGAACATACGTGACATTTTGGAAAAATTTGCCAAAAAGTGATTAGGTGAAAAAAT GAGTTGAAATAAATG[T/C]AAGTTGAATAATGACACTGTTGAAAAATGATGAATCTGCTTTCAATTCA CATGGAAAGGAGACTAGAACACACAGCGTTTATAGGGGAATACAT
WI-4698	135	C	G	---	---	ATGATGCTATCATGAGGAATCTGTAGAAAAATTTTCACTGGCAATGATTCAAATAAAGTTTGTCC TCACCTGGGAAACTGCTTATCTTGATGTCAGTGACATTTCTTTCTTTGACGGAAAGAAACTTCAA C[G]TTTCGAGAAAGGCTTAGATTATATCGCTGAAGCCCATTTCTG
WI-4722	88	G	A	AACCCACAC G	AATATGGAATC TGCATTCAAGTT G	CTTCCCATTTGCCAGTTAGATGACTGCCTCTCCACCGCTAGAAAAAGATGGGAGATTTATTTTC TGCACATATGGAACACACACAC[G[A/C]CAACTGAATGCAGATTCATATTGAATACTGGGAAATCAGTGA AAG
WI-2020	145	C	A	---	---	GCCACAGTAAAGAGGAAAAATGGAGCCATGTAAACAGAGGAGAGCTTTCTGAAGATCAGTGTATTGTCA TAAAGGTCAAGTAAATCACTTTGATGTTGAGATTTAGAAAAACGTGAAATATTGAGTAACCATGGG TCAACTATGAT[C/A]CCAAAAACAGCAGTGTGTCTAAAAAATATGATAGTTCTTCTCTGCTCCACC GCAATGAAAAAGGAGTT
WI-2028	176	T	C	CTGCTCATC GAA	GGTTGGAACCT CAAAATTACCTA GAA	GACTACAGCGCACAGACAGCGCATTTGTGGCTTGCACAGGTGTTGGTTTGTGTTTAAGTTAGATT TGAATCCTTTAAAGAAAGAAAGTGGCTCTTCAGTTTACTACAGACCTCATCATCTCTGTTCTCTTG CACCCAGTCCACTTCCACTGTTTACGTTCCCTGTCTCATCT[C/T]CTAGGTAATTTGAGTTTCCAACC TGTCG
WI-2033	183	T	C	A	CGTTCTCC	ATGTGTATGAGCTCCACATTCGCAGATTCACCAACTATGGATAGAAAAATATAGTATCCAGATGG GCAGCCCAAGGATCAGAGGGCTAATTTTAAATTTTCCAAGTTTACAGGACCAAGTGTGGAAATTT AGCATTTCTGGGTTTGGCATCCATCAGGGTGTAGAACTAATCCCTCA[T/C]GAGAACGTTGGAACC ACTGATATACCAAT
WI-4745	131	T	C	---	---	TTATGGATACATGTTTCTGTGGAGGACAAAGAGTTGAAGCAAAAGGACAAAGGAGATCAACTGGG TAGAATAACTCATCGATCCACCGGCTCTCTCCACCATTTCTCCATCTTCTACTCTGAT[C/G] AGGCAGACTTATATGGAATAAGGGA
WI-2034	150	T	C	CCAAGGAC CC	GGGTAAAGAT AGAGTCAGGT CC	CCACGACTATGCTTCAGAGTCCCTGGTACTGACAGAGAAGGCTTTGAGGACCATGTGGCGCCAAGA CCTCCTCTCGGGTTTCAAGTAAAGACGATGAATCTTCACTCTTACAGCAGCTGGACTTCACCA CAGTGCACCAAGGAGT[C/G]GGACCTGCACCTATCTTTACCCCTTCCGACACCCAGATGCTGAGATGCC ACACTCTGAGTG

WI-2038	155 C T	TGTGCTTTAAA GTGTGTAAGT CA	ATTTCTCTTG AAAGAAACAT CA	TCAGGTGACAAGAAAAAGTCACATTTCTCAATCACTCACCATTGCTCTGTTATTGCTCTTCGAGTGT ATCCAAGGATGTCACCTTTTGGAACTCTGTAGATCAGAAAAAAGTGTCTTTAAAGTGTGTAAGTATTA ATTAGATTTCTATTTTGATA[C/T]TGATGTTCTTTCAAGAGGAAATTTGTGAAGAGGATTCCTCAAT TGCATTTCCATTGGC
WI-4782	113 C T	GATGCAGAAG ATAACTAGAA AATGC	GAACTCTCTG GTTATTTTCT GTTG	TCATTGACTTTTAGAGTTCCTTCAGTCTTTATGCTTATTTCTTAGGAAAAAAGTGGTAGGAGAA CACAATTCAGGTTCTCCAGATGCAGAGATACTAGAAAAATGC[C/T]GAACAGAAAAAATAACCA GAAGAGTTCATTATGGTTTTTTTCCAGAACGATTAC
WI-4788	65 A G	GCATAGAATC ATCTTGCTAAG TTCC	GGATAAAAT AAAAATTTGGC ATAA	AGGAGAGTTTGGCTCTTTCCGACTCTTGGAACTCAGTCATAGATCATCTTGCTAAGTTCC[A/G] TTGAAAAAAATATGCCAAAATTTTAAATTTATCCAAACCTTAAAGTCGAGATTATAATTGATATTT AAAAAATATATGAGTCTTTCTTAAAGATGGCGTATCACTCTA
WI-5300	38 T C	TCCAGAGAC CACTTCATTC	CTACTCTTCT ATTCATAATC CAAAAA	CTTACTTCCAAAGTGTTCCTCCAGAGACCCTTCATTC[T/C]TTTTGGATTATGAATAGAAAAGAGT AGGTGTTATTATTCCTCTTTTACCAAGGTGAAATGAGGCTCAGAGACAAGGTAGATGATGAGCCCA AGGTCAGTGACAGAGCCA
WI-4818b	121 G T	TGATAATGGG GCCTGT	CCCTCCITTA TATGTATGCCA GA	TATAATGTTTTGTTCCATAGTTGCCATAGACTAGGTTATGTCCACACATGAATAACAATCTTATATA ATAATTTATCAAGAAGGAAATATACATATGGGTGATAATGGGCCCTGT[G/T]CTCTGGCATA CATATAAAGGAAGGCTAA
WI-4818a	43 A G C	TTGCCATAGAC TAGGTTATGTC	CATATGTATAT TTTCTTCTTG AATAAAT	TATAATGTTTTGTTCCATAGTTGCCATAGACTAGGTTATGTCC[A/G]CACATGAATAACAATCTTAT ATAATAATTTATCAAGAAGGAAATATACATATGGGTGATAATGGGCCCTGTGTTGCTCTGGCATA CATATAAAGGAAGGCTAA
WI-5317	139 T C	TTCCATTTCTG GTAGCAGGT	GATGCAAGA AGAAATGAGTC C	TTTTTCCATTTGTTGATTCTTTTGTGAGCCCTTAGATCTCCTTTAAATTAATAGCAAGGTTAAT AATATAATAATATGATGTTATATATTAACAATTCACACAGGAAATCCATTTCTGGTAGCAGGT ATA[T/C]GGACTCATTTCTTCTTGCATCTATTCTAGGTTATTTGCAGCCCCGAGATCTACCCAGG
WI-4888	56 G A	GCAAGATATA AAGATTAAAG AAAGATAACA	CAATCCACTA CCTCATTTAT CA	AAATGAGTAACCCAAAGTTACTCGGCAAGATATAAAGATTAAAGAAAAAGATAACAAG[A/G]ATGAAT AAATGAGGTAGTGGAAATTCCTTGATAACTGGAGTAGTGCCTT
WI-5328	44 A G	---	---	AACATTTTAAACCATGCTACATTTACAAACACTGAAAGACAG[A/G]AAAAAAGAAATATTTTG CCTCAAAAAGCTCTTAAGAGATTATGTAATAAAAAAATAATGAATCAGAAAAAGGAAAGAAAT AGAAACACGTGATACTGGAAAGGAG
WI-4897	93 A G	---	---	GCCTTTTGAGTTTAAGTCTTTTGTGAGTGTGCTTTTTTTTCCCCACTAGGTACTCTCGGCCCAAT CCCCAAAAGAAAAATAAGCGCTTGG[A/G]GATAAACACATCTTC
WI-5345	29 G A	---	---	CCCTGCTATAGGTCAGTTTAAAAATCCT[G/A]CCTGCTATGTTGTTGTTGAAGCCACATCCACT GAGGTATATCTGCTGCTATTTCTATATCACTCAGCTTTTTCAGATCCACTCCACTCACTTGCAG

WI-5370	143 T C	AATAAGATGG TACCTTAACTA	CAAAGTTGGTA CAGAGAATTTG AAA	TGCATGTTACTCTCTGGAAATCATAAAGGATCTGAGAGCCTACAGTATATGGCAACATTAACCAAT CTTTTGAAAAATTTACCTGTATCCCATCATGGTTTCATTTGCAAAAAATAAGATGGTACCTTAACCTA ATAAAACAATGCTTTGAAATCTCTGTACCAACCTTGGCTTTTC
WI-9711b	423 T A	---	---	GATCTCCTTCATCCCTCTCCAGAAGAGGAGAGGAAACACAAGAAAGAAACGCCCTGGTGCAGAGCC CCAATTCCTACTTCATGGATGTAAATGCCAGGTGAGGAGACGGCTTGTCTGTAGTGGGAAAGCAC TGGACCTCAACAGTTGAAATGTTGTAGTGTAGCTGTCTGTATCCCTTGAAGCTGTGCAGCAGCTT CAGTTCTTCGCCCTGTGGAAATATTTCCCTGATACCTCTTAAATTTGAATG
WI-9711a	390 C A	---	---	GATCTCCTTCATCCCTCTCCAGAAGAGGAGAGGAAACACAAGAAAGAAACGCCCTGGTGCAGAGCC CCAATTCCTACTTCATGGATGTAAATGCCAGGTGAGGAGACGGCTTGTCTGTAGTGGGAAAGCAC TGGACCTCAACAGTTGAAATGTTGTAGTGTAGCTGTCTGTATCCCTTGAAGCTGTGCAGCAGCTT CAGTTCTTCGCCCTGTGGAAATATTTCCCTGATACCTCTTAAATTTGAATG
WI-9702c	345 G A	---	---	GGAGGAATTCAGGGTGAATGGACTGCTCCCGCTCCTGAGTTCACCTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCCTATTCAGCAATTCCTACTGGTATGTATCAGGAT AGAGGTGAATCAAGCTGATATTTTGCAACTTCTCAGTTTATCTAACTTTAATGATCTCTGTGACTT TTATACTAGCTTTAAGAGGTTTTCATTCAGGTGTGCTACAGCATCTGATAG
WI-9702b	344 C T	---	---	GGAGGAATTCAGGGTGAATGGACTGCTCCCGCTCCTGAGTTCACCTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCCTATTCAGCAATTCCTACTGGTATGTATCAGGAT AGAGGTGAATCAAGCTGATATTTTGCAACTTCTCAGTTTATCTAACTTTAATGATCTCTGTGACTT TTATACTAGCTTTAAGAGGTTTTCATTCAGGTGTGCTACAGCATCTGATAG
WI-9702a	179 C T	---	---	GGAGGAATTCAGGGTGAATGGACTGCTCCCGCTCCTGAGTTCACCTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCCTATTCAGCAATTCCTACTGGTATGTATCAGGAT AGAGGTGAATCAAGCTGATATTTTGCAACTTCTCAGTTTATCTAACTTTAATGATCTCTGTGATGA CTTTTATAC TAGCTTTAAGAGGTTTTCATTCAGGTGTGCTACAGCATCTG
TIGR- A003N21	49 C A	---	---	TATAGTATTACGAAGCCTAGAAGCACGGCTGTGGGTGGTGGTTCAGTTCAGTTCAGCCTGAGGTTGCAG ATATAATACTTTGAAGCCATAACTTTTAACTGGAGTGGTGGTTCCTTTTAACTTTTAACTTTTAACTTTGGA GGTTTGGATTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTGGA TGATTACCTCTCAATCTATTGT
TIGR- A004V30	203 C T	---	---	AGAATGGCTACTTCATAGGGCAGAGCAGCCACTTTTGGCTAAATTTTAACTCCAAAGCTAATAAT AATCAAGAAGAAATAGAGAACATTAAACAAATAAATATGTCTATTTGGGAATACCTAATATCAG ATACTAACAAGTACAGTGATAAGAAATAAAAAAGATAATAATCACACATACCTTCTAGGTTAGTAGA AAAGTC/G, TCTCTAGGTTAGTAGAAAGTT

TGR- A004W22	232	C A ---	---	---	GGATAATCAGTACAAATAATGGGGACCTTAAAACTGCTGTGATGCAGGAGTGGAGGGCTGGCAGTG CCCGAGGCAGGGAGGAGCAGTGGGACAGGGATGCTCAGTGGTGGAGCCACAGCCCTGGGCTCTGGA TGGGGCATGGGAATGACCAGGTTCCACATCATGCACAGCAGGGCCCTGTAGCTTGAGTCCAGACAG GCCTGCCACACATTGGTGTGCTGCCCGCCCTA/C/ACTGGAGATGTCTCTAAAA
TGR- A005D24 b	138	C T ---	---	---	CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTGAATAATCTCTTTGAGATAATTGATTCATATTC TGTGGCTTTCAACCTCCATTACCTCTTGTCATTCACACATCTTTATAGAGAAATAAAACCCAAATTT CTC/TJTTTACCATTAGTTGATTATCATCTGGATTTTCACTCAAGATGCAGCTCCTAAGATTATT GTTATGTTAAATTCATAAACTCCTTCACCTTTAATAATTAGGAAACAAT
TGR- A005D24 a	123	A G ---	---	---	CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTGAATAATCTCTTTGAGATAATTGATTCATATTC TGTGGCTTTCAACCTCCATTACCTCTTGTCATTCACACATCTTTATAGAGAAATAAAACCCAA TTCTCTTTCAACCTTTAGTTGATTATCATCTGGATTTTCACTCAAGATGCAGCTCCTAAGATTATTG TTATGTTAAATTCATAAACTCCTTCACCTTTAATAATTAGGAAACAAT
U03735	74	C G ---	---	---	TGAGTGTGAGCAGGAGTTGCAGCCAGGGCCAGTGGAGGGGGTCTGGGCCAGTGCACCTTCGGGGCC GCATCC/C/GTTAGTTCCACTGCCTCTGTGACGTGAGGCCCATCTTCACTCTTTGAAGCGAGCAG TCAGCATCTTAGTAGTGGGTTTCTGTCTGTGGATGACTTTGAGATTATTCTTTGTTCTCTGTTGGA GTTGTTCAAATGTTCTCTTTAA
U39840b	42	T C ---	---	---	GGTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAAAAAT/C/CACAGCAAAACAAACCCACA CAAACCAACCGTCAACAGCATAATAAAATCCAACTATTTTATTTTCACTTTTTCATGCACAACC TTGCCCCCAGTGCAAAAGACTGTACTTTATTTATTTGATTCAAATTCATTGTGTATTTACTACAAA GACGGCCCCAAACCAATTTTTC
U39840	56	A C ---	---	---	GGTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAAAAATCAACAGCAAAACAA/C/CACCA CAAACCAACCGTCAACAGCATAATAAAATCCAACTATTTTATTTTCACTTTTTCATGCACAACC TTGCCCCCAGTGCAAAAGACTGTACTTTATTTATTTGATTCAAATTCATTGTGTATTTACTACAAA GACGGCCCCAAACCAATTTTTC
WI-8997	41	G A OCCC	GCCCCTTGCT	TGTTGTACGC AGTGCTCA	GTGGCCATCGATCTGGACCGTCCCTGCCACTTGCTCCCG/A/JTGAGCACTGGGTACAAACATCCA AAAGTTCAACAACACCCAGAACTGTGTCTCATGGT
WI-7008	180	A G ---	---	---	TATACACTTCCATTTGATGGAATGCTGCTGTTTCATGACCACTTTATGGCTAGATGGGTACAGAA AGCACCAGTTTCATGATAGGCAGTTCAAGGTATATGGTACTGTGATGACCCAGAGTCAAAACATTACAG TTTCCACCAAGGCCAGTAACAGGCCAAGAGCTGTCTCTCAAAG/A/GJAGAGTAGTTATCTGCAGA AGATGGCAGGGCCTTGCTCCGAAAGCCTAGAGACCGCCACTGTGATTCACCT
WI-9005	26	C T GGAATCT	CGAATTTGCTG	TCCAAAAGTC TTAAGAAGAA AAA	GGTCCACCAAGAAATTTGCTGGGAATCT/C/JGTTTTTCTTCTTAAGACTTTTGGGACATGGTTTGACTCC CGAATCATCCGACGCTCTCTGTTTTTCTGGGIGG

WI-7593	46 G A ...	---	TTTTGTGCTCTGGACACCCACTGCTCCAGGATGAAAGGAGAG[G/A]AATGAGATCAGTITTTGGA CACTTCCTCTTGAATATAAAGAATCAACAAGTTACAGTCATGTTGGGACTTCTTCTCTCTCCAA
WI-6962	78 A G ...	---	AGTGCATCTTGGGGAAGGCTCCAGTGTATCTGGACCAGTTCCTTCATTTTCAGGTGGACTCTT GATCCAGAGA[G/G]ACAAAGCTCCTCAGTGAGCTGTGTATAATCCAAGACAGAACCCAAAGTCTCC TGACTCCTGGCCTTCTATGCCCTCTATCCTATATCATAGATAACATCTCCACAGCCTCACTTCATTCAC CTATCTCTGAAATATTCCCTGAGAGAGAACAGAGAGATTAGATAAGA
WI-7059	43 C G ... AAGGCACCCA GCCATC	GCTCCTCGCTG GGTCA	GCAGAGAAAGAGAACCATGCCAGGGGAGAGGCCACCCAGCCATC[G/G]TGACCCAGCGAGGAGCCAA CTATCCCAATATACCTGGGTGAATATACCAAAATCTGCATCTCCAGAGGAAATAAGAAATAAA GATGAATTGTTGCAACTCTTAAAAAA
WI-9063	53 A C TT	TCTACTTTCTG OCTTGGGT	AGCAGCCATCACATGATCTGTTTTTCCACCCTTCACTGAAAGACACCATTTAT[G/C]TACCCCAAGGG CAGAAAGTAGAACCTTACTATTCAATTAATGTTTGACACAAATGGAATTGTC
WI-7079	293 T G ...	---	AAGGGCATTGAGACTATAAGCAGTAGACAATCCCCACATACCATCTGTAGAGTTGGAACGTGCATT CTTTAAAGTTTTATGCAATATTTTAGGGCTGTAGACTTACTTCTCTATTTTCTTTCCATTGCT TATCTTGAGCACAAATGATAATCAATTATTACATTTATACATCACTTTTGTACTTTTCCAAAGCCC TTTTACAGCTCTGGCATTTTCTCGCTAGGCCCTGTGAGGTAACCTGGAT
WI-9074	38 A G AAAAG GGTAAAAGTT CTTTTGCTCT	GACAGATTTTT GACCTAGTTCC TT	TGGATGCCAGGTAAAGTTCTTTTGTCTAAAAGAA[G/G]AAGGAACCTAGGTCAAAAATCTGTCC GTGACCTATCAGTTATTAATTTTAAAGGATGTTGCCACTGGCAATGTAACCTGT
WI-7104b	249 C T ...	---	GGAGTTGCCCTTCTAAGGGAAGGAGATCTTATCTTTCTGGTTGGCTTGACCAGTCACGTTGGGA GAAGAGAGAGAGTGCCAGGAGACCCTGAGGGCAGCCGTTCTACTTTGGACTGAGAGAAGGGAGCC CCAGGCTGGAGCAGCATGAGGCCAGCAAGAGGGCTTGGTCTGAGGAAGCAGATGTTTCATGCT GTGAGGCCCTTGACACAGGTGGGGCCACAGCACCCAGCATCTTGCT
WI-7104	157 C A ...	---	GGAGTTGCCCTTCTAAGGGAAGGAGATCTTATCTTTCTGGTTGGCTTGACCAGTCACGTTGGGA GAAGAGAGAGAGTGCCAGGAGACCCTGAGGGCAGCCGTTCTACTTTGGACTGAGAGAAGGGAGCC CCAGGCTGGAGCAGCATGAGGC[G/A]CAGCAAGAGGGCTTGGGTTCTGAGGAAGCAGATGTTTCAT GCTGTAGGCCCTTGACCCAGGTGGGGGCCACAGCACCCAGCATCTTTGCT
WI-8974	34 C T AAGAACTCA OCTGAGCCCTC	TGTAGGGCTGA GCTGGC	CATACAAATGAGAGCCCTGAGCCCTCAAGAACTCA[G/T]GCCAGCTCAGCCCTACACCAGTTTCCACC TGGAGTTTATGCAAGGGCAAAAGGCAGTGCCATGCAAGCTGTTAA
WI-9161	61 C T OCTGGC CCTAAGCATTG	GCTTACAGGAG AGACTAGACA GGAA	CTGTGAGGGTGACGTTAGCATTACCCCAACCTCAITTTAGTTGCCTAAGCATTGCCTGGC[G/T]TC CTGTCTAGTCTCTCTGTAAGCCCAAGAAATGAACATCCA
WI-9014c	93 T C ...	---	CCCTGTTCCCATGCTGACCTGTGTTTCTCCCAAGTCATCTTCTGTTCCAGAGAGGTGGGCTGGAT GTCTCCATCCTGCTCAACTTTAT[G/C]GTGCACTGAGCTGCAACTTCT

WI-9014b	44 C T ---	---	---	CCCTGTTCCCATGCTGACGTGTGTTTCCTCCCCAGTCATCTTTCC/TJTGTTCCAGAGAGGTGGGGCTG GATGCTCCATCTCTGTCTCAACITTTATGTGCACTGAGTGCACCTTCT
WI-7023b	206 C A ---	---	---	TCTGAGAGAAATGACTTGTGGGAGACACCCCTGCAGATCCTCATGGTTTGTGACAGACCCCTCGGTGCT CAGTGCCTTTAAGTGCATCCGCTGTGCTGACTTGGTGGGATCAACATCTGCTACGGTCCCC TCTTTTGGCCCCAGTATTCATGCGAGGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTCACAG A/C/A/CACACATCTTGTCTACCCAAAAGCTGTGGCTGGCAGCACTAA
WI-7023a	56 A C ---	---	---	TCTGAGAGAAATGACTTGTGGGAGACACCCCTGCAGATCCTCATGGTTTGTGACAG/A/CJCCCTGCGT GCTCAGTGCCTTTAAGTGCATCCGCTGTGCTGACTTGGTGGGATCAACATCTGCTACGGGTG CCCTCTTTTGGCCCCAGTATTCATGCGAGGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTCAA CACACACACATCTTGTCTACCCAAAAGCTGTGGCTGGCAGCACTAA
WI-7093	54 C T ---	---	---	CTGAAATCCCTCTCTGCTGCTGGTGGATCCGGGACCCCTTTCCTTCCCT/CJGGCTCCAGCC CTACAGACTTGTGTGACCTCAGGCCAGTGTGCCGACCTCTGCGCCTCAGTTTCCAGCTATG AAACAGCTATCTCACAAGTTGTGAAGCAGAGAGAAAGCTGGAGGAAGCCGTGGGCCAAT GGGAGAGCTCTTGTATTATTATATTGTTGCCGCTGTTGTGTTGTTA
WI-9171	62 G A ---	---	---	ACATATCTGAAAAATGTTGAAGCCTAAGCCAGGAATAAAGAAAAAGTAGAGATAATAATCA[G/A] TCTTTACACCGATGGTAATTAAGCTTGTTATTCACAAGACTTCATGC
WI-9174	47 T C T	CTAGAGGGTA TATAGGACAGG ACTG	CTAGGACCC ATTCTCTATT	GTGTGAGACCATCATGGTGCCAGTCTAGGACCCCATCTCTCTATTAT/CJGAGTCTGTCTCTATATA CCCTCTAGAAACAGAAAGCAATTTTAGGCAGCTATGGTCAAAITGAG
WI-7753	52 A G GAAGAACAGA A	CAGAGGCTTG AAATACAGGG A	CCATGTTCCGA GAAGAACAGA	AAGGCCAGATGCACATCCCTGGAAGGACATCCATGTTCCGAGAGAACAGAT/GJATCCCTGTATT TCAAGACCTCTGTGCATTTATGAACCTGCCCCTGCTCCACAGAACACAGCAATTCCTCAGGCTA AGCTGCCGGTTCTTAATCCATCCTGCTAAGTTAATGTTGGGTAGAA
WI-9186	76 G A CGCA	AAAGGGAAG TCTGACCTAGG T	CCACTTCTCCC CGCA	AAAGAACTACAGAGGAGCATGTCCAAAACAAAAATGGCATCACCTGTCAAAAATGGAGTCCCACT TCTCCCGCA[G/A]ACCTAGGTGACACTTCCCTTTTCATCTT
WI-9193	94 G A CA	AGATATTGT CTGCCTTAAAG TAGGGG	AGATATTGT CTGCCTTAAAG CA	TTGGACAAACCTAGAAATTTCTCCCTTTATGTATCTCTATCGATTGTAGCAATTGACAGAGAAATAA CTCAGAAATATTGTCTGCCCTTAAAGCA[G/A]TACCCCCCTACCACACACACCCCTGTCTC
WI-9015	48 C T ---	---	---	TTTGATTGATATCGTGAATCCTCAGCCGAGAAATGGGTGGATTG/CJGCTTTGGTTAATACAT CTTCCCTAAAGAAAGATAAACACAAAATCCATTCAGGTAGCTCGGCACCACTAAGAA
WI-7254	37 A G AGGAGCCAC	GGTCTGAGAG CATTAGGGA	GGTCTGAGAG CATTAGGGA	GGAGCCAGGAGACAGCGGTCTGAGAGAGGAGCCAC[G/G]GTCCCTAATGACACCCACTCCTAGCC CTGAGGCTCGTGCCTCCTAGACTGGGAAGAGTCCAAAGGAAGGGAGGAGCAGCCACTCCTCAATGC TCAATGGCTCCCTGAAATCAAGACAGG



WI-9231	32 G	CAGTCCCCA GATTGA	CAGTCCCCA ACTCAGAC	CACTTGCCAC ACTCAGAC	GTGACCCCTGTGAGGTCAGGTCGCCAGATTGA/CJGTCTGAGTGGGCAAGTGTGTCAAAAGGGGCTGCCCCCAGGAGATGAGGCTGAGAGCGGAGTTGAGGCCGAAGATCA
WI-7836	120 T C	CAAATAAACA ATGCAACGTT C	CAAATAAACA ATGCAACGTT C	GCTCTCAGAAC CAAGATTAGA AATC	TTGTTGGGAAATAGAGAGTTGAGATAAACACTCTCATTCAGTAGTTACTGAAAGAAAACCTGCTGA GAATGATAATGTCTGTTGCTATAAAGTCCAAATAAACATGAACGTTCC/CJGATTCTTAAT CTTGTTCTGAGAGCCATTGGTTTCAGTTGAGCAATCCCATACAGCT
WI-7286	65 T C A	CAGCTTCAGCT TAAGTGACAG	CAGCTTCAGCT TAAGTGACAG	AAACAATCTA ACCAGAAAGCT TTAA	TCCATTCTCTTTGGCCCTGCAGCATGTCCTCCAGAAITTCAGCTTCAGCTTAAGTACAGAT/C JGTTAAAGCTTTCTGGTTAGATTGTTTCACTTGGTGATCATGCTTTTCCATGTGTACCTGTAAATATT TTTCCATCATATCTCAAAGTAAAGTCA
WI-7858	91 T G TAAAT	CTAAGCATGT ACGTGAATTT	CTAAGCATGT ACGTGAATTT	CCCAATTTTA TTAAAAGTTTA CATCTAT	CAAATTCCTTGGAAATATCTCAAATGTTAATAACAATATGAATTTTCTCATGCATACTATTACTACT AAGCATGTACGTGAATTTTAAATTT/GJTATAGATGTAACCTTTTAATAAAATTTGGGTGTGG
WI-7860	50 C G	CGTACCTCCAA ACATAATTGA	CGTACCTCCAA ACATAATTGA	---	GAAGATTAAAGGAGGGTGTGCTCTGTGGTCTCCTCCCTGCCCTCTCCCA/C/A GTGGGGAGAGACC TGTGATTGCCAAGTCCCTGGACCTGGACAGCTACTGGGCTTATGGGTGGGGTGTAGGCAGG TGAGCGTAAGTGGGGAGGAAATGGGTAAAGTCTACTCCAAACCTAGGTCTCTATGTCAGACCAG ACCTAGGTGCTCTCTAGGAGGGAAACAGGGAGACCTGGGGTCTCTGTGGAT
WI-9064	29 A G TTC	CGTACCTCCAA ACATAATTGA	CGTACCTCCAA ACATAATTGA	GCTTGAGTGA AGTCTCGCAGA	CAAGGGGTACCTCCAAACATAAATTGATT/C/GJTATCTCGGAGACTTACACTCAAGCAATCCTGAGG AATACTGAGGAGGGCTGGCTACTGCTCTCTGCACTCTGCTGCTTG
WI-7307	128 GT	---	---	---	CACACTTGCTGTTCTTCAGTCTGGAGGTCCTGGCAGGTCAGGCTGGGTAGCCCGGGTTCACACA GGCCCCAGCCCTGGCAGGGTCTGGCCCCAGGTAGGGGAGAGCAGTCCCTCCCTCAG/GTAACT GGAGGAGGGGACTCCAGGAATGGGAAATGTGACACCAACATCCTGAAGCCAGCTTGCACCTCCAGT TTGCACAGGGATTGTCTGGGGCTGAGGGCCCTGTCCCAACCCCGCC
WI-9274	25 C T G	GAAATGTGAC TTCACITTTGGT	GAAATGTGAC TTCACITTTGGT	CAGGTAGAATT TTCGTGCCATT G	GAGGAAATGTGACTTCACTTTGGTG/C/JCAATGGACAGAAAATTCACCTGTGCTACATAGGAGAA GTTTGGAAATGCACCTAATAGCTGGTTTACACCTTGATTTCGAGGTGGAAA
WI-7313e	266 T C	---	---	---	AATTCCTTTCTGGTAATCAGGCACATGATGAACCTTTGATTAGTAGGCTGTGATTAAAGTTCTTAAAT TGTTTTCAGTCTTTTATGTTTATTATCATAGGTATAGGTGACCTAAATTCCTTATCATATCTTTATT AATTCAGCCAGTGTATCCACAGTTTTTGTGTTTAAAGTAACTATTATCTCTGGATTTCATG AAGGTGTAATATCGTTTTTGTAACTGAATAGATTGTATAGCGATGA
WI-7313c	256 C T	---	---	---	AATTCCTTTCTGGTAATCAGGCACATGATGAACCTTTGATTAGTAGGCTGTGATTAAAGTTCTTAAAT TGTTTTCAGTCTTTTATGTTTATTATCATAGGTATAGGTGACCTAAATTCCTTATCATATCTTTATT AATTCAGCCAGTGTATCCACAGTTTTTGTGTTTAAAGTAACTATTATCTCTGGATTTCATG AAGGTGTAATATCGTTTTTGTAACTGAATAGATTGTATAGCGATGA

WI-9281	68 G A ---	GCTAACACTTT TAAACCCGT	---	CATTATTG AAAGCTATTCA GACA	ACTGTGGGAGACTGTGAGGATCCAGGATTTCAGTATTCCTGGCCAGAGGGCCTTGCTGGCTACTGG [G/A]TGTTAGTTGCAGTCCTGTGTCCTCCCTCTCTTATGACTGTGTCCC
WI-7848	142 A G CTC	GTATATTACA ATGATCACCG	---	CCCCACAGAAC TATTGTA AAC AA	TTCTGAAATATAACCCAGCCATTGAGCTATTAAACCTTGTAATTTTAAATTTACAAAAATATAA AATATGAAGACATAAACCCAGTTGCCATCTGCGTGACAATAAAACATTAATGCTAACACTTTTAAAA ACCGTC[CA/G]TGCTGAATAGCTTTCAAAATAAATGTGAATGGT
WI-9304	70 G A ACTGA	---	---	CCCCACAGAAC TATTGTA AAC AA	TCACGTTTGGTGCTTCAGATTCTGAGGAAATGCTTTGTATTGTATATTACAATGATCACCGACT GA[G/A]AATATTGTTTACAATAGTTCTGTGGGGCTGTTTTTTGT
WI-7933b	314 C A ---	---	---	---	TTACAGAACTTGCCCTGTGCTGTGCTCCCCATGCTAGGGGGGAGGGGCTTTTCCTTCCTTTTC TACCTACCCCTTTCTCTTGGCCAGGGCCTCGTATCCTACCTTCTGTCCTGGCTGGCTGCAC AGAGGATTGCCCTTCTCTTTTCAGAGCTGCCCTCGATGCCAAATTAGCATTTAGTATTTGCACAA AGTCTAAGGGACCATGGCTGCCCTGGGGGAGGAACCATAGCTCCCT
WI-7933	96 G C ---	---	---	---	TTACAGAACTTGCCCTGTGCTGTGCTCCCCATGCTAGGGGGGAGGGGCTTTTCCTTCCTTTTC TACCTACCCCTTTCTCTTGGCCAGGG[G/C]CCTCGTATCCTACCTTCTGTCCTGGCTGGCTGGCTG CACAGAGGATTGCCCTTCTCTTTTCAGAGCTGCCCTCGATGCCAAATTAGCATTTAGTATTTGCA CAAAGCTAAGGGACCATGGCTGCCCTGGGGGAGGAACCATAGCT
WI-7374	182 T A ---	---	---	---	CCAGATGTGCCCATCACGTTTTTCTGAGGCTTTTGTACTTTAGTAAATGCTTCCACTAAACTGAAA CCATGTGAGAAAGTTGACTTTGTTAAATATTTGAAATGTAATGAAAGAAAGTACTGTATATTA AAAGTTGGTTGAACCAACTTCTAGCTGCTGTGAAGAATATATTG[T/A]CAGAAACACAAAGGCTT GAT
WI-9343	78 C T CCTTGCCA	CCAACAACAT CCTTGCCA	---	AAATGAAACTT ACGTTTGTG TG	GGTCTGCTCCTGCTACCTTGACCCCTCCCTTCTCTCTCTCTCTCATCATCCTCCCAACAACAT CCTCTGCCA[C/T]ACACAACAAACGTAAGTTTCATTTGGGCAAA
WI-7386b	104 T A ---	---	---	---	CTATATGTGAGAGGCGTGATATCTGGATGGAAGTTGGGCTGGATGATCTCCAAAGTCGTTTCAACTCT TAAAGACATCTTAACTCCTGAATGTAACAATTTGTTA[T/A]GTGTTTAGAATCAGAAATTTGATTTGA ACTTGAGTAATTCATCCTT
WI-9357	75 A G ---	---	---	---	AAGAAGGAGCTCAGTTACGGGGTTTTTAAACCTTCATGAAACCTGAAGAGTTCACTTTTGTATTAT GCTCTTA[G/G]TGATTACAGACTGATGCCAGACAAACCTTGGGAAGA
WI-9360	79 T C TGG	CTTAGAAAA TCTGCTTTAAC TGG	---	CCTAGGGAACA CAATTAGAGGA A	TGAAGGGGTGTGGCATCTGTTTCTGATGCTTACTACAATATGTGAACCACTACTTTAGAAAACTG CTTTAACTTGG[T/C]ATTCTCTAATTGTGTTCCCTAGGAAATGACTGTCCCAAG
WI-7423	107 T C GTTC	TTGCTGGGCTGT	---	GGTCCAGAAGA GCGG	TGCTCCCTGTCCCATCTGAGTGACCCAGGCCACCCCTTTGAGGAGGTGGGTGAAGTACTGCTCCTT GGCAGGGATTGTGACACTGCAATGCTGGGCTGTGTTCTGTTGAGGCTTCTTGACCTTGGACCCGTG GATACCAGGCCATGTGCCATGGTATTGGGTCCTGGAGGGTGGTGAATAAAGGCATCTGCT

WI-7424	131 T	A	CAAGAGAGAG AGAGGAAAGA	TGCAAAAGAAA GAATGAAAGTT G	CCAGGAGCACTAGAGAGGGGAGGAGCAGAAGTTAGAGAAAAAAGCCACCGGAGGAAAGG AAAAAACATCGGCCAACCTAGAAACGTTTTCATTCGTCAATCCAAGAGAGAGAGGAAAGAAAA TT/ATACAACTTTCATTCCTTTCATTCGACGTTTACATAAACATTCATACATA
X86400	118 A	C	---	---	TCCTGCAAGAAGTCTCAAGCCTTTTGATTTTGTGCAATAAAGTACAGCTTTCATAAGAGTGAAA TTGGGCTAGCTTAAATGGATCCATAAACCTTCTCTAAATTTAAGTGAGA/AC/CTCTTTTAAACACCT GTTAAATTTAATGTAGCAGCTGAGAATCTAAATATGTACCACTCGTTTATTTGTTTCATTCATCCA TCCCTTTCCCATGAATATTTCA
WI-8053	242 T	A	---	---	GTGGCCACTACATGTTATAGAAACCATCATCTTGTACACAGCAGCTATGTAATAAAGGCTGAG TTATCACTAAGCAGGAGAAAGCATTTAAAGGTGTCCTCAATTAAGGGGACTTTTAAATCAACCTAA TAAACTCTAATTCGTGCTGACTTTTAAAGATCTAAGGTCAATTTAATACATGCTGAAAAGGGTCACA ATTAATTCCTTGATCTTTTACTCACTGTTAACTTATATAAT/ATTCAGAAC
WI-6190	165 G	A	---	---	TACAAATGAATGTCTTTTATTCGGTATGCATCCACATTTTCAGCATTTAGTGTCTGAAACAGCAAG TGAAAGACGCGAGCAATTTGCCAGGAGTCAAGCCCAACCAATTCGGGGATCTGCTGTGCACACCGG GTCTCTTCTAATCCCTGCTGAGGATCTTG/AG/AGAGCAGCAGCAGCAAAACCAAGGCATGCA CCGGATTCAAGGTTCTTTTGTCCAGTTGTCAGATTCCAAACTAGACCCCA
WI-6275	148 G	C	---	---	AACAGTCAACCACCAACACATGACAACCTGCCAGGAGGCTTGTCTCCCTCCCTCTCTTGGCTCCC ATGTGCTTAGTCAGCAAGGTGGGGAGGACCGGATGTAGCTTCGCCCAAGGGAGTATTACAGAGA GAGGCTTGGGAAA/G/C/GGAAAGGAAACCTGGACAGGCTTTTCAGCACTGAGAAATCACTTAAAACTG ATTTGCTTTTCAGTAACTGGTATGCTGAA
WI-6421	41 G	T	---	---	ACCAAGAGATCAGCTGTCTAACACAGCAGCTTTTGTGTTG/TJGGGCTTCTGAAAGAACCTTGC TGACAGCTTCTCACTGACCTGCAGGACGGAACCGTACCTGAGAGGGGATGGGGCTCTCTCAGAAA GAATATTTGGGCGAGAACCTTGGAACCTGGCCACCGGACATCCCAAATATCCCTCTCTCAGGG CTCACCCCGACATCTCAGCCAAATGAAGGCTCTGAA
WI-6905	215 T	A	---	---	GGGTGAGACGGGTTTATTGTGCACATTTACACAGCTCAGCGTCTGGGCTGGCAGCGGCCATGCTC CTGTGTCGGGCTGCTACAAAGGGCGTTCACTTTTCTTCCACCACTATGTACAGTCAGTGCTCAA GGTATGGGCTACAGTGTGCTGATCAGTGTGCTGTACACACATTTTACATAAATTACACAGACTC ATACATGAAAAAT/AGAGCCTAAGGGCCTGATTTTATGAGAAAAAAA
WI-9420	202 G	A	---	---	AACCTGTTTACAAAATAGGCTTTGCAAACTTCATTACTGAATTTGAAAGTCAATGACTGTGTTT TAAAATATGTACCAAGGAAATACAAATTTGGATATGATCATTTTTCATGCTCAGGAGAACAGCAC AGAAATAAGGATACAGCAAGGTGCAAGGAAACCGGAAACCAATTTGTACACTGTCTTACACAG TG/AG/AGCATCTTCTCACCCTTAACTGCAGCTGTGCAAGATGCCTCAGTGTG

WI-9448	184	G A ---	---		TGGGGCTGCTTTAGACTTCATTTCTAGAGCAGAGCACCTAGTGAGAGGAATACCTGGGAGAGAGAC TGCCCTTGCCCATGGTGTAAACCTACATGAGGGGACTGAAATCTCTTTGGATGCCAGTCCAGATCCC TTTTAAGAAAATGGGCTTGTGTTCCAAAGGTGAGAGCTGGCACCAC[G/A]CACTGGTTTCTAAA TCTCTGGCTTGGATTTATCCAAGCGCATGTTCTTAACGTGCCCCGTGAGCAG
WI-9470	204	G A ---	---		ATGTCAGAAGAGACACAGACAAGGAGTTTTCCTTTTAAATGCTAAACAAGTGCCAACTAATCCACA GATCTGAAAAAGTACAGCTCTCCAGGTTGATAAATCAGATTCAGGCTTTTCTTGTCACTCCGCTTA TGAGATCACGAATATGATCTOCTTAAAGCCCCAGATTCTCTACTAGAGCCGCTGGGACACTGATGAC AA[G/A]GCAATCAACTCATCTCTCAAGCTCACAGGGCTCACTTCCCAG
WI-1245b	201	G T ---	---		GATGATTTCTGAAGTCTCAGCAGCCCTGATTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTGCTGCTGATGCAGATCTGCTGTGAGCCATGTCTGGCATCACAGGGTGGT TTATTAATTTCAATTATCATCTGGACAGCCCCCTCTTATAACGTACATCCTTGCCCTCTTCTGAGGC[G/ T]CTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1245a	85	T C ---	---		GATGATTTCTGAAGTCTCAGCAGCCCTGATTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTGCTGCTGATGCAGATCTGCTGTGAGCCATGTCTGGCATCACAGGGGT GGTTTATTAATTTCAATTATCATCTGGACAGCCCCCTCTTATAACGTACATCCTTGCCCTCTTCTGAGGC GCTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1031	149	G A ---	---		TCAGTGATAAGGACAGGCTAGAACAAAGCGTTCCCAACCCCTGGCACCATGACAGTTTGGACCAA TAACCTTTGTTTCAGGGGACTGTCTTACACATTGTGGGATGTTTAGAGCCTCCGTGGCTTCTACCCA CTAGATGCCAGCA[G/A]CACAAACACCCCTCCCCAACAAATCATGACAAATGAAATGTCTTTAGACATT GCCAAATATACCTTGTGGACAAAATGGCCCTGATTGAGAACCACCTGGTT
WI-5385	110	G A ---	---		AATGAGTCATTGTGGAGTTAGAGGAGGTTACTGAAATGGTGACTCCAATGGTGGGATTGAAAGAGG GAAGTCTCGATAATTTTAAACATATGGTTCTTGCCAGGAATCG[G/A]CAATGCTAATCTATTGCTTAA TCTTTATCAACAGACTCTTTGAATCAATTTAGAGATACTCAGTGACCCCATGGCTAGAGTTCCCTGAC CCCTGCTACGGGAAACATTGAATGCA
WI-5403	199	T G ---	---		ACCAACCCGTTGGCAAGGCTCCCCAAGACTCACCAACCCAACTTTGTGCTTACCCTATGCCGGGTG GGATTGAAGAAATAACCATAAATATAATTGCTACAATTTTCCAGTAGTTACCAGGACCCAGCCTAT TGGAAGAAATCATAAATGTAAACCCTACAATGTATTGCTCTCTGCTTGGTGGCCAGGCATAGAGTT/G JGGCCTACAACCCATTTATCATTTGAACCCCTCAGAAGCATCCAGTTGGGCT
WI-5801b	157	G A ---	---		TGATATTTTCCCTTCCCTAAATGTTATGATTAAATAGTGCTTTGTAGAAATTTGAAAAAATGTAAA TCAGAGAACAGAAAGAAAATAAGTATAGTTGAAACCCTCAACAATTTTAGATTTTAAAGGCCTAG GGAAAGAAAGAGAGCCCTGGGA[G/A]JAGGGAATGAGAAAAGCACACCAGAAAAAAGTGTGT GGCTTAAGGGGAAGCCCAAGGAAGTTAAGT

WI-5801a	48 A G ---	---	TGGTATTTTTCCTTTTCTAAATGTTATGATTAATAGTGTCTTTGTA/GJGAATTTGAAAAAATGT AAATCAGAGAACAGAGAAAGAAAAATAAGTAGTTGAAACCTCTAACAAATTTAGATTTTAAAGGCC TAGGGAAGAAAGAGAGCCCTGGGAAGAGGGAATGAGAAAAAGCACAAACAGAAAAAAGTGTGT GGCTTAAGGGAAGCCCAAGGAAAGTTAAGT
WI-5696	61 C A ---	---	TTCTATTTAAATCCTGTGCCCATTTGCAAGACTGCATTGAGTCTGCATGAGCCTTAGTTTC/AJTA AAGCCCCCTCACACCGAGGACAATGTTGAGAACTAAATGACTGCAGGTGAGCAATTTCTGTATTA TACAACTGGGACCAAGATGACTTTAATAGTGGCAAGAGACAATCAGGCAGACTGGGAGGACC TTATAATAGATTATAAGGCTGGTGAGTTTATTTAACTT
WI-7461	153 C T ---	---	TATTACTAGGTTTCATAGAGCCCCGTTGTATGATAAATAGCCAAATAGTTAAAGAGGCTGCAGGCC AATTCTAAGCTCCTCACCTCCCTTCGAAACCCAGCCTCAGAGATGACACTTAGGCTGCACATTCCCTG TGGCAGGGACTGTGTCT/CJTGTCCTGTGGTCCCGAACCCAGTGTGGTGCCTGGCACAGAG GAGGCCCTGAGTAGCATGTGCTGCA
WI-9716	221 G A ---	---	AGAAGACAGGAGCACTGGGATCAAGGACTGATAAACTCTGAGGCTTTAATGGTCCCTGTCTCTAAC GCCTTTGGTATACCTTCTCTTTCTGAAGACCAACCTTTCAAACCTCTCAGAACACAGGCAAGATGCAT ATTCTGTAGTTTCAGATGTGTACTTCTACATCTCGAAACCTAGATGAGTAGGCTCTCTTCATCT CAATTGAAATTTCTAGAA/GAJAAACACCTAATGGCTCATCTTGGATCA
WI-9760	49 C T ---	---	TTTTCGTTAAGCTTTGTGAAGCCACACAGAAGTATCTACTCTTTAC/CJJAAGTGTTACTTTGCA TATATTTATGGGATGATTTCTATCCCTACTTAAGATTTTCTCTCTCAGGTTAAATATTCATTTCT TTGTTCAAGGAGTTTCTATTGGCCCTTCTTTCTAAACCCCTTAACCATCTGCTTATTCTGCTTGACA CATGCTATTTAATCAAGGTGACATT
WI-9855	31 A C ---	---	GAAACCTCGTTGGCTCAAAGGAAACTGTAG/A/CJAAATCTTTTATTTTATTTTGTGTTTTAACTC AAAGAGTGGAGTTGCATTGACCTTGATGGCAGCTGCTCTTTTGTGTTGGTAAATCCTCTAGT GGGCACCTTGCAAAAGCAATTTAGAGCAAAAGGTGGTGGCATGGAGTTGTGTGAGGTTGCTGAAAAAG TAGCAAAATGGAAAGGTTAATGGA
WI-10312	41 A G ---	---	AAGGCCAGTGGGAAAGCAGACAAACACTCCAAGAATAC/JAGATATAAAACATCATCATCA GTAGAGATGGGATGACCTAGGAGGTATGCTGATGAGGCGATGTCAGACCAAAAGACATTTGGGTCT TGAGGGTTGAATAGGAGTTGTCTGGTGAGTCTTGCCAGTCCCATAGTAGGTGTTCCATAATAAAC AGTGACTAACTGAGGTAGAGTCAAGAAAGAAATTTCA
WI-11152	179 C T ---	---	GATTTCTTGGGACATGCAGAGCAGATACGGGAAGGCATCTTGGGCATTTGGAAGGAAACGAGCCCTA ATTATAGAAACAGACTCTACAAAGGACCAGTTAAAGGTCTCGCACCCAGGGGACTGGGTGGCCAAAG TCAGTCAAGGCATAAAGGGGGACAAAGTGGGACAAAGGCTTGTCA/CJCTGTGCAGAAACATTGAA AACAGCCAGTACATGOCACCTGATAGA

WI-1968	167 A G ---	---	TGTTGAGGAGCTGAAGGCTGAAAGATAGTCTCTGCTGGTCTTTTCGTTGGAAATGGATGAGTCCT TTTACAAAATTTTCTCTGGCATGGGTGTTATGTTTGAATCATGGAGTTGGAAGACTTAGATTCA ATTGGGGCTGTACAGTTTACTGGAAGTTGT/GJTGAACTTGAGCAAGTGTCTCTTAATGTCTCTCA GCCTCAATGCCCTTCCCTGTAA
WI-4701	198 G A ---	---	GGGTTCAITTAACAGCCTTCCCACTGGGTCTCAGATTGCACGGAGATGTAAAAATAGGAAGAGATAG AAAAATGGTGCCCACTATTGACTTGATAACACCTACAAAACACACATTAAACTCTCCCCACTCTA CCCGCCAAAGTCTACCTTTTGGTCTTTTATTCTGCTAATGACCATACTATTTCCCAATTAGA[G/A] CCATGTCATTTTTCAGAAAAGCAGTATA
WI-4823	164 C A ---	---	TTTATCTTCCAAACCATGTGTGTTTCTTCACATACITTTACGTAATTTTAAATCATGTCATTTAATTA TGCACITTAAGTTGGCTACCGACATTTGCTTCCAATTTGTAATTCCTTAACAACAGCAAGCATAACT GATGTCCATCTTTGTATTCCTAAA[C/A]AAAGAAAAGTGTCTTTTGTGCATCTGCCCTCTCTGT CTTCTGTGTTTCCCTTCTGTTTCCCTATTCAGCATTCATGATTA
WI-4860	72 A G ---	---	AAAAAACAACTTCATTTGACATTTCTAAGAGATAAGAAAAACAACGATCCACTGTGTGTTGCTT GATTT[G/J]GGAGATAAACCTGATCTCTAAGAAAATTAACCAAGCAGTACACTAAAATAGCCT TTGTGTGGTTTTCAGGAAAGAAAGCCAACTCAACTAAGTTGCTAAGAAAAATATGTTTCATATCA CTCTAATCTCCACATAGAGCATTATATAGCA
WI-9705	111 C A ---	---	TGAAGGACCAGTTTCCGAATGCCTACCAAGGTAAAGTAAATCGGAGGGCAGGAAGTAGGAGTTGCTT CCGGATGTTGCATAAATTGAGGTTCTTTAAGGAGTTTCGGCTGCC[C/A]AAAATTTTAACTGATGC TGCTACAAACGCCACATAGAAATCGGTGGTAGATTGCGGTTCTCTAGTAAGTAGCTAATGTTTAGATA TGATTGTTGAATATTGTTGCTGTGTTCTTGGTG
TGR- A004Z48	177 A G ---	---	CAAATACTCTGCTTAGAAGTTGCTCTAGGGCCCATGGATTCATGTAAGGTGGGCGAGGTGGACTG AAGATCTGTTGGCAGGGCTCACAGACGCGGGGTGAGGGGAGAGATCGTGGGTTTCATGAGATCCCAT CTTGGCAATACGGTTATCCCGTGGTCTTCATACGCCACAGA[G/J]TCTCCAAATTTAGGGGCTOCC GTGGGATGGTGGAGCCCAATGAAGACAGGTAGATGATGCCACCTAGAGATG
U17579	34 T G ---	---	GGGATTCAATGTGTCTGTCTCATCCAATAAGCACT[G/J]CATGACCTCAGCCCCATCTTTCTTCCC TATGTTCCAGAGACAGATAGACCTGGCCCTTCTCTAGGGATCACAATATTGGAAGGATGAG GACTCCAAACAGCCAGCTCCCATGCCAAATAGAACGATGAGTGTGGGATCAATTTCTATGGGAGCC TGGGAGAGGGATCCTTCTAGTTGA
WI-7747b	88 T G ---	---	GTGAGAGCGAGGCTGAGCCTACAGATGAACCTTTCTGGCCTGCTTTCGTTAACTGTGTATGTACATA TATATATTTTAAATTTGAT[G/J]AAAGCTGATTACTGTCAATAAACAGCTTCATGCCCTTTGTAAATT ATTTCTGTTGTTGTTGGGTATCTGCCAGTGTGTTGTTGTAATAAGAGATTGGAGCACTCTGA GTTTACCATTGTAATAAGTATATAATTTTTTAIGTTTTTCTGTA

WI-7747a	44	T C ---	---	GTGAGGCGAGGCTGAGCCTACAGATGAACCTCTTTCTGGCCTGCT/CJTTCGTTAACTGTGTATGTAC ATATATATATTTTAAATTTGATTAAAGCTGATTACTGTCAATAAAGCTTCATGCCTTTGTAAGTT ATTTCTGTTTGTGTTGGTATCCTGCCAGTGTGTTTGTAAATAAGAGATTTGGAGCACTCTGA GTTTACCATTTGTAATAAGATATAATATTTTATGTTTGTGTTCTGA
WI-7189	197	T C ---	---	TCCAGAAATTTCCCTTCCTCAGCTCATTTTGTCTCTCACAATTAAGGGAGTAGGTTAAGTGAAGGT CACATACCATTTATTTCCCTTCACAAATAATATTTTACAGAAGCAGGAGCAAAATATGCGCTTT CTTCTAAGAGATATAATGTTCACTAAATGTGGTTATTTTATATTAAGCCTACAACATTTT[C/JAG TTTGCAATAGAACTAATACTGGTGAAATTTACCTAAAACCTTGGTTATT
WI-7850	57	G A ---	---	AGCCCCAGCTGGACTCATGGATGTCACCCCTTTGCTCCCTGCTCTTTCTGCCCTGG[G/JCTCATGTA TCTGGCAGCTCTGGTACCTCTGTGGGTGCCATCTCTACCTCTGACACAGACTGCCTGCCCTTGAAGCT GAGAAGCACAGGGCAAGGAGCCAAAGACCACAGAGCCTCAGCAGCCAGGATCCGTCCTCATTTT ATTGGTGATGATGAATGGGAATGAAATCAGGGGCTGTCTACTAGAGCC
WI-7907	69	G C ---	---	CTCTTCTTCATCCCATCAOCCCTAAATAGGTCAGGTGAGGGAGGCTGGGAAGAGGTGGGAGGAGG G[G/C/JAGAGTGAAAGAGATAGGAAGGATATTACCTCTCTGTGTTATTTTAAAGAAACATTTGTTT GGTGGCAGCAATCTCCCTGTCCCTATCACTGTAGAGGCCATAATTTATATCTATAAATATATTAAAA AGCAAGTCAAACTTGGATGTATCAAGGTAAAATATTGTCAAAAGTTTAAAT
WI-7919	242	T C ---	---	GAAGGCAGCTGGATCACTTCCCGCAGCTCTTGGGCAGCGCTTTGCTGTGGAACACGAGAGCTCCTCT CAGGGGCTGGCAGCTCACTCACTCTATTCTGTATGATGTTATTTGGTTAAACACTGTCAATAATAGAGAT GTGCCAGATTTAGATTTTCTTACCCTAATCTGTTTAAATATTGTAACCTTTATCCATTTGAAAGTGCA AGCCCATTCAGATAAGCTATAATCTGGTCTTTAAGGAAT/C/JACAACTTT
WI-7928	101	T G ---	---	CTCCCTCCTATGTCTCAGCAGCAGCTTGGGCACACCTTGTTCATCTCTGACCCGTTTGGTGGCTA TTCCCTGCAGTGCAGACATCGTCAAAATTCAT/GJACAAGAGGAAATTTTCATGCAGAAAGCTGTA TGCAGGATGCTCACTGATGTTTGGCACTTTAAACTGAAATTCAACTCTTTATATAGGATTTTCTTTT CTATCTCCATCTCCCTCATTAAAAAATACGTACATTTTCGAGGTAATGGTA
WI-7936	131	T A ---	---	TTTTGAGTCAAAAGACTTAAAGGGCCCAATGAATTTATATACATACTGCATCTTGGTTATTCTGAA GGTAGCATTTCTTTGGAGTTAAATGCACATATAGACACATACACCAACACTTACACCAAACT[A] ACTGAATGAAGAAGTATTTGGTAACCAAGGCCATTTTGGTGGAAATCCAAGATTGGTCTCCCATATG CAGAAATAGACAAAAAGTATATTAAACAAAGTTTCAGAGTATATTGTTGAA
WI-7944	99	T C ---	---	TACAGGTTCCAGCCCGTTGCCCACTCATCTGCGCGCTTTGCTTTTGGTGGGGGAGAGATTGGTTGG AATGCTTTCCATCTCCAGGAGACTTTCTATG/T/JAGCCCCAAGTACAGCCTGGACCACCCTGGTGTG TGAGCTAGTAAGATTACCCTGAGCTGCAGCTGAGCCTGAGCCATGGGACAGTTACACTTGCACAGA CAAGATGGTGGAGATTGGCATGCCATTGAACTAAGAGCTCTCAAGTCA

WI-7805	101 A G ---	---	TTTCTAGGCTGTACAGTCTGATGATGATTTTATAAATATTTTCATACTCTTGTAATTTGGATCTT TTTACTTTGAGCATATATTTAGAATATGTGT[AG]TGTTAAAGGATCTCCACAATGTCTGCAGTGTG AAGCAGGTTTATTGTGGAATAGTTTAAACAGTCAAGGAGCTAAAGTGGTCAGTATTAAATGTGTAGC CCTACCAAAATAGCCAGTAGTATCTGAAAATGAAAAATAAATGAAGTAT
WI-7416	137 G T ---	---	GGCAGGAGATTAGCAACAAGGATTCACTCTGTACTACTTGCCCTTTTATCTTTCCCTCTTGCC CAGTCCCTTCTCTCCAGCTTCATGTGAAGCTCTGCACAGACAGACACTCAGTGTCTTGGCAGTGT [G/T]CTACTCCTCAGGTGCAGCATACATAACCAGTAAGAGACTAAATCTGCAATATATAAAGAGCTC CTACAAATCAGTAACATGAAGAACACTCAAAAATGGCAAAIGTCATCAG
WI-140	252 C T ---	---	ATTTGAAGATTGGAGGGCTTTGCAGAGGAAAATAGATTTCATTTGGATCCCCAACTATAATGACA AGTTTTTAATTAGGTGTGATCAAGGCTTCTAAAAGTGAATGCAAGTTGTTACCAGTAAAGTTTATA TCTTCATTACGCCAGCTCATTTGCCAGAAAATTCAGGTGAGTGGATTGGCCAGACTATCTGGCAAG GATGAAAATTTAGTTTAAAAATGTGTCATTTGCTGTATTGGCATTCCT[C/
WI-198	218 C T ---	---	GAGGTCTTTCAGCAACATGGAAGCCCTACTGCTTCAACCCCGAGTTCCCGGATCAAGTGTGGCACCC CATGATGGAACCTCTTGCCATGGTTTAGTACCCTGGACCAAGTAGTCAATCCATCCTGACTTTAAAA TTCTAACAGCCTTTGATGGGACATCTCTGCTAAAGACTAACCACTTCTTATCTTATCTTACGCTA CCTGCTTCCCTT[C/T]GTTTAAACAAGCATAGAATATCTGAACAAC
WI-205c	146 T C ---	---	TTATGGTCCCAAGACAGATTTTAAAGAAAGAAAATAAGCCTCATCTCTAATGACTTGGTCGG AAGCCAAGAACCTACTTCAACATTTGACCCATAACCTTCTTGAGATGATGGCTGACTTTTCAAT GCATGAGTTT[G/C]CCAAAGGCTTGATGGGAAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAAAGTGCATATGCCTTTATTTTGTAGTTCCC
WI-205b	146 T C ---	---	TTATGGTCCCAAGACAGATTTTAAAGAAAGAAAATAAGCCTCATCTCTAATGACTTGGTCGG AAGCCAAGAACCTACTTCAACATTTGACCCATAACCTTCTTGAGATGATGGCTGACTTTTCAAT GCATGAGTTT[G/C]CCAAAGGCTTGATGGGAAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAAAGTGCATATGCCTTTATTTTGTAGTTCCC
WI-234	165 G C ---	---	GAAGACTGAGTTTCCAGGAGGTTGCAGCCGTTTCTCTCGGGCCATATGGCTAATAAGGAGCTTGAGCA GGGATTCAACCTGTTTGCAACCCCAAGTNTTCCAAAGAGGTCTCAGACTACCTCCTCCATCTCCCCCT CTCCCCCACAACACACAATACAGAGATT[G/C]AATTCAGGAGCCAGTTCTAGGTGGGCTTTGAGC AATCATACACAGTAATCTCTTGGTGTCTTAGTTTCTCAAAATGGGAAATGG
WI-276b	25 A G ---	---	AGCTTTTGAATCCAAAACCCACAT[AG/C]TTGACTCTCTTATCTCTCTCTTGTGTAACTCTATCC CTGAGGCAGAAAATACAGAACACCCCTGTGGCTGCTGACCGGAGGAGGATGGGGCGGGGAGACAT CGGTCAATGTATCAAGCATCTCTCTGCTGAAAGACCTCTCCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTTGTCTTATCCTCTTGTCTATCCCTGATGACTGGGCAAA



WI-276	25 A G ---			AGCTTTGAAATCCAAAACCACATAGCTTGAAGCTCTCTTATCCTCCTCTTGTGTAACATCTATCC CTGAGGCAGAAAATACAGAACACCCCTGTGGCTGCTGAACGAGGAGGATGGGCGGGGAGACAT CGGTCAATGATATCAAGCATCTCTGCTGCTGAAGACCTCTCTGAAAGACATGAGCTATTAGGAGC TCTGGCAGGGCTTGTCTATCTCTCTGCTATCCTGATGACTGGGCAA
WI-427	59 G A ---			TTTCCCAATCCACAGGTAAACTAATAATGGATGTATAGAATTTAGAACTACTTCC[G/A]GTTT TTCCCTGGGAAATATTACAAAACATTTGTGGCTGCAATCAGGTTAAAGACATAGTGTGCCA TTTGTGTCATCAGACAGGTAGAGGCTGACTCTGGCAGGATTAGTACCACTAGCTGTGAGACTTTATGT ATTCAATTTATTAGAGCCAGGGTCTTGTCTGTCAACCCAGCTTTCAGTGCAGT
WI-562c	106 T C ---			CTCTTCACTCCAACTATATTGCTTACTTAATGGTTACAGATTAAAGCCAGAAAAGGAGCCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAA[T/C]AAATGGTCTTTTATTAAAAAAA AAAGNTATCTAAAGAGAAAACCATATAATCTCTCAGGTAATTATGGCCACAGCCAAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562b	106 T C ---			CTCTTCACTCCAACTATATTGCTTACTTAATGGTTACAGATTAAAGCCAGAAAAGGAGCCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAA[T/C]AAATGGTCTTTTATTAAAAAAA AAAGNTATCTAAAGAGAAAACCATATAATCTCTCAGGTAATTATGGCCACAGCCAAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562	103 T C ---			CTCTTCACTCCAACTATATTGCTTACTTAATGGTTACAGATTAAAGCCAGAAAAGGAGCCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAA[T/C]AAATAAATGGTCTTTTATTAAAAAAA AAAGNTATCTAAAGAGAAAACCATATAATCTCTCAGGTAATTATGGCCACAGCCAAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-597c	141 A G ---			GTGTAATTTGGTGGCTTTGCAACTTTCCACAGTAACCTTTAGAAATNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATG[A/G]TAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAATTATTAAAC TTGATCTAATAATTCTTCACTAATAATACCTGAGAGAAATAAGTCTATTTAAT
WI-597b	141 A G ---			GTGTAATTTGGTGGCTTTGCAACTTTCCACAGTAACCTTTAGAAATNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATG[A/G]TAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAATTATTAAAC TTGATCTAATAATTCTTCACTAATAATACCTGAGAGAAATAAGTCTATTTAAT
WI-597	136 A G ---			GTGTAATTTGGTGGCTTTGCAACTTTCCACAGTAACCTTTAGAAATNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGCTATGTTGAAGAAGTATCCTTAGGATATTCT GAT[A/G]CATGATAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAATTATTAAAC TTGATCTAATAATTCTTCACTAATAATACCTGAGAGAAATAAGTCTATTTAAT

WI-611	66 G C ---			TTCAATTTAACACCAATTGGGTATATTATAATTTTNGCTCTATCCATAGTTCTAACCCCTCTCTCTG/ CJACAGTGAGACACCTGCCCTTCTATGTCTTGAAGTATTACGTAATCGATCAGTCACCCATCTGGA ACCAAGGTTTCATTTCTGCTGACCCCTCCCTCTCACCCCTACTGGGCTCTGACTTCTCTTCTCTGGCT GAACCTTCTCTGTGGCTGTCCGCTTCTCTGCTTGGCTCCAATAC
WI-681b	156 A G ---			TGAAGCCCTCTCTATACCCAAAGTGTCTTTATCTTTAAATGCTGTGGTCAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTACAGGGGAAGCACTTTGNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATTJAGJTTATACTATGGCACCATTGGGACACAGATTATATATGTCAGA CACCACGNATGTCCTTTAAGATAIGCAGCAAGCACAAATCTGTCATGGTTT
WI-681	156 A G ---			TGAAGCCCTCTCTATACCCAAAGTGTCTTTATCTTTAAATGCTGTGGTCAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTACAGGGGAAGCACTTTGNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATTJAGJTTATACTATGGCACCATTGGGACACAGATTATATATGTCAGA CACCACGNATGTCCTTTAAGATAIGCAGCAAGCACAAATCTGTCATGGTTT
WI-867b	119 G A ---			AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCTCCAAGGCTCCCGATATCTGGCAGATCTTCCCTTTTCATCTCCGJAJTTTGTGTTTGGC CAATAATATCTCCCGAGGACGCTCTTCTTAATCCCTGAAACCTGAGAAAATGTTATCTTATGC AGTGCTATGGTTGAATGTGTCCCGCCACAAAGCACACATTAGAACTTA
WI-867	113 A G ---			AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCTCCAAGGCTCCCGATATCTGGCAGATCTTCCCTTTTCATCTCCGJAJTTTGTGTTTGGC CAATAATATCTCCCGAGGACGCTCTTCTTAATCCCTGAAACCTGAGAAAATGTTATCTTATGC AGTGCTATGGTTGAATGTGTCCCGCCACAAAGCACACATTAGAACTTA
WI-867	119 G A ---			AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCTCCAAGGCTCCCGATATCTGGCAGATCTTCCCTTTTCATCTCCGJAJTTTGTGTTTGGC CAATAATATCTCCCGAGGACGCTCTTCTTAATCCCTGAAACCTGAGAAAATGTTATCTTATGC AGTGCTATGGTTGAATGTGTCCCGCCACAAAGCACACATTAGAACTTA
WI-871b	123 C G ---			TCATCAGACCTGAGATTCAGCATGAAATCTACCAAGGTACCAAAATGTAACCTTGTCCTCAAAACGA ATCTCAGTTTCTGCATATGTAATAATGGGAATGATAAGAGCACCACCTACCTCATGJGJAACTGTT GAGAGAAATAAATGAGACATTGTAAGTAAAGTTGTAATGCACCTGTTATGGCTGAATTTGTATCCCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGNCCTGATTTGTACATAA
WI-871	123 C G ---			TCATCAGACCTGAGATTCAGCATGAAATCTACCAAGGTACCAAAATGTAACCTTGTCCTCAAAACGA ATCTCAGTTTCTGCATATGTAATAATGGGAATGATAAGAGCACCACCTACCTCATGJGJAACTGTT GAGAGAAATAAATGAGACATTGTAAGTAAAGTTGTAATGCACCTGTTATGGCTGAATTTGTATCCCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGNCCTGATTTGTACATAA

WI-884	198 T C ---	---	AGGTTCTGGACTTGATGCTGGGAACAATTTGGTNGTGGAGAAATTCCTATTTGAGTNTTTCACAGAT CAGTAGAGCCAAATGGGAAAGTATCCTAGTCCATCCCTTTATTAGGAATTTCTGATCTATTGGGA ACTTCCTCCTAATAGATCAGGAAATCCACCTCATTTAATCATGGACAACNNAAGGAATAIT/CJG ATCCGCGATGCAACATTTATTAGTGAAACATGATGAAATGAACATAAT
WI-921b	205 G A ---	---	CACITCCCAAGGGCTCTGGGGGANGAGCGGTGGGACGCTGCCGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGACGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGGACAGTTTACTGG CAGTGATGCCCTCAGCGCTGCCCGCCCAAGAAAGTCTNGCCAGGAAAGACGATCCATCTAC TCT/GA/GGGGAGAGATCTGACAAATTTAATCAGGAGGAAGAAATTTCTCCGAG
WI-921	205 G A ---	---	CACITCCCAAGGGCTCTGGGGGANGAGCGGTGGGACGCTGCCGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGACGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGGACAGTTTACTGG CAGTGATGCCCTCAGCGCTGCCCGCCCAAGAAAGTCTNGCCAGGAAAGACGATCCATCTAC TCT/GA/GGGGAGAGATCTGACAAATTTAATCAGGAGGAAGAAATTTCTCCGAG
WI-945c	90 G C ---	---	GGCTGGGATGAGAGGTCTACTTGTGGTACTGGAGTTTCACTGGCTTGTGCTAGAACTAGNAAAGNA GAAAGACACAGNATTGGCTAAC/GC/CATGGCAGTAGTGGGCCCAAGGCCCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAAACAAAGTTCAACACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGATCTCTTAAAGGGAATCATGACAGATTTTCTTGGCTTTA
WI-945b	90 G C ---	---	GGCTGGGATGAGAGGTCTACTTGTGGTACTGGAGTTTCACTGGCTTGTGCTAGAACTAGNAAAGNA GAAAGACACAGNATTGGCTAAC/GC/CATGGCAGTAGTGGGCCCAAGGCCCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAAACAAAGTTCAACACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGATCTCTTAAAGGGAATCATGACAGATTTTCTTGGCTTTA
WI-960b	167 C T ---	---	TTGCTTCAAGAAGTTCTTCTCAGGAAGTTATTCATTCAAGCAACCTAAATTTGTTTTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAATGAGTGTCTTCTACC CTGAGGAATTTATCAAGATGTTAAGTTATCT/CJCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-960a	155 G A ---	---	TTGCTTCAAGAAGTTCTTCTCAGGAAGTTATTCATTCAAGCAACCTAAATTTGTTTTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAATGAGTGTCTTCTACC CTGAGGAATTTATCAAGATG/AJTTAAGTTATCTCCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-1121	181 T C ---	---	TCCCACTGAGTATGGCTTTCAGTAGTTTATTATGATGTGCTTAGGTACATTTGTTTTATTGTTCTG CGAATTGTTGTTACTTTGGGAGAAATGCTCAACTATAAATATTGCTTCTGACCCCTTCTGTTCTG CTTCTTAAAGATACAAAATAAATGTAAACATTAGACCTCTCACTA/CJGCTGTTTTTACTCTCCTCTG ATTTTTTCCATTATTTTATTGCTCTGGCTTCATTTTGTAATNTG

WI-1147b	204	G A ---	---	TTTGCCATTATTGAAGATAACCCACACCTGGTGCCAGGGTTTTCACAGGTATTAGTGGTCAGTCA CATAGGCATATAGTACCTGTATGACTTCTATTCAGCCACCCGAACTTCTCCTCCCTGCTGGCTC CTGAGCCAAAACAGGCATTTACCATAAATCACTTTGTTAGGATGAACCTATCTGGCCAAACTGATA C/GA/GCATGACCCACAGCCTCAGGTATATAAACACTCTCATCAGGCAGA
WI-1158b	147	C T ---	---	GCATTGAGAGGGTTCGTTTAATGACATTCAGTGGCCCTGTCTATGTCAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAAATACAATGTGATGGTCTCCTGAGTGTCTGAATG/C/GGCCAGGT TAAGTCTGGGG/C/TTCTGGGGTCAGGCTGCCTGGGTACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1158a	124	C G ---	---	GCATTGAGAGGGTTCGTTTAATGACATTCAGTGGCCCTGTCTATGTCAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAAATACAATGTGATGGTCTCCTGAGTGTCTGAATG/C/GGCCAGGT GGCTAAGTCTGGGGCTCTGGGGTCAGGCTGCCTGGGTACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1304	124	T C ---	---	AAGTTTACAGAAAAAATACCAGAAAAAGTGACTTCAAGANTCAGCTGAGATAGAAACATATGCCCA TCATCTTCAANGTNCACAGACACATTAATCCCTAGACAGCCATTTCTTTGAATGN/T/C/GNCANT AAAAATGATTGAAATTTGGGAATAAAGCCCTCCCTCTAATGATTTGACAGTGTAGACCTTGCCTAG GCC
WI-1305d	202	C T ---	---	TTCTCAATCCAAATCTGTGTACTTTTATTTCTTTCTTTCCATTCTATGTTGGTAAATATAAAG ATGATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCCTC ACATCCACTGCTTTCANTAAATTNACTCCACTNATGTCTNACAAAATNACACTGTTTAAANTGNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATACAGCCCTGCCTACCA
WI-1305c	46	C T ---	---	TTCTCAATCCAAATCTGTGTACTTTTATTTCTTTCTTTCCATTCTATGTTGGTAAATATAAAG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAAT/C/TTNACTCCACTNATGTCTNACAAAATNACACTGTTTAAANTGNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATACAGCCCTGCCTACCA
WI-1305b	153	T C ---	---	TTCTCAATCCAAATCTGTGTACTTTTATTTCTTTCTTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAAT/C/TTNACTCCACTNATGTCTNACAAAATNACACTGTTTAAANTGNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATACAGCCCTGCCTACCA
WI-1305	202	C T ---	---	TTCTCAATCCAAATCTGTGTACTTTTATTTCTTTCTTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATTNACTCCACTNATGTCTNACAAAATNACACTGTTTAAANTGNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATACAGCCCTGCCTACCA

WI-1306b	248 A G ---	---	TTTCTGCATTGGAATAGTTGACITTCATGAGNNGCAATAAATGGACAAATCTTGNGNNNTNG GGCTGGGTGACTGTCCCTGGGTCAITTAGAAGCCATAGAGATGAAAGTAGCCGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGACCTAAGGNGAGAAGTGGCCCTNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTATCTTCCTTJAGJGC
WI-1306	240 A G ---	---	TTTCTGCATTGGAATAGTTGACITTCATGAGNNGCAATAAATGGACAAATCTTGNGNNNTNG GGCTGGGTGACTGTCCCTGGGTCAITTAGAAGCCATAGAGATGAAAGTAGCCGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGACCTAAGGNGAGAAGTGGCCCTNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTJAGJCTTCCTAGC
WI-1307b	118 T C ---	---	GACAAGGCTGGTACTAGTTCCAAATCCAAATCTATGTACACITTCCTCTCACITTTCTCAAGTGGACA GATTTTCTGCATTACTGCTGGGTGGGGAGCAGTGGTAGGCAATJGJGTGAGATTGCTCTTT CCTACCCCTCTTAATGTATCTTNTCTAATATNATGCTAAACCCGGTACTGTGATCTATCACTGGTT TCITTTGGGTGTTGTTGCTGTGTTTCTCCTGTAAAGNTGTTT
WI-1307	118 T C ---	---	GACAAGGCTGGTACTAGTTCCAAATCCAAATCTATGTACACITTCCTCTCACITTTCTCAAGTGGACA GATTTTCTGCATTACTGCTGGGTGGGGAGCAGTGGTAGGCAATJGJGTGAGATTGCTCTTT CCTACCCCTCTTAATGTATCTTNTCTAATATNATGCTAAACCCGGTACTGTGATCTATCACTGGTT TCITTTGGGTGTTGTTGCTGTGTTTCTCCTGTAAAGNTGTTT
WI-1325b	169 T C ---	---	GAGAGATGCCAAGACAAAGCAGAGGGAGAGAGAGCAACCNCTGTGGTTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATAGGCAACTACAATGTGCCCTTGTCTCTCTTJACCCCTCAGAACTTCCTTGAGGGGCAGGC ATTATGATTCACACTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
WI-1325	165 C T ---	---	GAGAGATGCCAAGACAAAGCAGAGGGAGAGAGAGCAACCNCTGTGGTTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATAGGCAACTACAATGTGCCCTTGTCTCTCTTJACCCCTCAGAACTTCCTTGAGGGGCAGGC ATTATGATTCACACTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
WI-1327b	162 T C ---	---	CTACGATAATTAGGTTGGCAGTGAGGGTATTAGCTGTGTAGTGAAGAGTCCCTGTTATTTGTAAA ACACCAAGTGCGGTTTAAATGGAATGCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGTCJGJGAAAGTTGGTAGCTACCAGGCTCCCAATGTAGT TCTTNGCTGAAAGTCTCTCTACTGAAGAGGCAATGGTTCATCTCTAAG
WI-1327	175 C G ---	---	CTACGATAATTAGGTTGGCAGTGAGGGTATTAGCTGTGTAGTGAAGAGTCCCTGTTATTTGTAAA ACACCAAGTGCGGTTTAAATGGAATGCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGTGAAGTTGGTAGCTGJGJACCAGGCTCCCAATGTAGT TCTTNGCTGAAAGTCTCTCTACTGAAGAGGCAATGGTTCATCTCTAAG

WI-1341b	136 G A ---	---	TATCAGCATGATTGTGGCTGTTGGACACAAAGTCAATTTGTGACATTTGNTGNNNTCCTTTTCNTTT ACCTGATCCACTATCTTCTCAAGATCANGTTCAAAATTTGGCTTNCCTTTGTTAAATATACCCCAAGC [G/A]GGATTGTGATGGATCTGTTATTTTCCCTGTGCTTGGACACAGCAGAGTCGTCTCTGNGAGTNTG GTTTCAGGATTGTCTCTGTTTCCCCAGCCCACTTGCACITAGCAAGTGT
WI-1349e	192 G C ---	---	CTGACAAATGTCATATCTCACTCCTTAAACCCACAGGTCATAGAAATCAGTTAGCTACCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGCTGGCCTGTGAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCACTGAGGATAGTGTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTCAGAAAAATA
WI-1349d	264 C A ---	---	CTGACAAATGTCATATCTCACTCCTTAAACCCACAGGTCATAGAAATCAGTTAGCTACCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGCTGGCCTGTGAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCACTGAGGATAGTGTGAATTTCCATCTCTGAGTTCAAAATA ATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTCAGAAAAATA
WI-1349c	192 G C ---	---	CTGACAAATGTCATATCTCACTCCTTAAACCCACAGGTCATAGAAATCAGTTAGCTACCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGCTGGCCTGTGAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCACTGAGGATAGTGTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTCAGAAAAATA
WI-1349b	264 C A ---	---	CTGACAAATGTCATATCTCACTCCTTAAACCCACAGGTCATAGAAATCAGTTAGCTACCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGCTGGCCTGTGAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCACTGAGGATAGTGTGAATTTCCATCTCTGAGTTCAAAATA ATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTCAGAAAAATA
WI-1349	264 C A ---	---	CTGACAAATGTCATATCTCACTCCTTAAACCCACAGGTCATAGAAATCAGTTAGCTACCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGCTGGCCTGTGAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCACTGAGGATAGTGTGAATTTCCATCTCTGAGTTCAAAATA ATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTCAGAAAAATA
WI-1403b	57 C T ---	---	TGGTATTTTGAATGGGTTTCAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTTG[C/T]TCCGAAT GCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACGT AAAGTTTACATCAACATAATTCTTGGCCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCCTCA TAATCCCAAGTGCCAAAAAGGGTTGTATCTGATTGT
WI-1403	58 T C ---	---	TGGTATTTTGAATGGGTTTCAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTTGCTT[C/T]CCGAA TGCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACG TAAAGTTTACATCAACATAATTCTTGGCCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCCTC ATAATCCCAAGTGCCAAAAAGGGTTGTATCTGATTGT

WI-1417c	31 C T ---	---	---	CAGGCCGGAAGAGATTACGTGGAGAGATGTC/TTTGGCCAGGGCGGAGATGTGAGCCACGGG GGTGACAGCATGCTGCTGGCATTTGGAGGCCCCAGAGGAATCCAGTGGCCCTCTCAATGACTTG GGGTCTCGACTTCGGAAGTTAAGGGCTCGGCTTCAAAAGCTGGTCCGGTTTGAGGGGGTTGC AGCGAGGCCCTTAGGTCGGTATTAAATGTTTGC/TTTGTAGAAAAAGTCGC
WI-1417b	31 C T ---	---	---	CAGGCCGGAAGAGATTACGTGGAGAGATGTC/TTTGGCCAGGGCGGAGATGTGAGCCACGGG GGTGACAGCATGCTGCTGGCATTTGGAGGCCCCAGAGGAATCCAGTGGCCCTCTCAATGACTTG GGGTCTCGACTTCGGAAGTTAAGGGCTCGGCTTCAAAAGCTGGTCCGGTTTGAGGGGGTTGC AGCGAGGCCCTTAGGTCGGTATTAAATGTTTGC/TTTGTAGAAAAAGTCGC
WI-1729	172 A ---	---	---	CCATGAGCAACAGCATGTTCTACTCTGTGTGTGTATGTTAGGGGCGCATGTATCTGTATTTCTT TTTTATTCTCTCCAAAAGAAATTTCAATTATGCAAAACATTTATCAGGCAATGCAAGCTCGTAATAAGA TGTTGGAGAACTGAAAAAGAGAGCTTACATGCACCCCAATAGCAAACTCTCCACACATTTCCAGCA GATGTATGTGCTCTCCGTGGTACCTTCTCTCCACCATCACCTGTGTTTTT
WI-1732b	122 T C ---	---	---	TGCTTACTTCTTTGTTCAATCCACCATACATTTTGTAAATTGGAACCTCTAGGAGGTAGAAGGA TATGCTGATCAAAAAAGGGGACATATTCAAGGAGTNTCCCTGGTCAACCTTTT/CJATTCAGTCT CTGCCACATGCTAGTAAGTGTGAGTGGTGCATCATGATATATCTGAGCCTCCCAAGGTACAGC CTTCACTACTATTCATATTTGGCTAAGGTATTCATCATATTTGGCTAAG
WI-1732	114 C T ---	---	---	TGCTTACTTCTTTGTTCAATCCACCATACATTTTGTAAATTGGAACCTCTAGGAGGTAGAAGGA TATGCTGATCAAAAAAGGGGACATATTCAAGGAGTNTCCCTGGTCAACCTTTTATTCAGTCT CTGCCACATGCTAGTAAGTGTGAGTGGTGCATCATGATATATCTGAGCCTCCCAAGGTACAGC CTTCACTACTATTCATCATATTTGGCTAAGGTATTCATCATATTTGGCTAAG
WI-1750	97 A G ---	---	---	GCGAATTTAATGACTCCAAAGGTAGTAATTCCTTTCCCCCAAAAAGGTTTAAATCTGTGTTGGA CATAATGTTTGAATTTGCAGTTCACCTTGG[A/G]TTAAGGTGTGCTGTTTCTGGCAAGAGTCAG TGGGAGTGTCCGGGAAAGGGCTAAAGTCTTTGTAGTCAGACAAACCGGCTTGCACTGCTGACTGAG CTACATTCACCTTTATGATCTCCAGCAGGTTCTTCCA
WI-1780	31 A G ---	---	---	GGTACACAAAGAAATGCTTCTGGAAATCTAC/A/GTAGCGCCTTAACATTTTGGCTGAGTATTAATC TGTACATGTGTAATGTGAACCATGAAGCTGGGAAAGAACAAATTCCTAGGAAAGTACAATTAC TGGGAACTGTAGAACAAATTAATTCATAGTTTACACATAGCTGGGAATCACTCATGTTCCCATCA ACTGGAGAGACCTTGTGTAGTACAGAGGACATTCAGAAATATCATAAAAAT
WI-1803c	77 A G ---	---	---	CCACTCAGTAATAATAGTGTGGAGATAAGTATATGGTAGGCACATAATAATTTTTCAGGCAGAA CCATTATGAT[A/G]AGTAGGGTAGAGCATCACACTTGGGAGGACATATTCTGGAGTINAGATATCCTG GGTGCTAATTTCAAAATATATCTACTAAAGCATGACTTCTAGAAAATTAATTTACTTGTGCTCAA GGAATGGGAATACCTATAATACAGTCTTATTGAGGAAAAATAACTGGAATCA

WI-1803b	77 A G ---	---	---	CCACTCAGTAATAATAGTGTGGAGATAAGTATATGGTAGGCACATAATAATATTTTCAGGCAGAA CCATTATGATAGAGTAGGTAGAGCATCACACTTGGGAGGACATAATCTGGAGTNAGATATCCTG GGTGCTAATTTCAAATATATCTACTAAAGCATGACTTCTAGAAAATTACTTATCTCTTGCTCCTCAA GGAATGGGAATACCTATAATACAGTCTTATTGAGGAAAATAACTGGAATCA
WI-1837b	112 C T ---	---	---	TTTACTTGGGATTTTCATAGCTGATCATAATTTACCAATTTGATAATTCACCTCTTTTCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGATAGACCCGTTTATACIC/TTCGTGCCAGTTTATTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAAACAAACCTCAAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACTGGGAAGTCTGGGAACGTTTTCGCTTTCGCTGGCT
WI-1837	112 C T ---	---	---	TTTACTTGGGATTTTCATAGCTGATCATAATTTACCAATTTGATAATTCACCTCTTTTCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGATAGACCCGTTTATACIC/TTCGTGCCAGTTTATTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAAACAAACCTCAAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACTGGGAAGTCTGGGAACGTTTTCGCTTTCGCTGGCT
WI-1840b	79 G T ---	---	---	TCACCTAGGGAGGTGCTAAAAATGTAGCTTCATTAAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCAGTGTGAGAACTCTGAATATTCAGCACATACAAAGTGTGACAACCACTTGTTTAGTAT ATTTATCTCCAGAGTGTGTTTGAATTTACTAAAAAGTTCCTAAAGAGCCATGAAGAAATTATAAGACT ATCGCA
WI-1840	79 G T ---	---	---	TCACCTAGGGAGGTGCTAAAAATGTAGCTTCATTAAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCAGTGTGAGAACTCTGAATATTCAGCACATACAAAGTGTGACAACCACTTGTTTAGTAT ATTTATCTCCAGAGTGTGTTTGAATTTACTAAAAAGTTCCTAAAGAGCCATGAAGAAATTATAAGACT ATCGCA
WI-1879b	110 C T ---	---	---	GGGCTCACTTTCATCAGAGCACATATCACGTGATAGTCTGTTTCCCTTTTCATAACTACTCCCCCG CACTGTAGGNTTCTTTTGAGGTNAAGGACCTGCCNTTTTATC/TGTCTGCNAAATAAACTCCCAAAA AAGTGGTTAGTCCACAGGGTTTAAATAGTCTTGTGTAATGAATTTCTGTGCGACCCCTGTGCCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTACCCACT
WI-1879	110 C T ---	---	---	GGGCTCACTTTCATCAGAGCACATATCACGTGATAGTCTGTTTCCCTTTTCATAACTACTCCCCCG CACTGTAGGNTTCTTTTGAGGTNAAGGACCTGCCNTTTTATC/TGTCTGCNAAATAAACTCCCAAAA AAGTGGTTAGTCCACAGGGTTTAAATAGTCTTGTGTAATGAATTTCTGTGCGACCCCTGTGCCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTACCCACT
WI-1900b	119 C T ---	---	---	TGTTCTCTGGTCCAGGCACCGGGTAAAGTCTTGTCTGCATAATGAATAATCAACTGGACAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGGIC/TGCTCTGAGAGGT AAAGTGCCTGCCCAACCGGCACAACTAGAGAGCAGCAACAGGTGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGTCTTAACTGCCATGAGAAACCACTTTCTTTTGCTCC



WI-1900	119 C T ---				TGTTCTCTGGTCCAGGCCGCGGCTAAGTCTTGCTGCTAATGAATAATCAACTGGACAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCACTTACAGCTGCAAAAGAGG[C/T]GCTCTGAGAGGT AAAGTCCCTGCCCAACGGCAGACAACTAGAGAGCAGCCAAACAGGTGTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGCTTAACTCCTATGAGAAACCACTTTCTTTGCTCC
WI-1943c	165 C T ---				ATTCCAGTTTCACAGTGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAAATGGTAGGGAAGACCAAGCC[C/T]CTCTGAANCTGGTCCCACGTTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCCAGATGACTCCAAAGCCCGGCTGGAGTAT
WI-1943b	165 C T ---				ATTCCAGTTTCACAGTGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAAATGGTAGGGAAGACCAAGCC[C/T]CTCTGAANCTGGTCCCACGTTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCCAGATGACTCCAAAGCCCGGCTGGAGTAT
WI-1943	164 C T ---				ATTCCAGTTTCACAGTGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAAATGGTAGGGAAGACCAAGCC[C/T]CTCTGAANCTGGTCCCACGTTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCCAGATGACTCCAAAGCCCGGCTGGAGTAT
WI-1960c	270 A T ---				CCAGGTGAGGCTGAAAGAAAGGAGGAGCAATTGCTGTTGGAGTGAGGATTCGGAGAAGCACCCCT GCAGAGCTTCATTCTGTTTCAAAAGTGTGCCATGCANGGTCNTCTGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGCTGAAAACTTAAAAATGCACCTCCCACTTT
WI-1960b	270 A T ---				CCAGGTGAGGCTGAAAGAAAGGAGGCAATTGCTGTTGGAGTGAGGATTCGGAGAAGCACCCCT GCAGAGCTTCATTCTGTTTCAAAAGTGTGCCATGCANGGTCNTCTGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGCTGAAAACTTAAAAATGCACCTCCCACTTT
WI-1977	203 T C ---				CTGATGCCAAGTGCAGCTTAGAGTNAGGAATCCAGAGAAAGTNTTTGGATCTGGTAAGTAGGAGTCA TTCTGGGCATTTCTTCATAGAGTNTGTTTAAAGTCTCGTAATAATACTGTGCCCTAGGAAGGTTGTT TTCTCTACTGCGTCTGTGAAAGCCCTTCCCACATCGAGTGATACAGTACTTCCAGTTATGGAGATTCT /C/TAAACATCAACACACTGGCTGAGGCTGTTGG
WI-2012	102 T C ---				AAATCTAGAAGCCAGAGTCAGCTCAGCTACGATTTATAAAGTTGAAGTAAATGCATTGTAGTTTCATGT TTTCTCTTAATTCTGCACAAACTAGCTAAAAAT[C/T]TTTAAATCAGTTACCAGAGGCAATACCT GGGTTAATGTAAGCACTCAAAAGTTATGTAGAGTAGCTGTCTCTGAGTCACCTTTTTTCTACTCTCATT GGCTTCAACCAATGCTTCCACTGGATC

WI-2013	127 C T ---	---	---	CTTTAGAGGTGGTCATTTGGGTTCCCTTCTGGAAGTATTGTTTAAAGAAAATAGATGCAACG TTGCTAAGTACACCTAACATTTAAACAGTCTCCAGCAGATAATATGCTGATGCTGACACTC/TCTCA CCAGAAAAAGAGAAATACCCATCATGAGGAAGAGAAATGACTTTTGTTCAGTTATGCTCCCGGGTCC CCTTCACTGGAGGGATATCTAGCTTTCTGAGCCCTGGTTACTGCAATCC
WI-2032c	166 G A ---	---	---	ACCAGACATCCCATCAGGAGTTAGTCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTCCCAAAAACC TCAATTTTCTTACTACTCATATATGCTAGGATATCCACATACCAAAAGCCAAACCTTAACC ACATACCCCAACTGGTTTCTAGATGTACACG/ATGTGGGACCTCTGTCTCAACCTCCGACTTTTCAC AGATCATGGTTAGGCTCACCTTCTGTAAATGCTCTGTTTTCAAAAGGG
WI-2032b	219 C G ---	---	---	ACCAGACATCCCATCAGGAGTTAGTCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTCCCAAAAACC TCAATTTTCTTACTACTCATATATGCTAGGATATCCACATACCAAAAGCCAAACCTTAACC ACATACCCCAACTGGTTTCTAGATGTACACGTTGGGACCTCTGTCTCAACCTCCGACTTTTCACAGA TCATTGGTTAGGCTCA/C/GTCTCCTGTAAATGCTCTGTTTTCAAAAGGG
WI-2032	219 C G ---	---	---	ACCAGACATCCCATCAGGAGTTAGTCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTCCCAAAAACC TCAATTTTCTTACTACTCATATATGCTAGGATATCCACATACCAAAAGCCAAACCTTAACC ACATACCCCAACTGGTTTCTAGATGTACACGTTGGGACCTCTGTCTCAACCTCCGACTTTTCACAGA TCATTGGTTAGGCTCA/C/GTCTCCTGTAAATGCTCTGTTTTCAAAAGGG
WI-2054b	188 C T ---	---	---	CGTTTCTCTACATCTTGGGNACATAAAGANGAAAGNAGCTGTCTTTTGTGGTAGTTTGTCT CAGAGCTGCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAATACCTTACAGACTTAGGATTGGA TTTTCATGGTGGTTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTGTCTC/TCTGCCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTACTGGATGGGCTGTCTTT
WI-2054	183 T C ---	---	---	CGTTTCTCTACATCTTGGGNACATAAAGANGAAAGNAGCTGTCTTTTGTGGTAGTTTGTCT CAGAGCTGCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAATACCTTACAGACTTAGGATTGGA TTTTCATGGTGGTTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTGTCTC/TCTGCCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTACTGGATGGGCTGTCTTT
WI-2573d	129 T C ---	---	---	TGGGATTAAACCCCTGTTTCTTCTCCCTCCAGTTCAGTGTGCCTTAATGTTGTGTAGAAATTAACA TTAACAGCAGTAAATAAGTCTTAAATGCACCTTCCCGTTACAAGGTGTTTCCGTGCTTTTGTGA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCCTAGGTAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGTCTTGCACAAAGGTATATGGCTGGGCTTGGACGAG
WI-2573c	165 A C ---	---	---	TGGGATTAAACCCCTGTTTCTTCTCCCTCCAGTTCAGTGTGCCTTAATGTTGTGTAGAAATTAACA TTAACAGCAGTAAATAAGTCTTAAATGCACCTTCCCGTTACAAGGTGTTTCCGTGCTTTTGTATAT CATCTGATCTTCCCAACAGGGCTTATTTA/C/TGCCTAGGTAGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGTCTTGCACAAAGGTATATGGCTGGGCTTGGACGAG

WI-2573d	129	T C ---	---	TGGGATTAAACCCTGTTTCTCCTCCAGTTCAGTGTGCCTTAATGTTGTGCTAGAAATTAAACA TTAACAGCAGTAAATAATAGCTCTTAAATGCACCTTCCGTTTACAAAGGTGTTCCGTGCTTTTCJGA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCCTAGTAAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGCACAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573c	165	A C ---	---	TGGGATTAAACCCTGTTTCTCCTCCAGTTCAGTGTGCCTTAATGTTGTGCTAGAAATTAAACA TTAACAGCAGTAAATAATAGCTCTTAAATGCACCTTCCGTTTACAAAGGTGTTCCGTGCTTTTGATAT CATCTGATCTTCCCAACAGGGCTTATTTACJTGCTAGTAAGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGCACAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573b	165	A C ---	---	TGGGATTAAACCCTGTTTCTCCTCCAGTTCAGTGTGCCTTAATGTTGTGCTAGAAATTAAACA TTAACAGCAGTAAATAATAGCTCTTAAATGCACCTTCCGTTTACAAAGGTGTTCCGTGCTTTTGATAT CATCTGATCTTCCCAACAGGGCTTATTTACJTGCTAGTAAGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGCACAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573a	129	T C ---	---	TGGGATTAAACCCTGTTTCTCCTCCAGTTCAGTGTGCCTTAATGTTGTGCTAGAAATTAAACA TTAACAGCAGTAAATAATAGCTCTTAAATGCACCTTCCGTTTACAAAGGTGTTCCGTGCTTTTCJGA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCCTAGTAAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGCACAAGGTCATATGGCTGGGCTTGGACGAG
WI-2868b	60	A G ---	---	GACTTCATGCTCATGAACAAGCATTTGCTTAATTTACAGACATTAAAGAACAAAGCTTTCCJAGJCTC CCACTTCCCTCCCACTATCACCTCAACCTCTTCATCCACTTTAAAGAGGTTTCTTAGGTCCTCTGCAT ATCATGGAAGCCAACTACTCTATTAAAGCTTTCCCAATGATGCAGCCAGTTCTGCATACAGTTTGTA CAGAAATGCTATATTTATGGAACAGCTGAAAAATGAAATATCGATATAC
WI-2868	60	A G ---	---	GACTTCATGCTCATGAACAAGCATTTGCTTAATTTACAGACATTAAAGAACAAAGCTTTCCJAGJCTC CCACTTCCCTCCCACTATCACCTCAACCTCTTCATCCACTTTAAAGAGGTTTCTTAGGTCCTCTGCAT ATCATGGAAGCCAACTACTCTATTAAAGCTTTCCCAATGATGCAGCCAGTTCTGCATACAGTTTGTA CAGAAATGCTATATTTATGGAACAGCTGAAAAATGAAATATCGATATAC
WI-2870b	131	T C ---	---	CATGCTGTGTAACCTCTGTGCTGCTTGTGCTGGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGATTCJ AGAAATGAATAGAGCCCCATTTAAATTATATACAGCTTTATGTCCACTTCCCTGTTCTGCCATCAC TGGGCTTTTACAAAGGAGGGCTTT
WI-2870	131	T C ---	---	CATGCTGTGTAACCTCTGTGCTGCTTGTGCTGGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGATTCJ AGAAATGAATAGAGCCCCATTTAAATTATATACAGCTTTATGTCCACTTCTGTTCTGCCATCAC TGGGCTTTTACAAAGGAGGGCTTT

WI-2954c	49 T A ---	---	TTAGCACACATATCTGTTGTGGGACTTAACTGAGACAAAGGCATAAAAAT/TAJGACGACCTGGGGCA CAGAGGGAGCTCTATGCATTNATTCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2954b	41 A G ---	---	TTAGCACACATATCTGTTGTGGGACTTAACTGAGACAAAGGC/AGTAAAAATCAGCACCTGGGGCA CAGAGGGAGCTCTATGCATTNATTCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2954a	38 G T ---	---	TTAGCACACATATCTGTTGTGGGACTTAACTGAGACAAAG/TAJGATAAAAATCAGCACCTGGGGCA CAGAGGGAGCTCTATGCATTNATTCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2971b	62 T C ---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTACCAGCATTTCTAAGAT/TCJG CTGCCAGCACCAATAAGCTTCTTTCAAAACAATTTGTGAACCTCCTCCTCTTAATAAACCTAAC ATTCTCTTTGTTCCCTGACATTCGAAGGCGACGCTGCTAGATGTATGCCAGATTGCCAATCCT AGTTCITTAATGTTATTCTGAAGAAACCTTTTACTTAGGGATTTGCT
WI-2971	62 T C ---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTACCAGCATTTCTAAGAT/TCJG CTGCCAGCACCAATAAGCTTCTTTCAAAACAATTTGTGAACCTCCTCCTCTTAATAAACCTAAC ATTCTCTTTGTTCCCTGACATTCGAAGGCGACGCTGCTAGATGTATGCCAGATTGCCAATCCT AGTTCITTAATGTTATTCTGAAGAAACCTTTTACTTAGGGATTTGCT
WI-2995d	133 A T ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTTA /TAATCTTTCTTTCTGGT/TAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995c	151 G C ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTTA AATCTTTCTTTCTGGT/GC/TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995d	133 A T ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTTA /TAATCTTTCTTTCTGGT/TAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGTT

WI-2995c	151	G C	---			TTCTGGGAAAGAAAGATGGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
WI-2995d	133	A T	---			TTCTGGGAAAGAAAGATGGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
WI-2995c	151	G C	---			TTCTGGGAAAGAAAGATGGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
WI-2995b	151	G C	---			TTCTGGGAAAGAAAGATGGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
WI-2995a	133	A T	---			TTCTGGGAAAGAAAGATGGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTTNA /TAAATCTTTCTTTCTGGTGT/TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG GAATGAGACAGAACTAGCAGAAAGTGT
WI-3147	85	C T	---			GTGGTGCAGTTTCATCCTCTGGAGCTCCCTGTGAGATCAGACTGGAGCCAGTCTCCAGCTTGAGACCCAC ATCTCAGTTAGCTCCTT[C/T]CCTGCCATATCCTGTTTCCCTACTCTCTATCTCCTGAGACTTCTTCCT GAATGAATTAGATGCACCTCAATCCCTGCCTCAGTCTCTGCTTTCAGGAACTTGACCTAAGACAGAA ATCTTAGTACCAATACCTTGCAAGG
WI-3234b	68	T C	---			ATTCTGTAATGTTTTCACTGCTTCCAGTAAATCTTTATTGAGGTCCATGTCCTACCTCTACTTA T/C/GACAAGCAAGAACAAACAGAAAGCCCTCTGTTTGCATCTGGCCTCTTATAAATACTTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATTACATCCTTAAAGCATATCAAAAATTTTAC TCAGTAATTCAGAAAGAAAGGACAATGGAATGTACTTATTATCTTAT
WI-3234	68	T C	---			ATTCTGTAATGTTTTCACTGCTTCCAGTAAATCTTTATTGAGGTCCATGTCCTACCTCTACTTA T/C/GACAAGCAAGAACAAACAGAAAGCCCTCTGTTTGCATCTGGCCTCTTATAAATACTTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATTACATCCTTAAAGCATATCAAAAATTTTAC TCAGTAATTCAGAAAGAAAGGACAATGGAATGTACTTATTATCTTAT

WI-3292b	106	G A ---	---	<p>GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACCTCATCC  TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCTGATGGTATGGATGGGATGGATTA  GCCATGAATATTTCCATTGTTTCTCATTAATGATTAATTAATTAAGTAAATATTAATTTNCCATGA  GACACAATGGAAAAATGGAAAAACATTCAATGGAAAAAACCCATTTCATC</p>
WI-3292	106	G A ---	---	<p>GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACCTCATCC  TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCTGATGGTATGGATGGGATGGATTA  GCCATGAATATTTCCATTGTTTCTCATTAATGATTAATTAATTAAGTAAATATTAATTTNCCATGA  GACACAATGGAAAAATGGAAAAACATTCAATGGAAAAAACCCATTTCATC</p>
WI-3355	19	G C ---	---	<p>CCATGAACCATGGGCTACA[G/C]ATATTCTCTAAACTTCAGAGTCCCTCTACTGGAGAGGGATCCA  CTTTTAAATATGATTTCTTGAAGTGGCTGCATACTATCCCTCCAGCACTTAAACTCATCAGAA  AAAAAATCATCAAAAAGTCGAAGTTAGTTTNNATACCTTCACCTTTCAATGGAAAACTTTATAA  ACTGTGGATCAATTTATATTACTTTTGGATCAGTTTAGATGACTTTNAGTTG</p>
WI-3408	194	G A ---	---	<p>CCATGAAGAATGAGTTCTCCCTCCCTGGTCCAGTCTAAGAATAGCACACCCCTTGAGAAATTTNACT  TAGCACGTGGCATTGTAATGGCTGGATTTCTCCGCTCTAAGACACACACCTTTATGCTTTCNAAGCTTT  CTGGAATGGGATGAATCTNACATCAATGTGCACCCCTCGTGTGGGATCACTTCTCC[G/A]TGCCCC  ATCTCTGNAGAAGCCACTGGGAAGTCGAAGGAGTGACTTCAATCAGG</p>
WI-3505b	131	G A ---	---	<p>TAACCTATGCCTCATCTGGCTTACTGCTTAGTTCCTCATCTAGTGCACCTTAAAAAATTAATTTT  GAAAAATGGCATTGTTAATATCTTTGGAACCTCTTAACACATTACCTATTTTNAACCAAC[G/A]  AGGTGATTCTTATGGGAAATATATACAGCAAGAAAAAANANGGAAAAAATGTTGATGATACCT  GTTTAAATGGGAAATATGTTGCATAT</p>
WI-3505	131	G A ---	---	<p>TAACCTATGCCTCATCTGGCTTACTGCTTAGTTCCTCATCTAGTGCACCTTAAAAAATTAATTTT  GAAAAATGGCATTGTTAATATCTTTGGAACCTCTTAACACATTACCTATTTTNAACCAAC[G/A]  AGGTGATTCTTATGGGAAATATATACAGCAAGAAAAAANANGGAAAAAATGTTGATGATACCT  GTTTAAATGGGAAATATGTTGCATAT</p>
WI-3564b	177	C T ---	---	<p>GCTAGTAAGGTTCCACCTAAATGGTTCCAAAGTCAGGAGTGCTACTAAATGTTTGAGAAATAAAAGT  GAAAAATCAATGTGCTTCCAGTGTATTACATGGCAGTGTCACAGAGGGCTTGAGCGTCTGAGCG  TGGGACTTCACTGGTTGACTAACGTTAACATGCTGTT[C/T]AACAAAGTGTGTTGTTGTTGTCATC  AGTGTACACATGCTACCTTCTTCAAAAAACAAA</p>
WI-3564	177	C T ---	---	<p>GCTAGTAAGGTTCCACCTAAATGGTTCCAAAGTCAGGAGTGCTACTAAATGTTTGAGAAATAAAAGT  GAAAAATCAATGTGCTTCCAGTGTATTACATGGCAGTGTCACAGAGGGCTTGAGCGTCTGAGCG  TGGGACTTCACTGGTTGACTAACGTTAACATGCTGTT[C/T]AACAAAGTGTGTTGTTGTTGTCATC  AGTGTACACATGCTACCTTCTTCAAAAAACAAA</p>



[illegible]



WI-4230	93 T ---				AGAGACGTTGAATGGGACATCTTTCTATTTCGATTTAGTTTAAACATTTGATAAGAAATGATGAAA GTTTGTCACATTCAGATTTATCTTTATAGCAGCAGAAAGTCTGGCAATAATAACAGCACACTGACT TTTCCATGGTAAAAAGATTAGAGAAAAACAGCCTATTTTCTTAATGTTAAATGTAATTCGAAT ACATTTTAATGGAGGAGATGAATAGTGACCTTTGAAATTTTGAATTTATG
WI-4241	118 C T ---				GAAATTCATTTGAAGTTTGACCTTGACCTGATCTCATTAATACTTTTNCCTTGAGTGGTTGATTTT CATTTTGACAAACAGACAGACGAAAAATTTCCACTTAAATTAATTTCTC/TJAAGTATCTATGAT TTAGCACTGTTAGCACCAAGAACTGTGAAATTAATCTCTAGATATCTTCAGAACTAGGATGGAAG AA
WI-4271b	151 A ---				CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGGAGCCCCAACCCCTCCCCCTTTGTCTCAGG CTCTTAGAAGGTCCAGTCAGGGGC
WI-4271	151 A ---				CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGGAGCCCCAACCCCTCCCCCTTTGTCTCAGG CTCTTAGAAGGTCCAGTCAGGGGC
WI-4389b	156 G A ---				AATCGAAACATTTGATTTTGTAAAGGAACCACTATTATGATATTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGATAAGAAAGGATATTATGCAACCTTTTGA AGGTAAGATGTGAACCTATACA/G/ATJNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACTGGAAGCGGTAA
WI-4389	156 G A ---				AATCGAAACATTTGATTTTGTAAAGGAACCACTATTATGATATTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGATAAGAAAGGATATTATGCAACCTTTTGA AGGTAAGATGTGAACCTATACA/G/ATJNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACTGGAAGCGGTAA
WI-4488	31 A G ---				GATGACAATATTGTGATTTGGCATTTTAAJ/G/GTACCATTCATTTTCTTCTGGCTTTCGTGTGTT TGTTGTTGAGAAGTCAGGGGTAGTCGTATTGCTCCTTTCTAGTTCTCTCAGTAGGAAGACTGATC CTAAACAACCTAATTACCCATGCCAAAGTACGTCCAAACTGATCTTTAAAGAACATAAATCAAAATTG TATTATCCTATGCTTAAATGCTCAG
WI-4491	145 G C ---				ACCATCAATGTATCACCTTCTAAAAATTTATTAGATGATTAACTGGCTCTGTTAAAAATAAAAACCT GTCTTGACATTTGAAAAATAAACATTAATTTGTTGCTACTTTCTGCTACTTACAAAGGTACTGCACTA AACAAAGTTAAG/G/C/GTTTTTGGAGGGGAAAAATCATAAAAATGCATAAAATTTCTACCACGTGCA TTTCTGTGCCATAAATAAATTTTACATGCTCT

WI-4584	144	A G	---			TTGGTTGGCATTAGCCTCATAACAATAATTACAATCAATGTTACTCTATTATTTACAAACAAG AAAAATGAGGCTTAACATCACACTTCTGCTTAGTCGAGAGCCAGATTGAAGCCAGGAATCCATT CACCGGTAC[A/G]TGCTACCTGGGTAAAAATGTTTAATTAATTAATGATGCGATTAGATTTCAAAGA GTCCTAATGTGGTTTGAATAAGGTGCTTAAATTTGTTTATCAGTATGC
WI-4639	185	C T	---			TTTGTCAATTTGAATGTGATGGTCAGACTTCAGAGAACCCAGGAATCTCATTTATTCAGTACAATA TGGTGGCCAGGTGCTCAGGCCCTATTATCAGAGAGATCTCAGTTTAACTTCCAAITCCACCATTTAC TGACCATATGACTTGGGAACATTATCTCACCTATCTGAGTCTGATC[C/TT]CATCTTTAAATTTGTA AATTTAAGGACACCTATCATAGTAATATTGTGAGGATAAAATGAAATAA
WI-5327	63	A	---			AAATGAATCCGCTTTAGAGCAAAATACCAAGGGCTGGTGCAGGATGGTGGTGGCTGAGAGA[A/-] JGATTACTCATAAAAGCATATTAAATTTATAAATATGAAAAATTTAACTAGATAATTAATGTAAT TGAGTTTGAAGGTTGCATGAGATGAGGAGGAGGTAGTTTCTACTTATAGGGTTTATATAAGTNTGCT TCAATAGAATGGCTCTTTCGGATGACAATGATGAATGTTCTAAGCAGACAG
WI-5390	87	C T	---			GCTTTTGAGAAATGAAAAGGGGAGCCTGGACCATTCGAGGGCTTCTCATCTCTGATTATTTGTGTAT TTATTGTTCACTATTATTC[TTG]CTGCTGCTCCCTTCTGGTATGCTTGTGTCATGAAACAATGAATTC CCAGTGCCTGGCCGATTCTGGCTCCTAGAGGTGTCAGAAAAAAGTTTCGGTGAATAGAATTG ACGAATGGGTTCAGAAATGAAACCTGTGAATCTATGGAAGACAAACGAAT
WI-5404b	87	G A	---			CCTTGCCTGCTTTATGCATAATGAGAATAGAGTTGACTCTCCTGCAAGAAATCAATTAAGCAGTT GCAACATTATTTAATTT[G/A]AAAGAAACTTGTCTGAACTTTGTACTCTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTCCATGGTGTGAATCCACCCCATCTCTTTCCACCAGTAGCAAGATT GCTACTTATATGGAAGGTTTAGAGTTTATGAGTTTATAACAA
WI-5404	87	G A	---			CCTTGCCTGCTTTATGCATAATGAGAATAGAGTTGACTCTCCTGCAAGAAATCAATTAAGCAGTT GCAACATTATTTAATTT[G/A]AAAGAAACTTGTCTGAACTTTGTACTCTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTCCATGGTGTGAATCCACCCCATCTCTTTCCACCAGTAGCAAGATT GCTACTTATATGGAAGGTTTAGAGTTTATAACAA
WI-5545b	77	A C	---			TAGGAAGGGGATGGTATGGCTCTGAGACATTTAAATCTATCTTCCACCCTCACACTGCCGCCA TATCTCTC[A/C]CCAAACACCTCTGTTTCTGACAGCCAAAGTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAATTTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAAGANTC GAGATACACCATGAATTTTATTTTCATTICA
WI-5545	77	A C	---			TAGGAAGGGGATGGTATGGCTCTGAGACATTTAAATCTATCTTCCACCCTCACACTGCCGCCA TATCTCTC[A/C]CCAAACACCTCTGTTTCTGACAGCCAAAGTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAATTTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAAGANTC GAGATACACCATGAATTTTATTTTCATTICA

WI-5860b	134 A G ---	---	---	ACTCAAGTTTGGGGATAAAATCAGAAAGTTTCTATGTACAACTTAAATTTTGTAAAGATTTTATTGT TTCTTTTATATAAATTATGGATTGTTTCTTACTCCCTAACCAACCTTCTAACTGAGGAACACTAC[A/ GTTTACTGGAATCATGTGAAGACATTCTAAAGGTACCCAGGTGCACATAGTTTAAAGGGAATCA ATTCCAAATCATCAACTTCTGTAT
WI-5860	134 A G ---	---	---	ACTCAAGTTTGGGGATAAAATCAGAAAGTTTCTATGTACAACTTAAATTTTGTAAAGATTTTATTGT TTCTTTTATATAAATTATGGATTGTTTCTTACTCCCTAACCAACCTTCTAACTGAGGAACACTAC[A/ GTTTACTGGAATCATGTGAAGACATTCTAAAGGTACCCAGGTGCACATAGTTTAAAGGGAATCA ATTCCAAATCATCAACTTCTGTAT
WI-6106	208 C G ---	---	---	GCAACAACCTATTATACCTGATTCCAACCCAGGTCTACTAACATTAATCAACCCTAACCAATAC TATATTGTCCTGTTCTGAATTATTCTTATAGAACTGTAGATTTAGCATGGGATAAGTGCAG TGCAGAGATAGTAAACACTGCTCTTTTGTCTCCAGGAGTCTCAATGTGAAGTATAATTCTTACAGAG TAATTTC/GJATAGTAGGTACCCACAAAGTCTATATTGTATGTGAAGGAAAG
WI-6109d	129 T C ---	---	---	AAGATAGACAAACATATGCCAGACCACAAACACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGGAAGGAAAAAACCT[C] AAACCTATATTNCTGCTTGTGCATACITTTAAATGTATAATGTGGGAGAGAAAGAAATTTTGATGT GNAAAATTATCCCTGAAAATTTTATACCA
WI-6109c	147 T C ---	---	---	AAGATAGACAAACATATGCCAGACCACAAACACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGGAAGGAAAAAACCTAA ACCCTATATTNCTGTC/CJCTTGTGCATACITTTAAATGTATAATGTGGGAGAGAAAGAAATTTTGATG TGNAAAATTATCCCTGAAAATTTTATACCA
WI-6109b	147 T C ---	---	---	AAGATAGACAAACATATGCCAGACCACAAACACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGGAAGGAAAAAACCTAA ACCCTATATTNCTGTC/CJCTTGTGCATACITTTAAATGTATAATGTGGGAGAGAAAGAAATTTTGATG TGNAAAATTATCCCTGAAAATTTTATACCA
WI-6109a	129 T C ---	---	---	AAGATAGACAAACATATGCCAGACCACAAACACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGGAAGGAAAAAACCT[C] AAACCTATATTNCTGCTTGTGCATACITTTAAATGTATAATGTGGGAGAGAAAGAAATTTTGATGT GNAAAATTATCCCTGAAAATTTTATACCA
WI-6112	96 T C ---	---	---	AATGCCTATCACCTCCATCATGCTGCATAACTGATTGATTCAATAATGCTTATTGTTAGCACCTGTC TTCCAAACACATGCTGTTTGTTCATGAT/CJGCATATCCCAAGTGCCTTAGACAATGCCTCCCATAC AGTGAACAGTATTGACTAAACATACCTTGTTAAATCAATAAAATTAATCAACTTGGCATATGCAGG GAAC

WI-6244	103	T C	---	---	TAATTGCACAACTTACATATCAGGGTTTCTGATTGAAAGGAGAGAAATATTCTCTTTTAGTGATT GCTTAATATTAAATCATAATAAGTGCACCATCTCTTCGCTCCTTATAAAATGTTTAGAAGAAGG AAATTGAGTGTGGGAATTAGCAACAGGAGACATTTTATATACTCTACAGTGGGGAAGACTT CCTATTCTTCCCAAGGATGGATACATTCTAC
WI-6268	124	C T	---	---	CTGGCCTTATAATCCAAAGTTTAGGATTAACTTACCCCACTTAATAGACTCCAGACAGTTGCAGTT GTCTACAAAGATTCTCTAGTAGGGCTTTGGGTGTGGCACCGTTTGGCTCATTCTCTACTCCCT GGGTCTTATTGACTTTCAGGGAGCCTAGAGAGCTGGACAAACCTGCTTCTTTGCAGAAAGAGTCG GGTTCCAAAGATTTCGTACGATTTTATA
WI-6336b	234	C T	---	---	AGGTGCCATTTAATCCATTCAAATTTGGAAGCTACATCTTCAAGGGTCTGAGAGAGCTCACTCCCCC ATATATCCCCCTTTACATGTTTCTTATAAGACATACAGTTTAACTAATTAACAACTAAACAGCTT ATATACTGGCAATATATACAGATGGTTTATGTCAGAGTAATAGATCACATGAAATGGACCATGTG GTACCCCGAGTGCATTATGTCTTGGTAGAGCCCTCTTGGAGACACTGACAGT
WI-6336	234	C T	---	---	AGGTGCCATTTAATCCATTCAAATTTGGAAGCTACATCTTCAAGGGTCTGAGAGAGCTCACTCCCCC ATATATCCCCCTTTACATGTTTCTTATAAGACATACAGTTTAACTAATTAACAACTAAACAGCTT ATATACTGGCAATATATACAGATGGTTTATGTCAGAGTAATAGATCACATGAAATGGACCATGTG GTACCCCGAGTGCATTATGTCTTGGTAGAGCCCTCTTGGAGACACTGACAGT
WI-6381	92	C A	---	---	TTGGATACAAAAATTCAGTTACACAATCAGTAGCATTCAAAAATTAGTTATGAGTATTTATACAATTA CAAAAATGNTTCATGTTTTAACAACTAAGTATTTTAAAGCTCAAAACATTTTAAACAGGCACAAT ATTCTAANGGCATATGCATTCACCATGGCTTTTGAATGTCTCTCACTCCCACTTCAACAATCAAAATC TACAGANGCGGCAAAAGATCAGAGTTTACAG
WI-6436	198	C G	---	---	GGTTGAGGCATTGGGAAAGGCAGAAATTGAGGCAGTAGAAAAATGGACATTTTAGGAAAAAGAGAAGT TCAGAGGCAAGTCATGACAGACAGGAATACAGGCTTAGGAAGACAGTAGTCTCTGTGTTGAA ATTTGGTGTCAATAAAGAGTTTAGACTTTGGTGGTTGAGTAGTTGAGTAGTAGGTAGCGTTCTC GJATTGGGTGATTCCACAGACAAGGTGATGTTCTAAGATTGATATTTATTGT
WI-6449	186	C T	---	---	GAGGCCTCTTTGCTTTTCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTGTTCTGATTGGTGGTGTGCTCAGACTGCCAGATTGTTAAATATTTGAAAAATC GTATCTGGTTCTATTATCATCTGCATCTCTGATCTTATGCTGGCTCTATTCTCTATCTCTCTGA TCTTATGTCAGACCTGAAGTTCTCTAAATTTTCTGTGGTGTATTATA
WI-6449	186	C T	---	---	GAGGCCTCTTTGCTTTTCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTGTTCTGATTGGTGGTGTGCTCAGACTGCCAGATTGTTAAATATTTGAAAAATC GTATCTGGTTCTATTATCATCTGCATCTCTGATCTTATGCTGGCTCTATTCTCTATCTCTCTGA TCTTATGTCAGACCTGAAGTTCTCTAAATTTTCTGTGGTGTATTATA

WI-6463	72 T C ---	---	GCTGGAGAGAAAAGACCTCCAAAAGAAAGAAACTAAATCAGAGTCTCTTGAGCAAGAGGAATTGAAA AGAACA[IT]GTGAAAAAAATTAAGTAGAACTCAAGAGAGCCAAAAGTCCCCAATTGTGTCCATTA TAAGAAATATTTGAATGGAAATCTTAAGAAATGATTTTATTGATCAGTTAAATGTTCTTCCTCTCCTC CAGTCCCATTTATAGACATTCGGCATGCTG
WI-6474b	76 C T ---	---	AAGCAGTAAATCTTCCATCATGCCATGGATGCCAGTGGGTAAATGTTATAGAAACTTCAGAGGANAC AGAGGCAAA[C/I]GTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGTAGAGCC AAGAAAAAGTAGGATTTTGAAGGCCACAGAGAAAAGGGGTGTAAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACATAAGTATAAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6474	76 C T ---	---	AAGCAGTAAATCTTCCATCATGCCATGGATGCCAGTGGGTAAATGTTATAGAAACTTCAGAGGANAC AGAGGCAAA[C/I]GTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGTAGAGCC AAGAAAAAGTAGGATTTTGAAGGCCACAGAGAAAAGGGGTGTAAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACATAAGTATAAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6478b	175 T A ---	---	GAACCTAAATTAACCTTGCAACACTGAGAAAATCGGATTTGGAGATCTGCAAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGAATGCCACGCTTCGAGGCTGTCTATATGCTTTATTTTGTGA CACTGTCTATTTACCTCCCTCCCAATAGTGGAGAAATCAGAGT[A/G]CTCCTTGTGCTGTTGCTACAGA GAAGATATACAGGATGGAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6478	175 T A ---	---	GAACCTAAATTAACCTTGCAACACTGAGAAAATCGGATTTGGAGATCTGCAAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGAATGCCACGCTTCGAGGCTGTCTATATGCTTTATTTTGTGA CACTGTCTATTTACCTCCCTCCCAATAGTGGAGAAATCAGAGT[A/G]CTCCTTGTGCTGTTGCTACAGA GAAGATATACAGGATGGAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6559	149 G A ---	---	CACATTTTGAATGCAACTGAGAAANTGGTTTNTAGGCCTACCTTTTATTTAAGAGTACATCTGGCTC CAATGTTACCCCAACATGCAAAACATAAGGCAACAATCTGATCATTTTATAGGNTCCCAAGCCCA TTAGCAATATCTTA[G/A]TCAAATTTTAAAGAGAACAGGAAATAAGGAAGGCCCTAACAGAGGAG TTAAATAATTGTGCAAAACTTATCAGTTCTTC
WI-6564b	54 G A ---	---	TTCTTTATTTGGTCCCTACCAATGTGACTCTTTACCCAGGCCCTGTTCTATGC[G/A]CACTGGCTTTG TAGGCATTACATCATATGTCTGTGCTCTGAAATCTCAATTAATTTCTCCTNCCTATTCCTTTTCCAT GCTCTGCCTCATTNCTCAGAAATGAAGGCATTTGATTATNATTTTGTGTTGGGCTGTGTAAAG GTTCTTGGCAGGAGAACATGCATATGACTTTTAAATAAAGACCAACA
WI-6564	54 G A ---	---	TTCTTTATTTGGTCCCTACCAATGTGACTCTTTACCCAGGCCCTGTTCTATGC[G/A]CACTGGCTTTG TAGGCATTACATCATATGTCTGTGCTCTGAAATCTCAATTAATTTCTCCTNCCTATTCCTTTTCCAT GCTCTGCCTCATTNCTCAGAAATGAAGGCATTTGATTATNATTTTGTGTTGGGCTGTGTAAAG GTTCTTGGCAGGAGAACATGCATATGACTTTTAAATAAAGACCAACA

WI-6608b	46 C	---	---	CTAATCACAGTAGCACTGAACATGGCTCTAGTGAGTGGGCTCAGT[C/- JAGTTGAGGAGCTAAAGGAGGGGATTTCCCTAGTCTCTCCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGATTTTCTAGAGGAAAAAGAACTGAACCTCCAGCACTAG GTAAACTGCAAAAAAGAAAAACACCTGTGCCCAGGCACTAGCTACAAGGCCACACCCAGAAAAAGGAA AGC
WI-6608	46 C	---	---	CTAATCACAGTAGCACTGAACATGGCTCTAGTGAGTGGGCTCAGT[C/- JAGTTGAGGAGCTAAAGGAGGGGATTTCCCTAGTCTCTCCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGATTTTCTAGAGGAAAAAGAACTGAACCTCCAGCACTAG GTAAACTGCAAAAAAGAAAAACACCTGTGCCCAGGCACTAGCTACAAGGCCACACCCAGAAAAAGGAA AGC
WI-6666	68 C A	---	---	GTTAGACAGTATCCAGCAAAAAAGGTTATTTATACCTCTACTTTTCCAAAAAGAGGAAACCTCCCC A[C/A]AATCCCATCAACACACAGTCATGCTGGAAGGCATTCTGTCTACTCTGTGTTTTCATGTAA ATGTTGGGGTGACTCATTCGCGCTCTCTNITCTCAAGTCCAGGCTTCTTGGGTAGACCAAACTA ATACAAATGTTAGAGCACACAAGAGA
WI-6670b	120 A G	---	---	AGATTAACATAATTATCTAGTGGGCCATTGTAGGGTNGGGAGGAGTGTTTTCTATCTGCAGCCAAA CAGAAATAGTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC[A/G]TTGTTAGCCA GCATTGCCATTGAGGCGGAGTCAGGGTTTGTGGGCCAGAGTTTAGACAAATTTGGGGAATTTCTGA AAAAAAAAGAAATACAGAAATTTGAACACAGACACAGAACTTTAGAAAGGGAT
WI-6670	120 A G	---	---	AGATTAACATAATTATCTAGTGGGCCATTGTAGGGTNGGGAGGAGTGTTTTCTATCTGCAGCCAAA CAGAAATAGTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC[A/G]TTGTTAGCCA GCATTGCCATTGAGGCGGAGTCAGGGTTTGTGGGCCAGAGTTTAGACAAATTTGGGGAATTTCTGA AAAAAAAAGAAATACAGAAATTTGAACACAGACACAGAACTTTAGAAAGGGAT
WI-6704c	33 T C	---	---	TTTGAAAAATAAATTCATGCACCAATGTTTTAACT[C/C]CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAGTTTTTCATGACACACGNC CTATTGCTCTTTAAATATGTTGTACATGTCATCATTATCGATTCTTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704b	33 T C	---	---	TTTGAAAAATAAATTCATGCACCAATGTTTTAACT[C/C]CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAGTTTTTCATGACACACGNC CTATTGCTCTTTAAATATGTTGTACATGTCATCATTATCGATTCTTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704	28 T C	---	---	TTTGAAAAATAAATTCATGCACCAATGTTTTAACT[C/C]AACACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAGTTTTTCATGACACACGNC CTATTGCTCTTTAAATATGTTGTACATGTCATCATTATCGATTCTTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG

WI-6710	106 G A ---				CCATGGACAGTTTAAATTAGGAAGCTTCGACTTGTAGAAATACAGAGGAAGTCCCAGTTATCTACCT ATTCCTTAAACACATTTTGTACAGGCTGGAATGATTCCC[G/AT]AGTAAACTCAACATCCACACCT GCATAACATCGCTCCCAAGTGACTATTTACTAGTCGACACAGGATGTCAACAGTGAGCCTC ATCTCCAGTCCAATGGAGGAGTTGACTTAGACCTTCCTTGGACAGGAAGGGTC
WI-6766b	148 G C ---				AAAACAAATGGTGCAATTGCAATAATTTGGGTCACAGTATAAAACAATAACAATTAGTTCATATAAC ATTGGATATGGACAAAAATACANGATCCTTTCTTGTCTACGGAAATNCTGCAGATCCTTTATGT GCCACACTTAAAN[G/C]AAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACACAGTGGAGNGAACCTTACCCAAATCCCAGTTCCCTTCTTC
WI-6766	148 G C ---				AAAACAAATGGTGCAATTGCAATAATTTGGGTCACAGTATAAAACAATAACAATTAGTTCATATAAC ATTGGATATGGACAAAAATACANGATCCTTTCTTGTCTACGGAAATNCTGCAGATCCTTTATGT GCCACACTTAAAN[G/C]AAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACACAGTGGAGNGAACCTTACCCAAATCCCAGTTCCCTTCTTC
WI-6787b	97 A G ---				ACAGATAAAGTCTTTATCCCTGTATGTTTACATAAGAAAGTCTTTACAGACTTTTTTTTATACA ATACTTGTGCAGCAATGTTCAAAATTTACAG[AG/TTT]TACTGCATAAGATATCTTCATGTACAACTGT ATGCTTTGTCTTCTTGGGAAGGACGCGTTAAAGACCTATGATAAACACACATCCACATGACAAAGGA GAGTCAATAGGGCAGAGTAGANTACTCACAGGAAAAGAGTAAATTCAGGT
WI-6793	105 C G ---				GAACCCACAGGTCCTGTTATTTTATAGGAGCATTTACATTATGATAGCAAGTTTCAACACATTCA TCAACAAGGCGTCTTCAATCAATCAGTCAACCC[C/G]GAGTTAGAAAGTAGAGTCATGAGGAA GAGCTGCTGGCTGTAGGAAGTAGGGTTAATGCCCTCTAATCCCGAAAGGGGAGACTGAAGCCA GAGCCAGANTCCTGGCAATTCACCAAGTTCTCATCACAGGTAAAAGGCAAC
WI-6810b	37 T C ---				CACAATAATAAAATCACTCCCTACCTACCTGAAAACCTTAT[C/J]AGAAAGCATTTTAAATTTACAACACA AAGCTCAACGNACCTACAATAAGTCTAGTAGTCTGTTACGNGCCAAAGGATAAGGCTGAACAATA AATTAACCCCTTTAAATGCTATGNACAAGTACAATTTCTTTTGGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT
WI-6810	37 T C ---				CACAATAATAAAATCACTCCCTACCTGAAAACCTTAT[C/J]AGAAAGCATTTTAAATTTACAACACA AAGCTCAACGNACCTACAATAAGTCTAGTAGTCTGTTACGNGCCAAAGGATAAGGCTGAACAATA AATTAACCCCTTTAAATGCTATGNACAAGTACAATTTCTTTTGGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT
WI-6817b	145 C A ---				GCATGATTAAACCAAGTGCAGAAAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTGTCTAGTA TTTGTCTTTTGTATCCAGTTAAGACCATCAGCATATACACATCATCACTAACTCAACAATGTAGCT GCAGGGTAAC[C/J]ATGTGGATACCTGTGTGCTCTACTNGCCTCCAAAGGCAATTCAGGGGATCATCA AAGATGTTGGACACCTTGTGTTCAAATCTTGGTTCAGGTCGGCCTGTGCAG

WI-6817	145 C A ---	---	GCATGATTAAACCAGTGCAGAAAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACAAACATCATCACTAACTCAACAATGTAGCT GCAGGGTAAC[C/A]TGTGGATACCCCTGTGTCTACTNGCCCTCCAAAGGCATTCAGGGGATCATCA AAGATGTTGGACACCTTGTTGTTCAAAATCTGGTTCAGGTGCGCCTGTGCAG
WI-6819b	221 C ---	---	GATGGAAGCCATTTATTTCTCTAAATTTAAATAGAAGACTTTAATGGAAAAACATTTAGTAC CATCATGTCAACCCTGAATGCCAGCAATACCTCGACTTTTACACAGCGAGGAGCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTATGGTCCCTCAACAGTTTGCATATACAAAAATTTTCTGCTATTTG CTTAGCAACACAGCAATAAGCTTTGTTGTTTCTATATGACACCTAATATCCAG
WI-6819a	175 GT ---	---	GATGGAAGCCATTTATTTCTCTAAATTTAAATAGAAGACTTTAATGGAAAAACATTTAGTAC CATCATGTCAACCCTGAATGCCAGCAATACCTCGACTTTTACACAGCGAGGAGCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTCTATGGTCCCTCAACAGTTT[G/T]CATATACAAAAATTTTCTGCTATT TTGCTTTAGCAACACAGCAATAAATTTGTTGTTTCTATATGACACCTAATAT
WI-6826b	154 A G ---	---	GCAAAAGCTTTATGGCTCCAACAAATATCCCTTTTAAACCTCCTCTCTCTTCTGGTCTCAGTG GAACAAACACATTTGAATTTGAGATTTGCAGTTTATAGCATTTTTCCTTAAGAACCATATAAATAC ATGCAAAACCTTGATATGAGCTTAAATATATCAAAATGCAAAATATAGATTGGGTGCACTGT TAAGCTGAATTGCAAAATATGGCAACACACACTGGAGTGGGTATACGTTG
WI-6826	154 A G ---	---	GCAAAAGCTTTATGGCTCCAACAAATATCCCTTTTAAACCTCCTCTCTCTTCTCTGGTCTCAGTG GAACAAACACATTTGAATTTGAGATTTGCAGTTTATAGCATTTTTCCTTAAGAACCATATAAATAC ATGCAAAACCTTGATATGAGCTTAAATATATCAAAATGCAAAATATAGATTGGGTGCACTGT TAAGCTGAATTGCAAAATATGGCAACACACACTGGAGTGGGTATACGTTG
WI-6857a	122 TC ---	---	AGTGCAAACTATTTGAACAAAAGTAAACTATGAGTCACAGCATTTCAAGAACATCAGACACGGA AGAGTGAACAATATTCACTAAGTAAATACAGCAGATGAGATGTCTCTACATGTAT[C]ATTTAAT TATTCATGCTTTTCAATAGTCTCTTAGTCAACTTTCAGTGTAATTTCCACAAATATATAGCAGCTCA AACACAAATGCAGGAGCACAATGGCAAGTTTGGCAACTGTTTGGGCTAAT
WI-6865	153 G A ---	---	TTATAGAATCTTATGGGGCATACNGTAAATGAACGTCAACCTTAAATCTAAACAAACAGCTTG TTTGTGGTTCGTCTGAAATCCTCCCTGCTCACAAAACAGCCAGCTACTNGGTTTCTAAAGACGTA ATTTGCAGGCAAACTTC[G/A]TAGAGCCATTCTGTGCAGAGAAGGGAAGGAGAGCTGTTTGT TTACCTGTAGTAGAAGATATCTTTGGCTGTTAGAACTGAGCTCATTA
WI-6909	73 C T ---	---	ATTGAAAACTGGTTAGCAACAGATAAATTACAAATAGAGCTGGATATAAAAATGAGAGAAGAATGC AGACTT[C/T]AAGCTTATAGAGAAAAGTCAAAAAGGAGCAAGTTTGAATCAGATTTTATGATAC GGAAAAAAATTCCTTTTGGCAACAGGATATTTTCGAATAAATAAATCTGCCAGTGCCAAATCAG AAACACCATTTCCACAATATTTGTCATGCCCCCTAGTTGCCTATTTTATACATATC



WI-6910b	163	GT	---			CACTCAAAACCCCTTTATTCAATTGATTTACAAACGTGTACAATATTTACAAAGTTTAGGCATTAAATCCCA TATTGACATGAATGCTGTGGAGAGCTTAAAAATAATATGTGGCACATAGCTTAATATACACATCAT GGCTCTTACACTTAAGCCATTACCAATA/G/JTGAGATGTAATGGAGAATTTAATGTGGTAGAAAA GTCAGAGTGGCTGACCAGTCCGGACCTTCATGTGAATGACTCTTCCTTGGC
WI-6915	144	A	---			GCTGTTTTTTGTTTTTTTAAAGTACACCTTGGCTTGTGGCATTTCTTCACCTTATCTTACCC AAAAGTGCCCTTTGGGCCAGCCACTGACTGATTTAAACCAGAAATGTGGTTTTAAACAATGTGGT CGTGTGAATCAGGTGATTTTCTATTTGGTAGTATTTTCAGATTTCCACAAAGAACATG TATTGCTTTGTAATTTGAAAAAAAATCAACACAGGATAGTAAAGATAT
WI-6928b	175	TC	---			CAATCAAAAAGTTCCAAAGTTTCAAAGCTGGGATGAAAAGCCAGGCTTCTGACTTGCACCTGTGCAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCTCCCATAGAAAGTTCACTCTTAATTCATGTCCCATG CTTTGTCTTGGTCCCTGTGAGGAAAGGGTCAGCTAAAGGT/CJAACTGTTCTATAAGGATGGTAGG TATCCTGGCAAGATATTTCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6928	175	TC	---			CAATCAAAAAGTTCCAAAGTTTCAAAGCTGGGATGAAAAGCCAGGCTTCTGACTTGCACCTGTGCAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCTCCCATAGAAAGTTCACTCTTAATTCATGTCCCATG CTTTGTCTTGGTCCCTGTGAGGAAAGGGTCAGCTAAAGGT/CJAACTGTTCTATAAGGATGGTAGG TATCCTGGCAAGATATTTCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6955b	79	GA	---			TTTTATGAACATTTCAAGTCCCTCATATCACAGCACATCAATAAAGCAGTATGTACATAGACTGA CTTTATAGTAC(G/A)NGTCATGTCCCAAATCCCAATCCTAGGTAGATATCAAGTTACAAANTAC AAGTCCGNTAATTAACATATAGGTAGTATTAANCAAAAATGNGTTTTTNGCAATTTATGTGAAT AAGGCTTTAACCAAAGC
WI-6955	79	GA	---			TTTTATGAACATTTCAAGTCCCTCATATCACAGCACATCAATAAAGCAGTATGTACATAGACTGA CTTTATAGTAC(G/A)NGTCATGTCCCAAATCCCAATCCTAGGTAGATATCAAGTTACAAANTAC AAGTCCGNTAATTAACATATAGGTAGTATTAANCAAAAATGNGTTTTTNGCAATTTATGTGAAT AAGGCTTTAACCAAAGC
WI-6957	47	CG	---			AACTAAAAACCCCTTATTGTCTCCAAAGTGTGGCAAAATAGAAAATC/GITTTCAATTACATTAGG AAATCGGGTGGATAACGGAGTATAGTTATCCACTTAAGAAGCATTCCAGTCAAAATAATCACAAA ACAAATTCAGATTGCTTGGATCTGGTCATTTATGGCTTGAAGAAGTGGATTTGAAACCACCTTTAGG CTAAATAAATGTATATGAATAATGCATAGACTGTGTATCTAGAAAATCATGC
WI-6996c	242	GT	---			ACTTCTAGTGCCCTGTGTACCACCCCTCTAATGCCCTTGGTCGCCGCACTTCTGTATGCCGTAGGCCCT TAAATCTGCCCTGGGTCCTCCCTCTGTCTTCCAGCACCCAGAGGAGAGCGCGCAGTTCCCTG CAGGAGAGAGGGGTGCTGGACCCAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGCTCCTGACT CTCTCCTGATGTTGGGCCCTCTGTGCTCTCTCTTCCTGGGTTGCGGATC

WI-6996b	242	G T ---	---	ACTTCTAGTGCCTCTGTTACCAACACCTCTAATGCCCTCTGGTGGCCGCACTTCTGATGTCGCTAGGCGCT TAAATCTGCCTGGCTCCCTCCCTCTGCTTTCAGCACCCAGAGGAGGAGAGCGCGGAGTTCCTG CAGGAGAGAGGGGCTGCTGGACCCAAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCCTGACT CTCTCCTGATGGTGGGCCCTCTGCTCTCTCTTCQJG/JTGCAGTC
WI-6996	228	T G ---	---	ACTTCTAGTGCCTCTGTTACCAACCTCTAATGCCCTCTGGTGGCCGCACTTCTGATGTCGCTAGGCGCT TAAATCTGCCTGGCTCCCTCCCTCTGCTTTCAGCACCCAGAGGAGGAGAGCGCGGAGTTCCTG CAGGAGAGAGGGGCTGCTGGACCCAAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCCTGACT CTCTCCTGATGGTGGGCCCTCTGJ/JGJGCTCTCTCTTCGGTCCGATC
WI-7021b	112	G A ---	---	TGGGAGGACAGGGAGATGCTGCAGTTCCTCCAAAGAGAAGGTTCTTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGCTCCTGAAAGCCACAGACAATATGGTCCCAATG/JA/CCTGACTGCACCTTCTGTG CTTCAGCTCTCTTGACATCAAGGCTCTCCGTTCCACATCCACAGCCAATCCCAATTAATCAAACC ACTGTTATTACAGATAATAGCAACTTGGAAATGCTTATGTTACAGGTTA
WI-7021	108	A G ---	---	TGGGAGGACAGGGAGATGCTGCAGTTCCTCCAAAGAGAAGGTTCTTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGCTCCTGAAAGCCACAGACAATATGGTCCCAATG/JA/CCTGACTGCACCTTCTGTG CTTCAGCTCTCTTGACATCAAGGCTCTCCGTTCCACATCCACAGCCAATCCCAATTAATCAAACC ACTGTTATTACAGATAATAGCAACTTGGAAATGCTTATGTTACAGGTTA
WI-7056c	118	C T ---	---	GGCAGTAGGACACAGTGCGGGTCTGCTGGACCTTGGAGAGCCTGCATCCAGGATGCGGGTGG CCCTGCAGCCTCCTCCACCTCACTCCATGACAGCGCTAAACGTTGGTGA/C/JGGTGGGAGCCTCT GGGCTGTTGAAGTCACCTTGTGTGTTCCAAAGTTTCCAAACACAGAAAGTCATTCCTCTTTTAA ATGGTCTTAAGTTCAGCAGATGCCACATAAGGGGTTTGCCATTGATA
WI-7056b	118	C T ---	---	GGCAGTAGGACACAGTGCGGGTCTGCTGGACCTTGGAGAGCCTGCATCCAGGATGCGGGTGG CCCTGCAGCCTCCTCCACCTCACTCCATGACAGCGCTAAACGTTGGTGA/C/JGGTGGGAGCCTCT GGGCTGTTGAAGTCACCTTGTGTGTTCCAAAGTTTCCAAACACAGAAAGTCATTCCTCTTTTAA ATGGTCTTAAGTTCAGCAGATGCCACATAAGGGGTTTGCCATTGATA
WI-7091b	153	A C ---	---	AATTCGCTGAAAAAGGAACCTACCTATCCTTACATTTACCTACTAATGTCCTCTAATCATCTTAGAG GTCCATGGAGAAGGCATATGGAGAACATGTTTATAGCTCTATAAATAGTATTCATCACTGTG CTTAATTTAAATAGCATT/JC/JCTTATCATTTATCAGCCTTTATGATTTTCCAAAGTAAAAATATTA ACATATTATTCATTGGTCTCTCTTTTATCTGTTCTATATGAATGCTAT
WI-7091	153	A C ---	---	AATTCGCTGAAAAAGGAACCTACCTATCCTTACATTTACCTACTAATGTCCTCTAATCATCTTAGAG GTCCATGGAGAAGGCATATGGAGAACATGTTTATAGCTCTATAAATAGTATTCATCACTGTG CTTAATTTAAATAGCATT/JC/JCTTATCATTTATCAGCCTTTATGATTTTCCAAAGTAAAAATATTA ACATATTATTCATTGGTCTCTCTTTTATCTGTTCTATATGAATGCTAT



WI-7175	194 C T ---			CTCTAGACTAGTCTTTACCTTTATTATGAACCTGTGACAGGAAGCCCAAGGCAGTGTTCTCTCACCA ATAACTTCAGAGAAAGTCAGTTGGAGAAAATGAAGAAAAAGGCTGGCTGAAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAAATATATAATGGTTTACTGCTGTCAATTGTCCATGCCTA[C]TAGAT AATTTATTTTGATTTTGAATAAAAAACATTTGTACATTCCTGATACTGGG TGATCAGGTCAGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCTCTGAGCCAGCTGCCTGGAG AGGCTCTCGCTGCTACCTGGCTGCTAGGGGAACAGACAGTGAACCCAGAAAAGCATAACACCA ATCCAGGGCTGGCTCTGCACCTAAGAGAAAATTCGACTAAATGAATCTGTTCCAAAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAAGCCAGTGAATGTGAAGGAA
WI-7178b	273 G A ---			TGATCAGGTCAGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCTCTGAGCCAGCTGCCTGGAG AGGCTCTCGCTGCTACCTGGCTGCTAGGGGAACAGACAGTGAACCCAGAAAAGCATAACACCA ATCCAGGGCTGGCTCTGCACCTAAGAGAAAATTCGACTAAATGAATCTGTTCCAAAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAAGCCAGTGAATGTGAAGGAA
WI-7178	273 G A ---			GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCACCAAAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATCACCAGTTCTCTGCAACCCACTCTGAGCCTA[C]TCTCTCCTCTATTT TACTTGAGGCTGCCAATTACCAGCCCCAGTTTCAGCTCAAGAGATGCCTTAAGATAATTATGTGAGG CCACTTGGTAGCAAGATGGCAGCTATTTCCTGAAGCCTAGTACCCCAATT
WI-7182b	116 A C ---			GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCACCAAAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATCACCAGTTCTCTGCAACCCAC[C]ATCTGAGCCTATCTCTCCTCTATTT TACTTGAGGCTGCCAATTACCAGCCCCAGTTTCAGCTCAAGAGATGCCTTAAGATAATTATGTGAGG CCACTTGGTAGCAAGATGGCAGCTATTTCCTGAAGCCTAGTACCCCAATT
WI-7182	106 C A ---			ATAATTGCTTGTTTCTAGCCTGGCAAGATATTTTCATAAAGAGGGGATAACAATGCTGATTACTAC CTTTTAAATATTTAGATAAATGCACAGCCAGCAGCACCACATCTAAGCATTAGTGATGGGTAGC TGATGTCAGCTTCATGTGGATTTAAGCACTCTAGAAACAATGAAGCTCTCTGGCATAATTTAAGGAG CTCCCAAAATGTGTTACCTATTAAATTGTAACCTCAGCAAGTAGAAGACCAATT CCAGTGGTGAACAGAACCTCCCAAAATTTGAGTTGCACCTTCCTCTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTGAGCTCCTTGACCTATGAGT[C]GGGGCCTGACTAGGAAAAGT TGGAGTTAAGGAGGAAATTAGCATTCCTTAATGTTTGTGTTGGTCTCTGAATTTCTCTTTATTAT AGTCTATAGTTTACTCTCAGTTCCTCACCATCATCTTGCTAA
WI-7191b	273 T A ---			CCAGTGGTGAACAGAACCTCCCAAAATTTGAGTTGCACCTTCCTCTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTGAGCTCCTTGACCTATGAGT[C]GGGGCCTGACTAGGAAAAGT TGGAGTTAAGGAGGAAATTAGCATTCCTTAATGTTTGTGTTGGTCTCTGAATTTCTCTTTATTAT AGTCTATAGTTTACTCTCAGTTCCTCACCATCATCTTGCTAA
WI-7199c	112 T C ---			CCAGTGGTGAACAGAACCTCCCAAAATTTGAGTTGCACCTTCCTCTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTGAGCTCCTTGACCTATGAGT[C]GGGGCCTGACTAGGAAAAGT TGGAGTTAAGGAGGAAATTAGCATTCCTTAATGTTTGTGTTGGTCTCTGAATTTCTCTTTATTAT AGTCTATAGTTTACTCTCAGTTCCTCACCATCATCTTGCTAA
WI-7199b	112 T C ---			CCAGTGGTGAACAGAACCTCCCAAAATTTGAGTTGCACCTTCCTCTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTGAGCTCCTTGACCTATGAGT[C]GGGGCCTGACTAGGAAAAGT TGGAGTTAAGGAGGAAATTAGCATTCCTTAATGTTTGTGTTGGTCTCTGAATTTCTCTTTATTAT AGTCTATAGTTTACTCTCAGTTCCTCACCATCATCTTGCTAA

WI-7216c	237	T C	---			TGACACTAACACTCTAATTCAAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGCTCTTCTCCCC AAGGACAAAATGTAGAAAGATGTAGATAACTTACTCAAGATTCCCTCCAGAAAAATACGTATGT TTAAAAACCTTCTCTGCTATACATAGGAAAAAGACACATCCACCTAAAATTGACTGTACTGTTTAA CTGTCAATTCTCTGAGGCTAAACACAGTTTGTTTT/CJCTTGTAATCAGTT
WI-7216b	237	T C	---			TGACACTAACACTCTAATTCAAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGCTCTTCTCCCC AAGGACAAAATGTAGAAAGATGTAGATAACTTACTCAAGATTCCCTCCAGAAAAATACGTATGT TTAAAAACCTTCTCTGCTATACATAGGAAAAAGACACATCCACCTAAAATTGACTGTACTGTTTAA CTGTCAATTCTCTGAGGCTAAACACAGTTTGTTTT/CJCTTGTAATCAGTT
WI-7220b	147	A T	---			AGGATGATGCTCCAAAGGGGACCTTGAACCTATTACCAATTATTGCTCTTTAAGCTGGCAACCCCA TCATTAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTAGACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAAJATJAATCTTGAGCACAGTGAATGACCTATCTCGAAACATCTAATGGATCTCTA AAGGGTAACAAACCCCTATAAATCTGGCTTACTGCACATATTAGTGTGTTT
WI-7220	140	A T	---			AGGATGATGCTCCAAAGGGGACCTTGAACCTATTACCAATTATTGCTCTTTAAGCTGGCAACCCCA TCATTAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTAGACAGCTTCAGTAATCAATGGGCA GTGGCJATJCTAGAAAAATCTTGAGCACAGTGAATGACCTATCTCGAAACATCTAATGGATCTCTA AAGGGTAACAAACCCCTATAAATCTGGCTTACTGCACATATTAGTGTGTTT
WI-7226	232	C	---			GATCGAATTTTTCAGATGATTCGGAAATTTTCATTACAGGTATTGTAATAGTGACATATATATGTATA TACATATACCTCCTATTCTCTTAATTTTGTAAATGTTAACTGGCAGTAAGTCTTTTGTGATCATTT CCCTTTCCATATAGGAAACATAATTTGAAGTGGCCAGATGAGTTTATCATGTGCAGTGAAAAATAA TTACCCACAAATGCCACCAGTAACTTAACGATTCTTCACCTCTCTGGGGTTT
WI-7228b	254	G A	---			ATAGCTTCAGATTACAAAGGCCAAGGTAATAGAAATGCATACCAGTAATGGCTCCAATTCATAA TATGTTCCACCAGGAGATTACAAATTTTGTCTCTTCTGTCTTGTATCTATTAGTTGATTTAATTA CTTCTGAATAACGGAAGGATCAGAAGATATCTTTTGTGCTAGATTGCAAAATCTCCAATCCACA CATATTGTTTTAAAAATAAGAAATGTTATCCAACATTAAGATATCTCAATGTI
WI-7228a	163	G A	---			ATAGCTTCAGATTACAAAGGCCAAGGTAATAGAAATGCATACCAGTAATGGCTCCAATTCATAA TATGTTCCACCAGGAGATTACAAATTTTGTCTCTTCTGTCTTGTATCTATTAGTTGATTTAATTA CTTCTGAATAACGGAAGGATCAGAA[G/A]ATATCTTTTGTGCTAGATTGCAAAATCTCCAATCC ACACATATTGTTTTAAAAATAAGAAATGTTATCCAACATTAAGATATCTCAA
WI-7233c	213	C T	---			CGATCGTACTGCCAGTAGCATTTGCTGTCTGTCCGGTCTGTTGTACATTTTCAATTTGTTACA GATGTGAACTTTATTCTTGTCACTAATTAATAATTTAAAAATTTCTAGGAAGTCAAAAAATAA TAAAGGGTTGAGCCCTCTACTTCTCTTGTCCACCTTTTGTGGCAATATTAAAGTGAAGTACTGCTAATA GTGTAAGTA[C/T]GTGCACAAAAACCACTGCCAGATAACAGAGGGGCTG

[illegible]

WI-7252a	520 T C ---			CCACAGGATCCAGCCCAAGGGCCCTCCGCCCCCTCCACTCGCAGACAGCCGGGACAGAG GCCTGCCGGGGGCGCAGCCCGGGCCCTGGCTCGGAGCTGCCCCCGCCCCCTGGTCTCGGTCCG GACACTCTAGAGAACGCAGCCCTAGAGCCCTGGCTGGAGCGTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACCTCAGTCATTAGACTCCTCCCA
WI-7265m	252 T A ---			AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCCATTCCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCTTT/
WI-7265l	231 T A ---			AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCCATTCCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCTTT/
WI-7265k	121 T G ---			AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCCATTCCTGTGGTTCATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCTTT
WI-7265j	174 T A ---			AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCCATTCCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCTTT
WI-7265i	227 T C ---			AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCCATTCCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCTTT
WI-7265h	80 T A ---			AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCCATTCCTGTGGTTCATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCTTT
WI-7265g	170 T G ---			AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCCATTCCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCTTT

WI-7265f	231 T A ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGCGCT
WI-7265e	227 T C ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGCGCT
WI-7265d	174 T A ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAATAACGATCTCT CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGCGCT
WI-7265c	170 T G ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAATAACGATCTCT CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGCGCT
WI-7265b	121 T G ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAATAACGATCTCT CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGCGCT
WI-7265a	80 T A ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAATAACGATCTCT CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGCGCT
WI-7281b	183 C ---	---	GATCACCCAGCCACAAAGCCCTTGAGGGCCCTATACCATGGCCACCTTGAGCAGAGAGCCAAAGC ATCTTCCCTGGGAAGTCTTCTGGCCAAAGTCTGCCAGCCTGGCCCTGCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTCTTGGCAAAAACGGAGTCCGAGGCCGCGAG GTGTTGTGAAGACCACTCGTTCTGTGGTTGGGGTCTGCAAGAGGCCCTCCTC
WI-7281	171 C A ---	---	GATCACCCAGCCACAAAGCCCTTGAGGGCCCTATACCATGGCCACCTTGAGCAGAGAGCCAAAGC ATCTTCCCTGGGAAGTCTTCTGGCCAAAGTCTGCCAGCCTGGCCCTGCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTCTTGGCAAAAACGGAGTCCGAGGCCGCGAG CAGGTGTTGTGAAGACCACTCGTTCTGTGGTTGGGGTCTGCAAGAGGCCCT



WI-7282b	159	G C	---			TGTCACCTGGCACATTCAATTTCTCAGTTGAAGAGAGAAAAATTTGAAAAATGTCCTTATGCTTTTAGA GTTGCAACTTAAGTATATTGGTAGGGTGAGTGTTCACCTCAAAATATGTCAACTNNNNNNNNNT AGGCCCTTTCATAAAACCAAACT[G/C]TAGCAAGATGCAATGCATGGCAATCTGTGGTCTCCA GTTGGTTATCTGAATAGTGCACCAATTCACCAAGACAGTCTGAGATTGG
WI-7292	92	T C	---			CTTGATTCTCCACTGAGTGGGAGCATCTCCAGTCTCCCAATATATCTCCCCCACTCCACTAC TCTCTCTCCACTTCATTTTCQ[T/C]TTGTCCTTCTCTCTAATCAGTGTTCGAGGCTGACTTG GGACAACGATATTATGATATTATGTCTGTTTCTCTCCCAATAGAAATAAGTCATGGAGCC TGAAGGTGCCTAGTTGACTTACTGACAAAAGGCTCTAGTTGGGCTGA
WI-7301f	133	A G	---			AACTATGGCAGTGGTCTGCTGTTATAGTAGTAGAGCGGGTATGGTGGTGGACCCAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTGGAGGATATGATGTTACAATGAAGGAGGAAATTTTG A/GJCGGTAGTAACATATGGTGGTGGGAACTATAATGATTTGGAAATACAGTGGACAAACAGCA ATCAAAATTATGGACACATGAAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301e	94	T G	---			AACTATGGCAGTGGTCTGCTGTTATAGTAGTAGAGCGGGTATGGTGGTGGACCCAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTG[T/G]TGGAGGATATGATGTTACAATGAAGGAGGAAATTTTGA TGACGGTAGTAACATATGGTGGTGGGAACTATAATGATTTGGAAATACAGTGGACAAACAGCAA TCAAATATGGACACATGAAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301d	138	A G	---			AACTATGGCAGTGGTCTGCTGTTATAGTAGTAGAGCGGGTATGGTGGTGGACCCAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTGGAGGATATGATGTTACAATGAAGGAGGAAATTTTGA CGGT[A/G]TAACATATGGTGGTGGGAACTATAATGATTTGGAAATACAGTGGACAAACAGCAA TCAAATATGGACACATGAAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301c	211	A C	---			AACTATGGCAGTGGTCTGCTGTTATAGTAGTAGAGCGGGTATGGTGGTGGACCCAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTGGAGGATATGATGTTACAATGAAGGAGGAAATTTTGA CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTGGAAATACAGTGGACAAACAGCAATCA AATTATGGAC[A/C]CATGAAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301b	182	C T	---			AACTATGGCAGTGGTCTGCTGTTATAGTAGTAGAGCGGGTATGGTGGTGGACCCAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTGGAGGATATGATGTTACAATGAAGGAGGAAATTTTGA CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTGGAAATACAGTGGACAAACAGCAA TCAAATATGGACACATGAAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301	88	G T	---			AACTATGGCAGTGGTCTGCTGTTATAGTAGTAGAGCGGGTATGGTGGTGGACCCAGGATATGGAA ACCAAGGTGGTGATATGGTGTGCGGTG[T/G]CGGTGTGGAGGATATGATGTTACAATGAAGGAGGAAATTT TGACGGTAGTAACATATGGTGGTGGGAACTATAATGATTTGGAAATACAGTGGACAAACAGCAA TCAAATATGGACACATGAAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG

WI-7301	205	A C ---	---	---	A A C T A T G G C A G T G T C C T G G T T A T A G T A G T A G A G G G G T A T G G T G G T G G C A C C A G G A T A T G G A A A C C A A G G T G G T G G A T A T G G T G G C G G T T G G A G A T A T G A T G T T A C A A T G A A G G A G G A A T T T T G A C G G T A G T A A C T A T G G T G G T G G G A A C T A T A T G A T T T T G G A A T T A C A G T G G A C A A C A G C A A T C A A A T T A C T G G A C A C A T G A A G G G G C A G T T T G G T G G A A G A G C T C G G G C A G
WI-7314c	49	G A ---	---	---	C T C T C C T T T T T C T C A G A T C T G C T C C T G G G T T T A A T T G G G A G G T C A G A J T T G T T C T A C C T C A C T G A G A G G G A A C A G A A G G A T A T T G C T C C T T T T G C A G C A G T G T A A T A A G T C A A T T A A A A C T T C C C A G G A T T T C T T T G G A C C C A G G A A C A G C C A T G T G G T C C T T C T G T G C A C T A T G A A C G C T T C T T T C C C A G G A C A G A A A T G T G T A G T C A C C T T A T T T T A T T A A C A A A A C T T G T T T T
WI-7314b	49	G A ---	---	---	C T C T C C T T T T T C T C A G A T C T G C T C C T G G G T T T A A T T G G G A G G T C A G A J T T G T T C T A C C T C A C T G A G A G G G A A C A G A A G G A T A T T G C T C C T T T T G C A G C A G T G T A A T A A G T C A A T T A A A A C T T C C C A G G A T T T C T T T G G A C C C A G G A A C A G C C A T G T G G T C C T T C T G T G C A C T A T G A A C G C T T C T T T C C C A G G A C A G A A A T G T G T A G T C A C C T T A T T T T A T T A A C A A A A C T T G T T T T
WI-7314	36	A G ---	---	---	C T C T C C T T T T T C T C A G A T C T G C T C C T G G G T T T A A G J T T G G G A G G T C A G T G T T C T A C C T C A C T G A G A G G G A A C A G A A G G A T A T T G C T C C T T T T G C A G C A G T G T A A T A A G T C A A T T A A A A C T T C C C A G G A T T T C T T T G A C C C A G G A A C A G C C A T G T G G T C C T T C T G T G C A C T A T G A A C G C T T C T T T C C C A G G A C A G A A A T G T G T A G T C A C C T T A T T T T A T T A A C A A A A C T T G T T T T
WI-7321b	199	C T ---	---	---	A C T C A G G G A A G G G A T G C C C C A T T A A A G T G A C A A A A G G T G G G T G T G G G C A C C A T G G C A T G A G G A A G A A C A A G G T C C C T G A G C A G G C A C A A G T C C T G A C A G T C A A G G G A C T G C T T T G G C A T C C A G G C C T C C A G T C A C C T C A C T G C C A T A C A T T A G A A T G A G A C A A T C A A A G N N N N N N N A G G G T G G C A C A C C C A T C C T T G T T G C T G G G T G T G C A G C C A C A T C C A A G A C T G G A G C A G C A G G C T G G C C A
WI-7321	199	C T ---	---	---	A G A C A T T C T C G C T T C C T G A A G A C T G A A G A A G T A G T A G C A T G G G A C C C A C G A A A C T G C C C T G G C T C C A G T G A A A C T T G G G C A C A T G C T A G G T C C A G A A G T C C T A T G T T A A G C C C T G G C A G G C A G G T G T T A T T A A A A T T C T G A A T T T G G G A T T T C A A A A G A T A T A T T T A C A T A C A C T G T A T G T T A T A G A A C T T C A T G G A T C A G A T C T G G G G C A G C A A C C T A T A A A T C A A C A
WI-7336b	248	A C ---	---	---	C T C T T T C T C A G C A C A T T G A T G G G C A A C T A G A A T T A C A G C A G T T T C A A A C T C T A C C A T G G A T A A T G C A A A C A A C C G A A G C T A C A T G C C A A T G A T A G G T G C A A A G A T A T T G G C A A A G G T G C T T T A C C C T T G A G C C A T T A T T G T G T C A G A G A A C A A A A G A A C A G A A T C A A T A T A A A T T C A A A G A C T A T C T G C A G C T A G T G T G T T C T T T A C A C A C A G J T A T A C A C A C A G A C A T C A G A A A A T T C T G T T
WI-7338c	221	A G ---	---	---	

WI-7338b	125 A C ---	---	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATGGCAAAAGGTCTTTAC/CCTTG AGCCATTATTTGTGTCAGAGAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAG CTAGTGTGTTCTCTTTACACACATATACACACAGACATCAGAAAATTCGTGTT
WI-7338	125 A C ---	---	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATGGCAAAAGGTCTTTACCTTGAGC CATTAATTTGTGTCAGAGAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAGCTA GTGTTCTCTCTTTACACACACATATACACACAGACATCAGAAAATTCGTGTT
WI-7338	221 A G ---	---	CCTATGTCATGAATGCTAGGGGCCAGGGAACAAATTTTAAATAATAAATTCACCATAG CAATACAGAAATACTTTAAATACCATTAATACATTTGATTTTCAATGTAACAGGATTTCTTCA CAGATCTCATTTT/AJAAAATCTTAATGATTATTTTATTAATCTACTGTTGTTTAAAGGGATGTTA TTTTAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAGAA
WI-7384c	146 T A ---	---	CCTATGTCATGAATGCTAGGGGCCAGGGAACAAATTTTAAATAATAAATTCACCATAG CAATACAGAAATACTTTAAATACCATTAATACATTTGATTTTCAATGTAACAGGATTTCTTCA CAGATCTCATTTT/AJAAAATCTTAATGATTATTTTATTAATCTACTGTTGTTTAAAGGGATGTTA TTTTAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAGAA
WI-7384b	146 T A ---	---	CCTATGTCATGAATGCTAGGGGCCAGGGAACAAATTTTAAATAATAAATTCACCATAG CAATACAGAAATACTTTAAATACCATTAATACATTTGATTTTCAATGTAACAGGATTTCTTCA CAGATCTCATTTT/AJAAAATCTTAATGATTATTTTATTAATCTACTGTTGTTTAAAGGGATGTTA TTTTAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAGAA
WI-7384	145 T A ---	---	TGAAATCCTGGGTCCTTGGGCTGCTGAGTGGTTATTTTACTTTGCCCTCCCTCCCTTTT TGAGATCCATCCTTTATCAAGAAAGCTGAAGCGACT/AJAAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAGGTTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTGA CTTGTGCTGTCCAGAACTTTTCCCCCAAGATGTGTATGTTATGG
WI-7388c	106 A T ---	---	TGAAATCCTGGGTCCTTGGGCTGCTGAGTGGTTATTTTACTTTGCCCTCCCTCCCTTTT TGAGATCCATCCTTTATCAAGAAAGCTGAAGCGACT/AJAAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAGGTTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTGA CTTGTGCTGTCCAGAACTTTTCCCCCAAGATGTGTATGTTATGG
WI-7388b	106 A T ---	---	CTTGTGCTGTCCAGAACTTTTCCCCCAAGATGTGTATGTTATGG

WI-7388	94	T A	---			TGAAATCCTGGGCTCTTGGCCTGCTCTGTAGCTGGTTATTTTACITTTGCCCCCTCCCCACITTTTT TGAGATCCATCCTTTATCAAGAAAGT/AJCTGAAGCGACTATAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTTGCAACAAGGTTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTTGA CTTGCTCTGTCCAAAGAACTTTTCCCCAAAGATGIGTATAGTTATTGG
WI-7438	64	A G	---			TTAGATTTAATTGGCAACAGCAACTCACTGCCACCATTCCTGAGATCTNCTATTCCTGG[A/G] GTTGATATGACAAGGAACCCCTATTGGAACCAAGTCTTCAGATTGNCATGTGCAGACAGGCTCCT TGCTGTAGGTGTAGTAGCATGTACACTGTACTGTTCACTGTAAACATAGTTTGTTGCTGTTATTTGTTA TTGGAAATGAATATCGCTCCACTGACTTTTACCA
WI-7454b	152	T C	---			CCATGATCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAAGCCCCAAACC CAGTACAACTGAGAAATGAGAGAACCCCTGATAGCACTGTCTGAATGGCCAGGAGCCTCCAAAGGCTAA TCCTACCCCTGGATTCTT/CJTGTTGTTTAAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCATTTGTCTACTTCTCAAAATGTTTTGACA
WI-7454	152	T C	---			CCATGATCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAAGCCCCAAACC CAGTACAACTGAGAAATGAGAGAACCCCTGATAGCACTGTCTGAATGGCCAGGAGCCTCCAAAGGCTAA TCCTACCCCTGGATTCTT/CJTGTTGTTTAAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCATTTGTCTACTTCTCAAAATGTTTTGACA
WI-7464c	177	G C	---			AATTTGAAAATCTGAAAAAAGTGCAATAAGCAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTTCAGTCAGTCCATCTTAACCATGTACAAATGCACTAAATTAATTTTAAATTTCCCTATGTA CAACAGAGCCACAGCACAAGAGGGTGGGCATAAGCAGTTGCCA[G/C]CCAGAAAGAGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCCCAGGAGAGCAACGTTTCCCAACAATTAT
WI-7464b	168	C A	---			AATTTGAAAATCTGAAAAAAGTGCAATAAGCAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTTCAGTCAGTCCATCTTAACCATGTACAAATGCACTAAATTAATTTTAAATTTCCCTATGTA CAACAGAGCCACAGCACAAGAGGGTGGGCATAAG[C/A]AGTTGCCAGCCAGAGAGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCCCAGGAGAGCAACGTTTCCCAACAATTAT
WI-7464a	103	C A	---			AATTTGAAAATCTGAAAAAAGTGCAATAAGCAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTTCAGTCAGTCCATCTTAACCATGTACAAATG[C/A]ACTAAATTAATTTTAAATTTCCCTAT GTACAACAGAGCCACAGCACAAGAGGGTGGGCATAAGCAGTTGCCAGCCAGAGAGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCCCAGGAGAGCAACGTTTCCCAACAATTAT
WI-7499b	134	T G	---			CAATTTCTCAATCCAACTAGTCTGTGTCCTAAACCATTCAGACAACTTCCACTTCGAAGGTTTTTA AATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCACGTTCTTTGAATGCTTCAIT /GJTATAGTCTCTTCAATTTAGCAATCAGTGAGGCAATACACTGGCATCATGCCCTTTTTTTTAGGA ACTCTGTACAAAATTCCTTTGAAAATATAAATTTTGGAAATGAGTGATGA

Accession	Length	GC Content	Sequence
WI-7499a	33 A G ---	---	CAATTCTCAATCCAAOCTAGTCTGNTGCCATAA/GJCCATTCCAGACAAACCTTCCACTTCAAGGTT TTAAATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCACGTTCTTTTGAATGCTTC ATTATAGTCTCTTCATTAGCAATCAGTGAGGCAATACACTGGCATCATCCCTTTTTTTTAGGAA CTCTGTACAAAATCCCTTTGAAAATATAAAATTTGGAAATGAGTGATGA
WI-7506b	118 A C ---	---	TGGGAATAGTAAGAGAAAGATGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAGTGAAT GCATCCAGCAGCAGACCACTTNAAGAGTAGTCTGGTGTGATTGCCTAGC/ACJGGAGAGTTGAG TGCCACAGGTAAGAAATGAGTGAAGAGGAAAAATCATGATGTCATGATGCAGTAATTACTATGTCA GAAGAAAATATTTTAAATATTGGACCACCTCTTGTCTACCATCCCTACCCACT
WI-7506	118 A C ---	---	TGGGAATAGTAAGAGAAAGATGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAGTGAAT GCATCCAGCAGCAGACCACTTNAAGAGTAGTCTGGTGTGATTGCCTAGC/ACJGGAGAGTTGAG TGCCACAGGTAAGAAATGAGTGAAGAGGAAAAATCATGATGTCATGATGCAGTAATTACTATGTCA GAAGAAAATATTTTAAATATTGGACCACCTCTTGTCTACCATCCCTACCCACT
WI-7534b	143 C T ---	---	TGTGAATCTTAGCTCTGGAAGGTGTTTATGCCCTTTCGGGTTCTTGATGTTCCGAGTGTCAACCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCGTGGAAACACATCCCGGTGATAGAATTGCT AAATTGT/CJGTGAAATAGGTTAGAAATTTTCTTAAATATGTTTTCTTATTCGTGAAAAATTCGG AGAGTGTCTGCTAAAATTTGGATTGGTGTGATCTTTTTGGTAGTTGTAATTT
WI-7534	135 T C ---	---	TGTGAATCTTAGCTCTGGAAGGTGTTTATGCCCTTTCGGGTTCTTGATGTTCCGAGTGTCAACCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCGTGGAAACACATCCCGGTGATAGAATTGCT /CJAAATTGTCGTGAAATAGGTTAGAAATTTTCTTAAATATGTTTTCTTATTCGTGAAAAATTCGG AGAGTGTCTGCTAAAATTTGGATTGGTGTGATCTTTTTGGTAGTTGTAATTT
WI-7543b	162 G A ---	---	GGGAAAGAATAAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACC AGTCTGTTTGACAGGAAGCCCCACTTGAAGGAAGAGTCTAAGAGTGAAGTAGGTGTGACTTGAAC TAGATTGCATGCTTCTCTCTTGTCTT/GJGGAAGACCAGCTTTGCAGTGACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTTCTCTGGCTCTTGGATGTAGTCAGTTA
WI-7543	162 G A ---	---	GGGAAAGAATAAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACC AGTCTGTTTGACAGGAAGCCCCACTTGAAGGAAGAGTCTAAGAGTGAAGTAGGTGTGACTTGAAC TAGATTGCATGCTTCTCTCTTGTCTT/GJGGAAGACCAGCTTTGCAGTGACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTTCTCTGGCTCTTGGATGTAGTCAGTTA
WI-7555c	60 T C ---	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAAATTTGTAGAGGT/CJCTCA AAAAAGAAAGTGGTATGTTGTGATGATCAGCACTAAGTCTCGATCTCTGTTAAAGCCACTTGGGTC ATAAGAAGGGGAAGTAAAAAATGAAGTCTGACTAGAAATTTCTATGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTGATGTGCAATTTTGAATTTGAG

WI-7555b	60	T C ---	---		GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCCTCAAAATTTGTAGAGGTT/CJTCTA AAAAGAAAGTGGTATGTTGTGTGATGATCAGCACTAAGTCTCTGCAATCCTGTTAAAGCCACCTTGGGTC ATAAGAAAGGGAAGTAAAAAATGAAGCTGACTAGAAATCTATTGCAGAGGCCAAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTTGATGTGCATTTTGAATTTGAG
WI-7555	60	T C ---	---		GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCCTCAAAATTTGTAGAGGTT/CJTCTA AAAAGAAAGTGGTATGTTGTGTGATGATCAGCACTAAGTCTCTGCAATCCTGTTAAAGCCACCTTGGGTC ATAAGAAAGGGAAGTAAAAAATGAAGCTGACTAGAAATCTATTGCAGAGGCCAAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTTGATGTGCATTTTGAATTTGAG
WI-7567b	290	G T ---	---		TGAGCCATCTAGTAAAGAAAGCCCATTTTCAACTGCTTTGAAACCTGGCTGGGCTGAGCATGAT GGGAATAGGGAGACAGGGTAGGAAAGGGCGCTACTCTTCAGGGCTAAAGATCAAGTGGCCTTGG ATCGTAAAGCTGGCTGTTGATGCTATTATGCAAGTTAGGGTCTATGTATTAGGATGCGCCTAC TCTCAGGGTCTAAAGATCAAGTGGGCTTGGATCGCTAAGCTGGGCTGTTT
WI-7569b	63	T C ---	---		AATGATCCCTTTCCGTCCAAACAACAGGAAACCTGACTGGGCAGTGAAGGAAGGATGGCAIT/CJ AGCGTTATGTTAAAAAACAAGTATCTGTATGACAACCCGGGATCGTTGCAAGTAACTGAATCCAT TGGACATTTGTAAGGCTTAAATGAGTTTAGTGGGAAATAGCGTTGTTATCGCTTGGGTTTAAAT ATTGATGAGTTCCACTTGTATCATGCGCTACCCGAGGAGAAGAGGAGTTTG
WI-7574c	216	A G ---	---		GCCACAGCAGAAATGGAGCGGTGTGAGGAAGTGTCCTTTTCTCTGTTTGTGTTGCCAAGGCCAAAC TCCCACCTCTGCCCCCTTTAATCCCCCTTCTACAGTGAGTCCACTACCCCTCACTGAAATCATTTTG TACCACCTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTCTTG ATAGCCCAGGGC/A/GTCTGCTGGGCTGACCACGTTACTCATCCCCGTTA
WI-7574b	216	A G ---	---		GCCACAGCAGAAATGGAGCGGTGTGAGGAAGTGTCCTTTTCTCTGTTTGTGTTGCCAAGGCCAAAC TCCCACCTCTGCCCCCTTTAATCCCCCTTCTACAGTGAGTCCACTACCCCTCACTGAAATCATTTTG TACCACCTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTCTTG ATAGCCCAGGGC/A/GTCTGCTGGGCTGACCACGTTACTCATCCCCGTTA
WI-7574	216	A G ---	---		GCCACAGCAGAAATGGAGCGGTGTGAGGAAGTGTCCTTTTCTCTGTTTGTGTTGCCAAGGCCAAAC TCCCACCTCTGCCCCCTTTAATCCCCCTTCTACAGTGAGTCCACTACCCCTCACTGAAATCATTTTG TACCACCTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTCTTG ATAGCCCAGGGC/A/GTCTGCTGGGCTGACCACGTTACTCATCCCCGTTA
WI-7576c	168	A T ---	---		AATGATGATGATAATGATGATGACGACGACAACGATGATGCTTGTAAACAAGAAAAACATAAGAGAGC CTTGGTTTCATCAGTGTAAAAAATTTTGAAGGGGCTACTAGTTGACACACTTTTGAAGTTTGTGT TCTGTTTGTAAAAACTGGCATCTGACACAAAAAATGTTGTTGAAGGCTTATTCTACATTTCACTAC TTTGTAAAGTGAGAGACAAAGAAAGCAANNNNNNNNAAAAAGAAAAAATAAAG

WI-7576b	168 A T ---	---	AATGATGATGATAATGATGATGACGACGACGATGATGCTTGTAAACAAGAAAACATAAGAGAGC CTTGGTTCATCAGTGTTAAAAATTTTGAAAAGGCGGTACTAGTTTCAGACACTTTTGAAGTTTGTGT TCTGTTTGTTAAACTGGCATCTGACACAAAAA[A/T]GTTGAAGGCCCTTATTTCTACATTTCCACCTAC TTTGTAAGTGAGAGACAAAGAAGCAANNNNNNNNNNAAGAAAAATAAAC
WI-7577g	77 T C ---	---	AACCATGTTCCCTTCTTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTAA AAATATGCA[T/C]CAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTAQACGTAGGAAGAGAGAAQCATCAAAGTGGAGATATGTTAACTAT TGATATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTAATTC
WI-7577p	50 G C ---	---	AACCATGTTCCCTTCTTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTAA TAAAAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTAQACGTAGGAAGAGAGAAQCATCAAAGTGGAGATATGTTAACTAT TGATATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTAATTC
WI-7577o	157 G A ---	---	AACCATGTTCCCTTCTTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAA AGAAGTTCAATTTGGTTTAQACG[A/T]AGGAAGAGAGAGAAQCATCAAAGTGGAGATATGTTAACT ATTGTAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTAATTC
WI-7577n	48 A G ---	---	AACCATGTTCCCTTCTTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTAA TAAAAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTAQACGTAGGAAGAGAGAAQCATCAAAGTGGAGATATGTTAACTAT TGATATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTAATTC
WI-7577m	84 G A ---	---	AACCATGTTCCCTTCTTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTAA AAATATGCATCAAAATCG[A/T]CTCTCATTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTAQACGTAGGAAGAGAGAAQCATCAAAGTGGAGATATGTTAACTAT TGATATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTAATTC
WI-7577l	93 T C ---	---	AACCATGTTCCCTTCTTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTAQACGTAGGAAGAGAGAAQCATCAAAGTGGAGATATGTTAACTAT TGATATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTAATTC
WI-7577k	154 C A ---	---	AACCATGTTCCCTTCTTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAA AGAAGTTCAATTTGGTTTAQACGTAGGAAGAGAGAAQCATCAAAGTGGAGATATGTTAACT ATTGTAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTAATTC

WI-7577j	117 A G ---	---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTTCTGAGGGTTTGTAGTA/GJACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGATTTC
WI-7577i	77 T C ---	---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGATTTC
WI-7577h	50 G C ---	---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA TAAATATGCATCAAAATCGTCTCTATTCTTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGATTTC
WI-7577g	157 G A ---	---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AGAAGTTCAATTTGGTTTACACG/GATAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGATTTC
WI-7577f	48 A G ---	---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA TAAATATGCATCAAAATCGTCTCTATTCTTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGATTTC
WI-7577e	84 G A ---	---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGATTTC
WI-7577d	93 C G ---	---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA TAAATATGCATCAAAATCGTCTCTATTCTTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGATTTC
WI-7577c	114 C A ---	---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA TAAATATGCATCAAAATCGTCTCTATTCTTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGATTTC



WI-7576b	168	A T ---	---	AATGATGATGATAATGATGATGACGACGACAAATGATGCTTGTAAAGAAACATAAGAGAGC CTTGGTTCATCAGTGTTAAAAATTTTGAAGGCGGTACTAGTTTCAGACACTTTGGAAGTTTGTG TCTGTTTGTTAAACTGGCATCTGACACAAAAA[A/T]GTTGAAGCCCTTATTCTACATTTCCACCTAC TTTGTAAGTGAGAGAGACAAGAAGCAANNNNNNNNNNAAGAAAAATAAAC
WI-7577g	77	T C ---	---	AACCATGTTCCCTTCTTTAGCACCACAAATAATCAAAACCCCAACATAA[G/C]GTTTGCCTTTAA AAATATGCA[T/C]CAAAATCGTCTCTCAATTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGTAATATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577p	50	G C ---	---	AACCATGTTCCCTTCTTTAGCACCACAAATAATCAAAACCCCAACATAA[G/C]GTTTGCCTTTAA TAAATATGCAATCAATCGTCTCTCAATTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGTAATATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577o	157	G A ---	---	AACCATGTTCCCTTCTTTAGCACCACAAATAATCAAAACCCCAACATAA[G/C]GTTTGCCTTTAA AAATATGCAATCAATCGTCTCTCAATTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AGAAGTTCAATTTGGTTTACAC[G/A]TAGGAAGAGAGAGAGCATCAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577n	48	A G ---	---	AACCATGTTCCCTTCTTTAGCACCACAAATAATCAAAACCCCAACATAA[G/C]GTTTGCCTTTAA TAAATATGCAATCAATCGTCTCTCAATTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGTAATATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577m	84	G A ---	---	AACCATGTTCCCTTCTTTAGCACCACAAATAATCAAAACCCCAACATAA[G/C]GTTTGCCTTTAA AAATATGCAATCAATCGTCTCTCAATTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAGAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGTAATATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577l	93	T C ---	---	AACCATGTTCCCTTCTTTAGCACCACAAATAATCAAAACCCCAACATAA[G/C]GTTTGCCTTTAA AAATATGCAATCAATCGTCTCTCAATTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAGAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGTAATATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577k	154	C A ---	---	AACCATGTTCCCTTCTTTAGCACCACAAATAATCAAAACCCCAACATAA[G/C]GTTTGCCTTTAA AAATATGCAATCAATCGTCTCTCAATTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AGAAGTTCAATTTGGTTTACACGTAGGAAGAGAGAGAGCATCAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC

WI-7577j	117 A G ---	---	AACCATGTTCCCTTCTTAGCACCACAAATATCAAAACCCCAACATAAGTGTGCTTTCCCTTAA AAATATGCATCAAAATCGTCTCATTACTTTCTCTGAGGGTTTAGTA/GJACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAATTGACTGTATTTC
WI-7577i	77 T C ---	---	AACCATGTTCCCTTCTTAGCACCACAAATATCAAAACCCCAACATAAGTGTGCTTTCCCTTAA AAATATGCAT/GJCAAAATCGTCTCATTACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAATTGACTGTATTTC
WI-7577h	50 G C ---	---	AACCATGTTCCCTTCTTAGCACCACAAATATCAAAACCCCAACATAAGTGTGCTTTCCCTTAA TAAAAATATGCATCAAAATCGTCTCATTACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAATTGACTGTATTTC
WI-7577g	157 G A ---	---	AACCATGTTCCCTTCTTAGCACCACAAATATCAAAACCCCAACATAAGTGTGCTTTCCCTTAA AAATATGCATCAAAATCGTCTCATTACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AGAAGTTCAATTTGGTTACAC/GJTAGGAAGAGAGAGAGCATCAAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTCTGAATTGACTGTATTTC
WI-7577f	48 A G ---	---	AACCATGTTCCCTTCTTAGCACCACAAATATCAAAACCCCAACATAAGTGTGCTTTCCCTTAA TAAAAATATGCATCAAAATCGTCTCATTACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAATTGACTGTATTTC
WI-7577e	84 G A ---	---	AACCATGTTCCCTTCTTAGCACCACAAATATCAAAACCCCAACATAAGTGTGCTTTCCCTTAA AAATATGCATCAAAATCG/GJCTCTCATTACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAATTGACTGTATTTC
WI-7577d	93 T C ---	---	AACCATGTTCCCTTCTTAGCACCACAAATATCAAAACCCCAACATAAGTGTGCTTTCCCTTAA AAATATGCATCAAAATCGTCTCATTACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTCTGAATTGACTGTATTTC
WI-7577c	154 C A ---	---	AACCATGTTCCCTTCTTAGCACCACAAATATCAAAACCCCAACATAAGTGTGCTTTCCCTTAA AAATATGCATCAAAATCGTCTCATTACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AGAAGTTCAATTTGGTTA/CJACGTAGGAAGAGAGAGAGCATCAAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTCTGAATTGACTGTATTTC

WI-7577b	117 A G ---	---	AACCATGTTCCCTTCTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCATTACTTTCTCTGAGGTTTGTAGTAA/GIACAGTAGGAGTTAA AAAGAAATTCATTTTGGTTACACGTAGGAAAGAGAGCAATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTATACATGACACTCTCTGAAATGACTGATTTTC
WI-7577	107 G A ---	---	AACCATGTTCCCTTCTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCATTACTTTCTCTGAGTGTAGTAA/GIACAGTAGGAGTTAA AAAGAAATTCATTTTGGTTACACGTAGGAAAGAGAGCAATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTATACATGACACTCTCTGAAATGACTGATTTTC
WI-7619q	106 C G ---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAAGGGCCAAATGGGTCATCCCTCCCTAACGAGACTCTGCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGATGGGGCTCTAAGGGGAGTGTGGGCTCTGCTCTCCCTTTTTCATCTTTTCCCT CTCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619p	150 T C ---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAAGGGCCAAATGGGTCATCCCTCCCTAACGAGACTCTGCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGTGGGCTCTGCTCTCCCTTTTTCATCTTTTCCCTCTC TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619o	228 A G ---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAAGGGCCAAATGGGTCATCCCTCCCTAACGAGACTCTGCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGTGGGCTCTGCTCTCCCTTTTTCATCTTTTCCCTCTC CGCTTTCTTCTTACACAGAAACATTA/GIACATACCGAGAAACCTATTTC
WI-7619n	237 G C ---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAAGGGCCAAATGGGTCATCCCTCCCTAACGAGACTCTGCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGTGGGCTCTGCTCTCCCTTTTTCATCTTTTCCCTCTC CGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619m	99 C T ---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAAGGGCCAAATGGGTCATCCCTCCCTAACGAGACTCTGCTGTGCTGGGGTGCTAATTACATGG TGGCAGGAAGAAATGGGGCTCTAAGGGGAGTGTGGGCTCTGCTCTCCCTTTTTCATCTTTTCCCTC TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619l	189 T A ---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAAGGGCCAAATGGGTCATCCCTCCCTAACGAGACTCTGCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGTGGGCTCTGCTCTCCCTTTTTCATCTTTTCCCTC TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619k	90 C G ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCATCC[C/G]CTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCTCCCTTTTCCATCTTTTTCCT CTCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619j	206 T G ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCTCCCTTTTCCATCTTTTTCCTCTCT CGCT[G]TCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619i	106 C G ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG ATGGCAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCTCCCTTTTCCATCTTTTTCCT CTCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619h	150 T C ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCTCCCTTTTCCATCTTTTTCCTCTC TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619g	228 A G ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCTCCCTTTTCCATCTTTTTCCTCTCT CGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619f	237 G C ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCTCCCTTTTCCATCTTTTTCCTCTCT CGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619e	99 C T ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG TGGCAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCTCCCTTTTCCATCTTTTTCCTC TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619d	189 T A ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCTCCCTTTTCCATCTTTTTCCTC TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619c	90 C G ---	---	---	ACAAGCGGACCTGAAGAGGACGCGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAGGGCCCAATGGGTATCC[C]GCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGATGGGGCCTTAAGGGAGTGGGGCTGTCTCCTCCCTTTTCCATCTTTTCCCT CTCTCGCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619b	206 T G ---	---	---	ACAAGCGGACCTGAAGAGGACGCGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAGGGCCCAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCCTTAAGGGAGTGGGGCTGTCTCCTCCCTTTTCCATCTTTTCCCTCTCT CGCT[G]TCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619	189 T A ---	---	---	ACAAGCGGACCTGAAGAGGACGCGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAGGGCCCAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCCTTAAGGGAGTGGGGCTGTCTCCTCCCTTTTCCAT[G]CTTTTCCCTC TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7626d	105 A G ---	---	---	CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACCAAAAGCAACAGTAA TCATGTGTTTCTGTAACAAATGGGATCTGTCTGGC[G]GTTAAACCCACATCATGGACCAATGTG CCATACTAATGATGAGCAATTTAGCAAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTGCCTGCTGTATTTATAGTAACCAATTTCCCTTTGGACTGTTCA
WI-7626c	155 C T ---	---	---	CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACCAAAAGCAACAGTAA TCTATGTGTTTCTGTAACAAATGGGATCTGTCTGGCATTAAACCATCATGGACCAATGTGCCA TACTAATGATGAGCAATTTAG[C]TACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTGCCTGCTGTATTTATAGTAACCAATTTCCCTTTGGACTGTTCA
WI-7626b	28 T A ---	---	---	CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACCAAAAGCAACAGTAA TAATCTATGTTTCTGTAACAAATGGGATCTGTCTGGCATTAAACCATCATGGACCAATGTG CCATACTAATGATGAGCAATTTAGCACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTGCCTGCTGTATTTATAGTAACCAATTTCCCTTTGGACTGTTCA
WI-7626	144 T C ---	---	---	CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACCAAAAGCAACAGTAA TCTATGTGTTTCTGTAACAAATGGGATCTGTCTGGCATTAAACCATCATGGACCAATGTGCCA TACTAATGAT[G]GAGCAATTTAGCACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTGCCTGCTGTATTTATAGTAACCAATTTCCCTTTGGACTGTTCA
WI-7689c	134 A G ---	---	---	TCCATAACCGCTGATTCAGGGTCTCTGCTGCCGCCACCCAGATGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTTGTTCTCTAAAJA /GTTAAGGGCAGATCACACTGGGGCAGCTGATACAAATTCAGACTGTGTAAAGAGAGCTTAAT GATAATATTGTGGTGGCCACAAATAAAATGGATTTATTAGAATTCATATGAC

WI-7689b	134	A G	---	---	---	TCCATAACCGCTGATTCACAGGTCTCTGCTGCGCCGCCACCCAGATGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGAGCCGCCACCCAGCAAAAGTTGTTCTCTAAAJA /GJTAAGGCGAGATCAGACTGGGCGAGCTGATACAAATTCGAGACTGTGTAAAAAGAGAGCTTAAT GATAATATTGTGGTGCCACAAATAAAATGGATTTATTAGAATTCATATGAC
WI-7689	121	G A	---	---	---	TCCATAACCGCTGATTCACAGGTCTCTGCTGCGCCGCCACCCAGATGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGAGCCGCCACCCAGCAAAAGTTGTTCTCTAA AATAAGGCGAGATCAGACTGGGCGAGCTGATACAAATTCGAGACTGTGTAAAAAGAGAGCTTAAT GATAATATTGTGGTGCCACAAATAAAATGGATTTATTAGAATTCATATGAC
WI-7690	45	G A	---	---	---	TGGAGAACATTCATCTGCCGTCACTATTCATCAATGAAGATTG/AJCACTGAGATCCAGAGAGG CTGGATGACTTGTCAAGTTCACCGATGGTAGTGGCAAGAGAGAGTCCAGAGTCTGGCCCTTGAT GCCAGCTCAGTGCCACAAAGCTCAGTAGGAGGGATGTTCCAGTGGATGAGGGCCACAGGAAGCAC AGGTCCAAGGCTGGTCCACACTTATCAGCAGCAACAACCTGTCAGTTCATCC
WI-7703b	164	T C	---	---	---	ACAGAAAAGTTGAATTTACATGGCTGGAGCTAGAAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGGTTTTTACATTTGGAAACAAGTCAGTCATTCAGATATGATTCAAA TGCTATAAACCAAACTGATGAAGTAAATTCJGJGCTCTCACTGTTTTTATTTAACCTCTAAATTCCT TTCATTTAGGGGTAGCATTTGTTGAAGAGGTTTTAAAGCTTCATGTT
WI-7703	156	T C	---	---	---	ACAGAAAAGTTGAATTTACATGGCTGGAGCTAGAAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGGTTTTTACATTTGAAACAAGTCAGTCATTCAGATATGATTCAAA TGCTATAAACCAAACTGATGTCJAGTAAATGGTCTCACTGTTTTTATTTAACCTCTAAATTCCT TTCATTTAGGGGTAGCATTTGTTGAAGAGGTTTTAAAGCTTCATGTT
WI-7743e	106	C A	---	---	---	TAAATGAGTGTGTTTGTCAACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGAGCCAAAG GTTTCAGAGACTCAGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTACCTCACTGGGGTCTGGGGCTCGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCTCTCAGCCAACG
WI-7743d	275	C T	---	---	---	TAAATGAGTGTGTTTGTCAACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGAGCCAAAG GTTTCAGAGACTCAGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATTCGTACCTCACTGGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCTCTCAGCC
WI-7743e	106	C A	---	---	---	TAAATGAGTGTGTTTGTCAACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGAGCCAAAG GTTTCAGAGACTCAGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATTCGTACCTCACTGGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCTCTCAGCC

WI-7743d	275 C T ---	---	---	TTAAATGAGTGTGTTTGTCAACCGTTGGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAACTCTGCTACCTCACTGGGTCTTGGGGCTCGAGCCCTCATCCGAGGAGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTGCCAGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7743e	106 C A ---	---	---	TTAAATGAGTGTGTTTGTCAACCGTTGGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAACTCTGCTACCTCACTGGGTCTTGGGGCTCGAGCCCTCATCCGAGGAGGTCAGGAGAG GAGGGGCAGAACAGCCGCTCTGTGCCAGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7743d	275 C T ---	---	---	TTAAATGAGTGTGTTTGTCAACCGTTGGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAACTCTGCTACCTCACTGGGTCTTGGGGCTCGAGCCCTCATCCGAGGAGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTGCCAGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7743c	106 C A ---	---	---	TTAAATGAGTGTGTTTGTCAACCGTTGGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAACTCTGCTACCTCACTGGGTCTTGGGGCTCGAGCCCTCATCCGAGGAGGTCAGGAGAG GAGGGGCAGAACAGCCGCTCTGTGCCAGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7743b	275 C T ---	---	---	TTAAATGAGTGTGTTTGTCAACCGTTGGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAACTCTGCTACCTCACTGGGTCTTGGGGCTCGAGCCCTCATCCGAGGAGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTGCCAGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7743	106 C A ---	---	---	TTAAATGAGTGTGTTTGTCAACCGTTGGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAACTCTGCTACCTCACTGGGTCTTGGGGCTCGAGCCCTCATCCGAGGAGGTCAGGAGAG GAGGGGCAGAACAGCCGCTCTGTGCCAGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7743	275 C T ---	---	---	TTAAATGAGTGTGTTTGTCAACCGTTGGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAACTCTGCTACCTCACTGGGTCTTGGGGCTCGAGCCCTCATCCGAGGAGGTCAGGAGAG GAGGGGCAGAACAGCCGCTCTGTGCCAGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7758	144 A G ---	---	---	TGACATTTATTCAAAGTTAAAGCAACACTTACAGAAATTATGAAGAGGTATCTGTTTAACTTTCC TCAGTCAAGTTCAGAGTCTTCAGAGACTTCGTAATTAAAGGAACAGAGTGAGAGACATCATCAAGTG GAGAGAAATCjA/GjTAGTTTAAACTGCATTATAAATTTTATAACAGAAATTAAGTAGATTTTAAAAA GATAAATGTGTAATTTGTTTATATTTTCCCATTTGGACTGTAACTGACTGCC

WI-7765b	126	G C ---	---	ACAGGGCCTTTGGCAGGTGCAGCCCCCACTGCTTTGAOCTGCCTCCCTTCATGCATGGAATTCCTCTCATCTGGAACCATCAGAAACCCCTCACACTGGACTTGCAAAAAGGGTCAAGTATGG[G/C]TTAGGGAACCATCCACTCCTTGAAGTCAAAAATCTCAATCTTCCCTATCTTTGCCACCCCTCATGCTGTGTGACTCAAAACCAATCACTGAACCTTTGCTGAGCCTGTAAATAAAAGGTCGGA
WI-7773b	237	C G ---	---	TTAATTACTGATTCAGCAAGACCAATCATTTGTATCAGATTATTTTAAAGTTTATCCGTAGTTTTGATAAAAGATTTTCTTATCTTGGTTCTGTCAGAGAACCTAATAAGTGTACTTTGCCATTAAAGGCA GACTAGGGTTGATGCTTTTACCCCTTNNNNNNNNNTTGTAAAAGTCTAGTTACCTACTTTTCTTTGATTTGACGTTTGACTAGCCATCTCAAGCAA[C/G]TTTCGACGTTTGA
WI-7774b	170	T C ---	---	TGCAACCTCTTTTCGTATGGCAGCCTGCTGGTCAGCACTCCAGTAGCGAGAGACGGCACCCAGAATCAGATCCCAGCTTCGGCATTTGATCAGACCAACAGTGTCTTTCCCGGGGAGGAAACACTTTTAAATACCCCTTTGCAGGCACCACTTTAATCTGTTT[C/J]ATACCTTGCTTTAATAATGAGCGACTTAAATGATTGAAAATAATGCTGTCTTTAGTAGCAAGTAAATGTGCTTGCT
WI-7785c	165	G ---	---	GCAGAGACCTTCCAAAGGACATATTGCAGGATCTGTAAATAGTGAACATATGGAAGTATTAGAAATATTTATTGCTGTAAATACGTAAATGCATTGGAATAAAACTGTCTCCCATTTGCTCTATGAAACTGCACTTGGTCATTGTGAATANNNNNNNNNGCCAAAGGCTAATCCAATTATTATTCACATTTACCAATAATTTATTGTCCATTGATGATTTATTATTGTAAATGTATCTTGGTGTGC
WI-7785b	165	G ---	---	GCAGAGACCTTCCAAAGGACATATTGCAGGATCTGTAAATAGTGAACATATGGAAGTATTAGAAATATTTATTGCTGTAAATACGTAAATGCATTGGAATAAAACTGTCTCCCATTTGCTCTATGAAACTGCACTTGGTCATTGTGAATANNNNNNNNNGCCAAAGGCTAATCCAATTATTATTCACATTTACCAATAATTTATTGTCCATTGATGATTTATTATTGTAAATGTATCTTGGTGTGC
WI-7785	156	- T ---	---	GCAGAGACCTTCCAAAGGACATATTGCAGGATCTGTAAATAGTGAACATATGGAAGTATTAGAAATATTTATTGCTGTAAATACGTAAATGCATTGGAATAAAACTGTCTCCCATTTGCTCTATGAAACTGCACTTGGTCATTGTGAATANNI- /TJNNNNNNNGCCAAAGGCTAATCCAATTATTATTCACATTTACCAATAATTTATTTGTCCATTGATGATTTATTATTGTAAATGTATCTTGGTGTGC
WI-7789c	84	G A ---	---	TCTCCCCCTCATCCAACCTCCGAAAGTCTGAATCTCCCAAGGAGGGCAACCATCTTACAGAGACTCTCCC TGACGGTGGAAATTTAA[G/A]TTTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGTCCCTTCAGGCCCGCTGCCCTAGGATATGCCCTCCTGGTGACTCGGGGGCTGCTCAGACGACTAGCCCAAGACCCATCT
WI-7789b	84	G A ---	---	TCTCCCCCTCATCCAACCTCCGAAAGTCTGAATCTCCCAAGGAGGGCAACCATCTTACAGAGACTCTCCC TGACGGTGGAAATTTAA[G/A]TTTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGTCCCTTCAGGCCCGCTGCCCTAGGATATGCCCTCCTGGTGACTCGGGGGCTGCTCAGACGACTAGCCCAAGACCCATCT



WI-7789	73 GA ---	---	TCTCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCACATCTTACAGAGACTCTCCC TGACG[G/A]TGGAAATTTAAGTTAGGGTCCCTAAAGCAATTTGACACACAGATGTTGAATGACTGAC CCAAAATGTAATGAAGCTAATGTAATGTGAGTGAAGCTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCCTCCTGGTGAAGTGGGGCTGTCTCAGACGACTAGCCACAGACCCATCT
WI-7790b	190 CT ---	---	AATTGTCAGTCACTCTTCAAACCTTACAGTCTTCCCTAAGGTACTCTTCATGAGATTCAATCCATT TACTAATACTGTAATTTTGGTGGACTAGGCTTGCCTATGTGCTTATGTAGCTTTTACTTTTATGG TGTGATTAAATGGTGATCAAGGTAGGAAAAGTTGTCTCTATTTCTTGAAGTCTC/TJTTCTATACTTT AAGATACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAAC
WI-7790	190 CT ---	---	AATTGTCAGTCACTCTTCAAACCTTACAGTCTTCCCTAAGGTACTCTTCATGAGATTCAATCCATT TACTAATACTGTAATTTTGGTGGACTAGGCTTGCCTATGTGCTTATGTAGCTTTTACTTTTATGG TGTGATTAAATGGTGATCAAGGTAGGAAAAGTTGTCTCTATTTCTTGAAGTCTC/TJTTCTATACTTT AAGATACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAAC
WI-7795b	81 CA ---	---	CAGATGTTCTGGTAAACTGATTGCTGGCAACACAGATTCTCTGGCTCATATTTCTTTCTTCAT CTTGATGATGATC/AJGTCATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTCTCT TAATAAGCCACATATAAATGATCTTTTCTCCAGAAAATTCCTTGAGGAAAATGTCCAAA TAAGATGAATCACTTAATACCGTATCTTCTAAATTTGAAATATAATCTG
WI-7795	81 CA ---	---	CAGATGTTCTGGTAAACTGATTGCTGGCAACACAGATTCTCTGGCTCATATTTCTTTCTTCAT CTTGATGATGATC/AJGTCATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTCTCT TAATAAGCCACATATAAATGATCTTTTCTCCAGAAAATTCCTTGAGGAAAATGTCCAAA TAAGATGAATCACTTAATACCGTATCTTCTAAATTTGAAATATAATCTG
WI-7814c	41 GA ---	---	TTCTCTCATTTTATCCCTCACTGTAGCATGCCAGTCCG[G/A]TTTCATTTAGTCATGTGACCACTC TGCTTGTTGTTCCACAGCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTAGGATAAAAATATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGTATATTTTAAAGAAATAACAGAA
WI-7814b	41 GA ---	---	TTCTCTCATTTTATCCCTCACTGTAGCATGCCAGTCCG[G/A]TTTCATTTAGTCATGTGACCACTC TGCTTGTTGTTCCACAGCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTAGGATAAAAATATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGTATATTTTAAAGAAATAACAGAA
WI-7814	28 GA ---	---	TTCTCTCATTTTATCCCTCACTGTAGCATGCCAGTCCG[G/A]CATGCCAGTCCGTTTCATTTAGTCATGTGACCACTC TGCTTGTTGTTCCACAGCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTAGGATAAAAATATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGTATATTTTAAAGAAATAACAGAA

WI-7830d	150	C T	---			GCAGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGGATAGGGGGCAAATCTTTCCCTTTCTGTAAATAGTCATCACATTTCTATGCCAAACAGGAACG ATCCATAACTTTAGTC[CT]TAATGTACACATTCGCAATTTGATAAAATTAATTTGTGTTTCCCTTG AGGTTGATCGTTGTGTTGTTGCTGCACATTTTACTTTTTGCGTGIGGA
WI-7830c	54	GA	---			GCAGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGATGGATAGGGGGCAAATCTTTCCCTTTCTGTAAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTCGCAATTTGATAAAATTAATTTGTGTTTCCCTTG AGGTTGATCGTTGTGTTGTTGCTGCACATTTTACTTTTTGCGTGIGGA
WI-7830b	134	GA	---			GCAGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGGATAGGGGGCAAATCTTTCCCTTTCTGTAAATAGTCATCACATTTCTATGCCAAACAGGAAC[ G/A]ATCCATAACTTTAGTCTTAATGTACACATTCGCAATTTGATAAAATTAATTTGTGTTTCCCTTG AGGTTGATCGTTGTGTTGTTGCTGCACATTTTACTTTTTGCGTGIGGA
WI-7830	44	A G	---			GCAGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGATGGATAGGGGGCAAATCTTTCCCTTTCTGTAAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTCGCAATTTGATAAAATTAATTTGTGTTTCCCTTG AGGTTGATCGTTGTGTTGTTGCTGCACATTTTACTTTTTGCGTGIGGA
WI-7865e	25	C T	---			CCACTTCCTATCTGATTTTCCAG[CT]AAATGAGCGAGGCAATTTCTAGTCTCCACAAAACATCTA GCCATCTAAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGG GGTATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865d	191	C T	---			CCACTTCCTATCTGATTTTCCAGCAAATGAGCGAGGCAATTTCTAGTCTCCACAAAACATCTAGCC ATCTAAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGGGT ATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTA[CT]GAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865c	25	C T	---			CCACTTCCTATCTGATTTTCCAG[CT]AAATGAGCGAGGCAATTTCTAGTCTCCACAAAACATCTA GCCATCTAAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGG GGTATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865b	191	C T	---			CCACTTCCTATCTGATTTTCCAGCAAATGAGCGAGGCAATTTCTAGTCTCCACAAAACATCTAGCC ATCTAAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGGGT ATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTA[CT]GAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTACCCAGTAAACCCAAA

WI-7865	25 C T	---	---	CCACTTCTATCTGATTTTCCAG[C/T]AAATGAGGAGGCAATCTAGTCTTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGG GGTATGCTACTCATAAGATTTCAAGGTGCTTCCAACCTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865	191 C T	---	---	CCACTTCTATCTGATTTTCCAGCAAAATGAGGAGGCAATCTAGTCTTCCACAAAACATCTAGCC ATCTAAATGGAGAGATGAATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGGGT ATGCTACTCATAAGATTTCAAGGTGCTTCCAACCTGAAATCTCAATGTTCTCAGTA[C/T]GAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7867c	92 A C	---	---	TTCAACACCTGCTTCCACCTCCACCATCTGTGCAATCACTTCACCTTCAGCCTACTAGTCCOC CTAACAATTACCCTGTCAAGAGG[C/G]AGTGCAGCTCAGGTGGATTAAATGTGGTTTAAATATGGC CTGTTGAGTTTAAATGTTTAAATGTTTCTTTAAGTAACCATTTCTGTTCTTCTATAAATCTATGT CTATATGCTATGCTTAAATTTGGATGATGAGGCAACTTTGGATTAAAGG
WI-7867b	92 A C	---	---	TTCAACACCTGCTTCCACCTCCACCATCTGTGCAATCACTTCACCTTCAGCCTACTAGTCCOC CTAACAATTACCCTGTCAAGAGG[C/G]AGTGCAGCTCAGGTGGATTAAATGTGGTTTAAATATGGC CTGTTGAGTTTAAATGTTTAAATGTTTCTTTAAGTAACCATTTCTGTTCTTCTATAAATCTATGT CTATATGCTATGCTTAAATTTGGATGATGAGGCAACTTTGGATTAAAGG
WI-7868c	173 C T	---	---	TTGATCGATCTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGGCTTT CACCCAACTGCTCCCTCTGATCCTCCATCAGGCGCAGATCTCCACGTCTCCATCTCAGTACACAAT CATTTAATTTCCCTGCTTACCCCTATTCAAGCA[C/T]TAGAGGCCAGAAAAATGGGCAAAATTAT CACTAACAGGCTTTGACTCAGGTTCCAGTAGTTCAATCTAATGCCTAGAT
WI-7868b	173 C T	---	---	TTGATCGATCTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGGCTTT CACCCAACTGCTCCCTCTGATCCTCCATCAGGCGCAGATCTCCACGTCTCCATCTCAGTACACAAT CATTTAATTTCCCTGCTTACCCCTATTCAAGCA[C/T]TAGAGGCCAGAAAAATGGGCAAAATTAT CACTAACAGGCTTTGACTCAGGTTCCAGTAGTTCAATCTAATGCCTAGAT
WI-7868	66 T C	---	---	TTGATCGATCTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGGCTTT /C/TCAACCAACTGCTCCCTCTGATCCTCCATCAGGCGCAGATCTCCACGTCTCCATCTCAGTACAC AATCATTTAATATTCCCTGCTTACCCCTATTCAAGCAACTAGAGCCAGAAAAATGGGCAAAATTAT CACTAACAGGCTTTGACTCAGGTTCCAGTAGTTCAATCTAATGCCTAGAT
WI-7870b	85 T C	---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAGAAAGCACTATTAACTCTGCAGTGATTAGAAGGG GTGGGTGGCGGGAATCC[C/T]ATTATCAGACTCTGTAATTGAATATAAATGTTTACTCAGAGGA GCTGCAATGGCTGCAAAAAATGAAATCCAATGAGCACTAGATATTAAAAACATCATTTACTGCCAT CTTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTG

WI-7870	76 C T	---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCAGCACTAATTAATCTCTGCAGTGATTAGAAGGG GTGGGTGG[C/T]GGGAATCCTATTTATCAGACTCTGTAATGAAATATAATGTTTACTCAGAGGAG CTGCAAAATTGCCTGCAAAAATGAAATCCAATGAGCACTAGAAATATTTAAACATCATTAATGCCCATC TTTATCATGAAGCAGACATCAATTACAAGCTGTAGACCACCTAATATCAATTTG
WI-7889c	54 C	---	---	TTAGGTCATCGCCACTCCCCAGGAGCAGCTGGCACTGACAGCTGGGGGGCGCTCTCCCCCTG CAGCCGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACTACAGGACTGGGCCGGCCAGGGCCTCT GGCTCCCTGCCCAATCCTCCCTGGAGAAAGGACATGGGAATGAATTGAAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCCTCCAAGGCTGTCTTCTCCAGAGACACAAGAAG
WI-7889b	54 C	---	---	TTAGGTCATCGCCACTCCCCAGGAGCAGCTGGCACTGACAGCTGGGGGGCGCTCTCCCCCTG CAGCCGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACTACAGGACTGGGCCGGCCAGGGCCTCT GGCTCCCTGCCCAATCCTCCCTGGAGAAAGGACATGGGAATGAATTGAAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCCTCCAAGGCTGTCTTCTCCAGAGACACAAGAAG
WI-7894c	142 A G	---	---	AGCCACCCCAATATAACTGTTATCCAGAAGCTGTTATGTCCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGTCCTATGTTTGTGAATTTATATTTGCGTATAC ATTATC[A/G]ATGTAAATTTGCATTTTTTATTGAAAATTATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTAACCGCTATAGATATCCATA
WI-7894b	142 A G	---	---	AGCCACCCCAATATAACTGTTATCCAGAAGCTGTTATGTCCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGTCCTATGTTTGTGAATTTATATTTGCGTATAC ATTATC[A/G]ATGTAAATTTGCATTTTTTATTGAAAATTATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTAACCGCTATAGATATCCATA
WI-7900e	84 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAACAGTGATTAAAGTTGATCAAGCCATGGTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACTCAACTATAGAAAGACATTAAAGAAATC
WI-7900d	128 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAACAGTGATTAAAGTTGATCAAGCCATGGTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACTCAACTATAGAAAGACATTAAAGAAATC
WI-7900e	84 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAACAGTGATTAAAGTTGATCAAGCCATGGTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACTCAACTATAGAAAGACATTAAAGAAATC

WI-7900d	128 C T ---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAACACAGTGATTAAGTTTGATCAAGCCATGGTGA/C/TAACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900e	84 C T ---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG/C/TCCTGCCATTGAACACAGTGATTAAGTTTGATCAAGCCATGGTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900d	128 C T ---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAACACAGTGATTAAGTTTGATCAAGCCATGGTGA/C/TAACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900c	84 C T ---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG/C/TCCTGCCATTGAACACAGTGATTAAGTTTGATCAAGCCATGGTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900b	128 C T ---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAACACAGTGATTAAGTTTGATCAAGCCATGGTGA/C/TAACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900	84 C T ---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG/C/TCCTGCCATTGAACACAGTGATTAAGTTTGATCAAGCCATGGTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7901c	33 C T ---			AGACTTAGGTACAATTGCTCCCTTTTATATA/C/TAAGACACACACAGGACACATATATTAACAG ATTGTTTCATCATTTGCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAACATGGTAAGAC CCCTTTTAAACAACTCCAGGCCCTGGTGGCGGCTGGTGGTATTTGGGGCAGCGCCGCGTGGTGGT CACTCAGTCGCTCTGCATGCTCTGTCTATACAGACAGGTAACCTAGTCT
WI-7901b	33 C T ---			AGACTTAGGTACAATTGCTCCCTTTTATATA/C/TAAGACACACACAGGACACATATATTAACAG ATTGTTTCATCATTTGCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAACATGGTAAGAC CCCTTTTAAACAACTCCAGGCCCTGGTGGCGGCTGGTGGTATTTGGGGCAGCGCCGCGTGGTGGT CACTCAGTCGCTCTGCATGCTCTGTCTATACAGACAGGTAACCTAGTCT

WI-7901	33 C T	---	---	AGACTTAGGTACAATTGCTCCCTTTTATATA[C/T]AGACACACAGGACACATATATTAACAG ATTGTTTCATCATTCATCTATTTCCATATAGTCATCAAGAGACCATTTTTATAAAACATGGTAAGAC CCTTTTAAACAAACTCCAGGCCCTTGGTTGCGGGTCGCTGGTTATTGGGCGAGCGCGGTGGTCGT CACTAGTCGCTGTCATGCTCTCTGTACATACAGACAGGTAACCTAGTTCT
WI-7901	271 T G	---	---	AGACTTAGGTACAATTGCTCCCTTTTATATACAGACACACAGGACACATATATTAACAGATT GTTTCATCATTCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAAACATGGTAAGACCCT TTTTAAACAAACTCCAGGCCCTTGGTTGCGGGTCGCTGGTTATTGGGCGAGCGCGGTGGTCGTAC TCAGTCGCTGTCATGCTCTCTGTACATACAGACAGGTAACCTAGTTCTGTGT
WI-7926c	150 C A	---	---	CATCCGCATCTGTCAACCCAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAGATGATGCACCT TTGGAGATCAGAAAATTCATATTTAAGCAAAGTGATACAAACACAGTGATTTGGGAATGCCCTTCATT TACAATGCAATACCTT[C/A]ATTTTAATACTCTTGAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAAATTACACTGTGGGAA
WI-7926b	28 A T	---	---	CATCCGCATCTGTCAACCCAGGACAGAA[A/T]GCATGGACAAGGGATGAGCTTTACAAAGATGATGC ACTTTGGAGATCAGAAAATTCATATTTAAGCAAAGTGATACAAACACAGTGATTTGGGAATGCCCTTC ATTTACAATGCAATACCTTACATTTTAATACTCTTGAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAAATTACACTGTGGGAA
WI-7926	150 C A	---	---	CATCCGCATCTGTCAACCCAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAGATGATGCACCT TTGGAGATCAGAAAATTCATATTTAAGCAAAGTGATACAAACACAGTGATTTGGGAATGCCCTTCATT TACAATGCAATACCTT[C/A]ATTTTAATACTCTTGAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAAATTACACTGTGGGAA
WI-7947b	203 G T	---	---	AAGAGCCAGCAGGTCAAAAGGCCAACACAAACCATTAAGCAGCCACACAGCCACAGGCCAGGTCCTGT GCTATCACAGGTCACCTCTTTACAGTTAGAAACACACAGCCAGGCCACAGAAATCCCATCCCTTCC TGAGTCATGGCTCAAAAATCAGGGCCACCATTGTCTCAATTCAAATCCATAGATTTCCGAAGCCACA GA[G/T]TCTCTCCCTGGAGCAGCAGACTATGGCAGCCCGAGTCTGCCACCTG
WI-7947	203 G T	---	---	AAGAGCCAGCAGGTCAAAAGGCCAACACAAACCATTAAGCAGCCACACAGCCACAGGCCAGGTCCTGT GCTATCACAGGTCACCTCTTTACAGTTAGAAACACACAGCCAGGCCACAGAAATCCCATCCCTTCC TGAGTCATGGCTCAAAAATCAGGGCCACCATTGTCTCAATTCAAATCCATAGATTTCCGAAGCCACA GA[G/T]TCTCTCCCTGGAGCAGCAGACTATGGCAGCCCGAGTCTGCCACCTG
WI-7963b	145 T C	---	---	CATGTGCTGCATGAAGAGCTAATTTAAAAAGCAAAGTAAGACTAATTTATTTAAAAATAAAATGCC ACAAATTTCAATTTCTCCTCTAAGTATTACAATGGAGTTTATCTCGCTCAAAAGTGGAAGAAAT TGAGTGAATGA[T/C]AATTTTGTAATTTAGGATAAGATCCAAGTATTTTCCCCAACTCTTGTTTCCC CCATAAAGTTAGGCATGAGGAGGAGCAGCTCAATTAAGGCGAGAAGACGCGGAAA

[illegible]

WI-8021b	57	C T ---	---	ACAACTCAGAGGACTGTGCAAGTCAATGAGTCGGCTTGTAATTCTCATCTGGAAC[CT]GATCCC ACGCTTAGAACCTTCAACACAGGAGTTTCTTGAGTAGTCTCAAAGTCTTGGTAGGCATTGGA ACTGGTCTTTACATTTGAGATTTCTTTTGGCCCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTTTAGGGGTGATTCGAATTCGGTGAATTGCCA
WI-8021	57	C T ---	---	ACAACTCAGAGGACTGTGCAAGTCAATGAGTCGGCTTGTAATTCTCATCTGGAAC[CT]GATCCC ACGCTTAGAACCTTCAACACAGGAGTTTCTTGAGTAGTCTCAAAGTCTTGGTAGGCATTGGA ACTGGTCTTTACATTTGAGATTTCTTTTGGCCCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTTTAGGGGTGATTCGAATTCGGTGAATTGCCA
WI-8024c	206	A G ---	---	CTGAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTTCCACAGACACAGTCAATGTCAGTCA GCTTGATTCAGGAGGACAGGGCAGAGGGATCCCAAGTGGCACTTCCCATGGGAAGACAGAAGAGAGT GGCCCCAGAGATGGAAGGACCCCAAGTGTATCATCAACCAACACCATTTAGCCGCTTAGCCTCTAA TTCC[AG]CTCTAGAACAGCTGGCCCTGGTCTGTCAGTACACAAAGGAAGAGC
WI-8024b	206	A G ---	---	CTGAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTTCCACAGACACAGTCAATGTCAGTCA GCTTGATTCAGGAGGACAGGGCAGAGGGATCCCAAGTGGCACTTCCCATGGGAAGACAGAAGAGAGT GGCCCCAGAGATGGAAGGACCCCAAGTGTATCATCAACCAACACCATTTAGCCGCTTAGCCTCTAA TTCC[AG]CTCTAGAACAGCTGGCCCTGGTCTGTCAGTACACAAAGGAAGAGC
WI-8077	167	A G ---	---	GAATGAGCCTTCTAGCGCCGAGGGACCTGCTGCTGTTGGCCTGCACATGCATCTATGGAATGC TTTTTGCCAAAGCGGGGCACTGAGGACTAAGCTCTGANNNNNNNNATCTGCCCAAACTCTTTCT AAGGAGTCTGGGTGTCATGCCCTACAAAC[AG]TAAATTCATCAGATGGATTTTATTAAACGTT GTGTATTGTGACTTACTTTCCAACTCTGACTCTGGCATAACAAGGGAAAAA
WI-8118f	114	G C ---	---	TCTAGGTTTAAATCAAGCAATTTGCANTTTGGATTTTGGAAATGACCCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACCTGGCAATACAGAATGAGCTTGT[GC]TTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCTCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118e	40	A G ---	---	TCTAGGTTTAAATCAAGCAATTTGCANTTTGGATTTTGGAAATGACCCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACCTGGCAATACAGAATGAGCTTGT[GC]TTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCTCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118d	118	T G ---	---	TCTAGGTTTAAATCAAGCAATTTGCANTTTGGATTTTGGAAATGACCCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACCTGGCAATACAGAATGAGCTTGT[GC]TTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCTCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA



WI-8118c	44 C T ---	---	TCTAGTTTAATCAAAGCAATTGTCANTTTGGATTTTGGAAATGA[C]TCACTCCCTTCTAAGGAAGC TATGTACTTCATGCTGTGGAACCTGGCAATACAGAATGTAGCTGTGTTGTTTCTTAGCCTTGAAGA TGACAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCCCT AAAAATCAGACTCATTGTGACAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118b	88 T C ---	---	TCTAGGTTTAATCAAAGCAATTGTCANTTTGGATTTTGGAAATGACCCTCCCTTGTAAAGGAAGCTAT GTACTTCATGCTGTGGAAC[C]TGGCAATACAGAATGTAGCTGTGTTGTTTCTTAGCCTTGAAGA TGACAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCCCT AAAAATCAGACTCATTGTGACAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8171d	299 C T ---	---	TTTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGCATACAAATGGCAGCGGCTCGGGAAG AGGGTAGGAGACCGAGCAGCATTTCTGTAGAGGAAGACAGAAAGGAGACCCCTTTGGCACACA TTTATGGAGGTTGTCCCTGAAGAGAAGGGCAGGTGGGAGAGGTTCCCTGTACTTAAGAGAAGGC ACCAGTGGGCAAGAGCACAAATGAAGAGGATGATATAAAACAATCACGGCA
WI-8171c	46 A G ---	---	TTTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGCATACAA[C]GTGGCAGCAGGCGCTCGGG AAGAGGGTAGGAGACCGAGCAGCATTTCTGTAGAGGAAGACAGAAAGGAGACCCCTTTGGCAC ACATTTATGGAGGTTGTCCCTGAAGAGAAGGGCAGGTGGGAGAGGTTCCCTGTACTTAAGAGAA GGCACCAGTGGGCAAGAGCACAAATGAAGAGGATGATATAAAACAATCAC
WI-8171a	46 A G ---	---	TTTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGCATACAA[C]GTGGCAGCAGGCGCTCGGG AAGAGGGTAGGAGACCGAGCAGCATTTCTGTAGAGGAAGACAGAAAGGAGACCCCTTTGGCAC ACATTTATGGAGGTTGTCCCTGAAGAGAAGGGCAGGTGGGAGAGGTTCCCTGTACTTAAGAGAA GGCACCAGTGGGCAAGAGCACAAATGAAGAGGATGATATAAAACAATCAC
WI-8171b	298 T C ---	---	TTTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGCATACAAATGGCAGCAGGCGCTCGGGAAG AGGGTAGGAGACCGAGCAGCATTTCTGTAGAGGAAGACAGAAAGGAGACCCCTTTGGCACACA TTTATGGAGGTTGTCCCTGAAGAGAAGGGCAGGTGGGAGAGGTTCCCTGTACTTAAGAGAAGGC ACCAGTGGGCAAGAGCACAAATGAAGAGGATGATATAAAACAATCACGGCA
WI-8314b	85 G C ---	---	GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTCGAATTGAGCACATTTCTTGGGTCTGT TTCTCTATCTTAAGGG[G/C]AGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTCTCTGTAGTCTTATGATGATCTAGAAGAGCAGCTGTCCAATAGAACTTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATTAGGGGTAAACCACT
WI-8314	78 C G ---	---	GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTCGAATTGAGCACATTTCTTGGGTCTGT TTCTCTATCTTAAGGG[G/C]AGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTCTCTGTAGTCTTATGATGATCTAGAAGAGCAGCTGTCCAATAGAACTTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATTAGGGGTAAACCACT

WI-8321	178	G A ---	---	TTTTAAATATGCCCGTTAGAGCAGACACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGATATACCCAGGNAATCCATCTTGGTACTTTCAAGAGCTGCTGTTACTAGTCTCTGAGAAAG TCCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTGAGAAATG/AJAGTATCTAGTATCTTCTTA TTTGGCTATGGTCTAGTTATCAACCTACTTTATTAGCTGAACGTGTGGC
WI-8321	178	G A ---	---	TTTTAAATATGCCCGTTAGAGCAGACACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGATATACCCAGGNAATCCATCTTGGTACTTTCAAGAGCTGCTGTTACTAGTCTCTGAGAAAG TCCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTGAGAAATG/AJAGTATCTAGTATCTTCTTA TTTGGCTATGGTCTAGTTATCAACCTACTTTATTAGCTGAACGTGTGGC
WI-8332b	123	A C ---	---	TATGTACTCACTTTCAGTTACCCCGTGCCTCCAGAAATCGCATGTGTCTCCACCTGGGGGGGATATA AATTACCTCTAGATTGTCCAAAGCCAGTCTTCCCTTCCCTGTGCG/AJGCTTAGAACTAAGTAG CAGTACTGTTGGTGTGTTTCTTCCCGAGCAATGCCTACTGCACTAGTACTAGTAAACAACCTAG AGGTGGAGGGTNTCCGGGGAAGCAGTTAGATGATGATTAAGTGTGATGCACA
WI-8332	114	A C ---	---	TATGTACTCACTTTCAGTTACCCCGTGCCTCCAGAAATCGCATGTGTCTCCACCTGGGGGGGATATA AATTACCTCTAGATTGTCCAAAGCCAGTCTTCCCTTCCCTGTGCG/AJGCTTAGAACTAAGTAG CAGTACTGTTGGTGTGTTTCTTCCCGAGCAATGCCTACTGCACTAGTACTAGTAAACAACCTAG AGGTGGAGGGTNTCCGGGGAAGCAGTTAGATGATGATTAAGTGTGATGCACA
WI-8378b	311	T C ---	---	TGCGGGCTTAACAGGAAGCATGACTGGAGGCTCAGGAAGCTTATAATCATGGCAGAGGCGAAGG GGAAGCAAGGACCTTCTTACATGGCAGCAGGAGAAAGAGAAAGGAGAGTGTACACACTTTT AAACAACCAAGATCTCATGAGANTTCCATCGGGAGACAGCACTAGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCAATCACTNTCAACAGGCCCTCCTCCAAACACGTGGGG
WI-8378	308	T C ---	---	TGCGGGCTTAACAGGAAGCATGACTGGAGGCTCAGGAAGCTTATAATCATGGCAGAGGCGAAGG GGAAGCAAGGACCTTCTTACATGGCAGCAGGAGAAAGAGAAAGGAGAGTGTACACACTTTT AAACAACCAAGATCTCATGAGANTTCCATCGGGAGACAGCACTAGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCAATCACTNTCAACAGGCCCTCCTCCAAACACGTGGGG
WI-8426	184	T G ---	---	TTTAGCACATATTAGCATTAAAGCCTCAAAGATACAGCAATATGTTACATTCTCTGTGAAAAACAG TTGTTGTAGACTGTTAANNNNNNNAATGTAACTCCGACTGTGCTTAATAGGATTTGACCNNTAA GAGGNTCTTTTGTGTGGGAGGGTGGCTTGTGCTTGAACCTCCATCTGT/GJGCTTGTAGCTGGTG AGGCTGGGAGTATGGANGNCGGGGCTTGGCNATGNATTCAGTGAG
WI-8450h	61	C A ---	---	TTGAGCCTCCACAAATATGCAACCAAGTTTACATTTTAAACAGCCCTCTACATACACTC/AJCA TCTCTCTATCTTAGTCCAAAGTTTAGTTTCAATCCCAATATACCAATTCATTGTTATTTAAGA AAAAACCTCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTAT

WI-8450g	55 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTCACACTCCAT CTTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTCAAT
WI-8450f	108 T A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATATACCAATTCATTTGTTATTC/TTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTCAAT
WI-8450e	125 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATATACCAATTCATTTGTTATTC/TTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTCAAT
WI-8450d	125 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATATACCAATTCATTTGTTATTC/TTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTCAAT
WI-8450c	108 T A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATATTC/TTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTCAAT
WI-8450b	61 C A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTTC/CAJCA TCTTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTCAAT
WI-8450a	55 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTC/CAJCA CTTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTCAAT
WI-8458b	60 A G ---			CAAGGAAAGCTGCAGTCTTCATAAACTTCAAGAGTTACAAAAATACGTATTTTAAJAGJCTA CAATTCAGATTAGCATCCAAACCTACAAACATGATGATACATTGTCACACACCATACAACTTCAC ACCTGGCTACAGCAATGTTGACTTACATCACCATGTTTACTTGTGAAAACTTTATTGTGCACAGT GACATCCATTCGCCAGACTTAATGTTTATAAAGCAGCTGAGCAGAGTTCTCA

WI-8461c	105	A T ---	---	CTTCTCTCCAAATCTACATGAATCTTGAAGACAATATAACTACAACCTTACAAATGCCAATT GACAAAGAGANTAAATGATATAATAATAAATCATTTTTT[A/J]NNNNNNNNCCTTGTCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAAACAACATTACAANTTNTTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAGAAAANTCAAGGATTTCGAAAAAGGGGG
WI-8461b	38	T C ---	---	CTTCTCTCCAAATCTACATGAATCTTGAAGACAAT[TC/J]ATAACTACAACCTTACAAATGCCAA TTAGACAAAGAGANTAAATGATATAATAATAATCATTTTTTNNNNNNNNCCTTGTCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAAACAACATTACAANTTNTTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAGAAAANTCAAGGATTTCGAAAAAGGGGG
WI-8461	38	T C ---	---	CTTCTCTCCAAATCTACATGAATCTTGAAGACAAT[TC/J]ATAACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAATAATAATCATTTTTT[A/J]NNNNNNNNCCTTGTCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAAACAACATTACAANTTNTTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAGAAAANTCAAGGATTTCGAAAAAGGGGG
WI-8461	105	A T ---	---	CTTCTCTCCAAATCTACATGAATCTTGAAGACAATATAACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAATAATAATCATTTTTT[A/J]NNNNNNNNCCTTGTCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAAACAACATTACAANTTNTTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAGAAAANTCAAGGATTTCGAAAAAGGGGG
WI-9438	77	A G ---	---	ACAGAAATGACCTTTATTTGTTGTACTAAAGCCTGTTTAACTTTTGATACAAAGTAACATTTTAGTA CAGAAATCCAGCTGTGACGTCAGTACCTGT[TC/J]TGTGCACACTGTACCATCTCAGTCCCACCT GCCTGTAACCTTAGAAAACAGCCCCCTACCCCCAGAGGCTGCGAGTTAATACCTTGAGAAATAGCTTA CAGTTTTTCATAGTTTGTCTGAGCTAGAAAACCTTGACCTGTAAACAAAAG
WI-9439b	101	C T ---	---	ACAGAAATGACCTTTATTTGTTGTACTAAAGCCTGTTTAACTTTTGATACAAAGTAACATTTTAGTA CAGAAATTC[TC/J]CCAGCTGTGACGTCAGTACCTGTCTGTGCACACTGTACCATCTCAGTCCCACCT GCCTGTAACCTTAGAAAACAGCCCCCTACCCCCAGAGGCTGCGAGTTAATACCTTGAGAAATAGCTTA CAGTTTTTCATAGTTTGTCTGAGCTAGAAAACCTTGACCTGTAAACAAAAG
WI-9439a	76	C T ---	---	GAAGGCTTGATTAAAGGAGGNTTTATTTGATGTNAACCTTACCATTCCATAGACTATAAAGANCATTA TAAAAAAAT[TC/J]CCTCTAAAGNGACACATGCCCCAAATGACCANGNCATAGGCAACCTTTTAAAT TACTCATCTTTCATATGTGTGTTTGTNCCCCTACTNTTATCACTGTGCTTCTGCTTGTCTACCTTA TGNGAACTGCACACTATCTGTGGCAATTGTT
WI-9446b	75	T C ---	---	

WI-9446	75	T C	---			GAAGGCTTGATTAAAGGGAGGNTTTATTTGATGTTNAACCTACCATCCATAGACTATAAGANCATTATA TAAAAAAT/C CCTCTAAAGNGACACATGCCCCAAATGACCANGNCATAGCAAGCCTTTTAAAT TACTCATCTTCATATGTGTGTTGTCNCCCTACTNNTATCACTGTGCTCTCTGCTCTTTGCTACCTA TGNGAACTGCACACTATCTGTGGCAATATGT
WI-9497b	185	A	---			ATTAAATGTCAAGGTTTCATGTTTACATTTCTTATATCAAGTACAATGGTATATATACATTTTTTT GAGATAATTATTCTAGATCCAGGCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTAAACAGTCTCCAAATTTNCTTAAATTAATCAAAGTATGTTAATGTCACTT GGAATCTACATGGAAGGCCAACAAAATAACTAAAACCTTGACTAATGAAG
WI-9497	185	A	---			ATTAAATGTCAAGGTTTCATGTTTACATTTCTTATATCAAGTACAATGGTATATATACATTTTTTT GAGATAATTATTCTAGATCCAGGCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTAAACAGTCTCCAAATTTNCTTAAATTAATCAAAGTATGTTAATGTCACTT GGAATCTACATGGAAGGCCAACAAAATAACTAAAACCTTGACTAATGAAG
WI-9523b	193	C A	---			GTGAAAAAGTTTCTATTCTATCCATCATACAATAGATTGTGCTAAGGATCATTTTGGAAAGATGTG CAGCATTGAGAAAGTTGTATCTCATGTCAGTCACTCAGCAGCATTTTATCTAAAGTACGTGCACA GACTCAGACAAATTACAACTATTTCCAGCCATGATCTATGGTGATTTCCACACATTTGTA/C A AGTG AAAGCTCTTCAGCTTGGAAACAACCTTGTCAGGCGAGACTGCATGCACATATAT
WI-9523a	47	G A	---			GTGAAAAAGTTTCTATTCTATCCATCATACAATAGATTGTGCTAAGGATCATTTTGGAAAGAT GTGCAGCATTCAGAAAGTTGTATCTCATGTCAGTCACTCAGCAGCATTTTATCTAAAGTACGTGCA CAGACTCAGACAAATTACAACTATTTCCAGCCATGATCTATGGTGATTTCCACACATTTGTACAGTGA AAGCTCTTCAGCTTGGAAACAACCTTGTCAGGCGAGACTGCATGCACATATAT
WI-9554	202	T C	---			AAAAACACAAGTTTCTATACATCACAAAAACCTTCCATTATACACAGAAGTGATTATTACCAGAC AAGCATCAGTGATGATACCTGCTTCTTACTGTTTGTATTTGATACATGCTGTAGATAATGCAGCCCATG CAATACACCCCAAGAACACTAGAGTCTCTACACCCCAAGTACAATATGATAAAGCAGCCCTCTGCAAGTG GTT/C G GCTGGATACCCTAAGAAAGTCTACTGCAGCCATGTTGGTTATGATTTT
WI-9555	97	G A	---			CCAAAAAGCCAAACCATTCATATGTTGATTTTCATAAAACATTTATTTGATCCTTTTTTGAGGTAAGTAT AAATACCTTTTACATGGCTAACCTTCTAACG G A CTTGAAAAATCAATTTCAAGGACTCTTTAATCA GTTAAATAATCTGCTTTAGAAGGCGACAAATGATCATACTTCAGATTAAAAATACAGGTAAGTATTCAG GGNTAAAAATGGTACAAAAAGGCTGAACCTTTTNTCTTCACATTGATCACA
WI-9625b	172	A T	---			TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAAATAGCTACCATAATTTGTATCTNCTCTCTGGGAAAAACCTTTGGAAAAAACAACACGCACA TAAGTATCATAACTGAGGGTTGTGGACAAGTTACTTCT A T GTTTACCAATTTTATATTGACATAA AGTAGCAGACTAGTTATTTTCATTTAAAAAACAACACTGACAAATCTTTTC

WI-9625	172 A T ---	---	---	TTGAACATTTAATGAATGACAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAACAATAGCTACCATATTTGTATCTNCTCCTGGGAAAAACCTTGGAAAAAACAACACGCACA TAAGTATCATAACTAGGGTTGTGGACAAGTTACTTCTATGTGTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCAATTAATAAAAAACACACTGACAAATCTTTTC
WI-9647	144 C T ---	---	---	TTTTCTGAGATTCAAAGAGCTACATTTTGGTAGTGATGTCTACTATACCTTTTTCATCCTTTCA ACATCTTTTGTACATTTTAGGTGATGCTCTGTAAACAGTGATGCTAGACCTAAAAATCCAAAGCT TACAACTC/TGTCTTTACCTGATACATTTATCCATTTACTTTCATTTGGATTTTAAAAATGTTA ACTTAATACGTCTCTTCAGATGTCCTGCTTTTAGTTAATTGTTT
WI-9676n	114 A G ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCA/GATGTGGCTTTCCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676m	184 G T ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGC/G/TTCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676l	84 A C ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676k	202 C T ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA C/TTCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676j	92 C T ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676i	173 T C ---	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTTCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT

WI-9676h	134	C A	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCTGCCCC[ C/A]ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGCGCATGAAATAACTTG AGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676g	202	C T	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCTGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGCGCATGAAATAACTTGAGG[ C/T]CAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676f	184	G T	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCTGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGCG[ G/T]CATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676e	173	T C	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCTGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTT[C]CCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676d	134	C A	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCTGCCCC[ C/A]ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGCGCATGAAATAACTTG AGGCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676c	114	A G	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCA[ A/G]GATGTGGCTTTCTCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676b	92	C T	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676a	84	A C	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCCATATGGCAAAGATGAAGAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT

WI-9738b	40	C A ---	---	TGGACCAACACAGACAGATGATTCCTGGTGCCTGTGTA[C/A]ATTACAACATCATGTGATCAGATGC AGCAACATCAACATCTCAAGGAGTCCATTTGTTCAAAACACAGATAAGTACTCCACATTTTCCCTTT GAGTCAACAAAGACTCTGCTTGTCACCTTGCCTGGAGCGGGTGGTTTTCACATGTGAGTATCTA TCTTTTATTCTGTCCCTTATGTTGGTGGCCACATGCTGTGATTGCTGTC
WI-9738	40	C A ---	---	TGGACCAACACACAGACAGATGATTCCTGGTGCCTGTGTA[C/A]ATTACAACATCATGTGATCAGATGC AGCAACATCAACATCTCAAGGAGTCCATTTGTTCAAAACACAGATAAGTACTCCACATTTTCCCTTT GAGTCAACAAAGACTCTGCTTGTCACCTTGCCTGGAGCGGGTGGTTTTCACATGTGAGTATCTA TCTTTTATTCTGTCCCTTATGTTGGTGGCCACATGCTGTGATTGCTGTC
WI-9756	47	A -- ---	---	ACTGAAATGTAAATGGCCAAAGGCCACCCAGGACCTTAAATCATAGAAGTTAATCTGTGGGAAAA GAGTAACATCAAAAGCATCTAAACAAGAGCAGGATGTGATGTAATGTGTCCTTATCATTAGTC AGTAAAGATAAGAAAGCCCTGGTGAGTATCCACTCCACAACACACAGATATACACACTTTTGGGAG ATTCCACTTAACCACCTTGATTCTTCACCTTTTAAIGATTAAACATCTCCGTGG
WI-9758	135	A G ---	---	GATGGTCCCTTAAGGATTTGCATTGGTTAATGGGCAGACTGGTGCAAAAGAGGCTGAATTGAATAAT TAGGAACTGGGAGAAATCAATTCAAGGAAGAAATCTTGTTCGCAAGGTCAATTTTATACATTTA A[G]TAAATAACTCTGGTAGGTTCTATAGCAAAATGCTAAGTAAAGTAACCGCTGGTTTCTAAAT ATTACG
WI-9778	127	G A ---	---	ATTAAATCCAGGCAGCGGGGAAAATGGATACCTTTCATATGCTCTGTACCCAACTATAAATTTTG GTTCTCATGCACCATTTTCATTTTGCCTTCTCACTCCAAAGTACCAGTATTTACCAATTTG[A]CTCTC ATAATTGACTTTGCTACTGGAAGAACTCTTAGAATGTTGGAATTTCTATTACACACTTTGCTCA AAGATGTGTCAGTCAGGACTAAAGGCAATAGTCTCAGGGCAGACAGCC
WI-9832	116	C A ---	---	TCTCCCTTTGCCTCCTCATGCCACTCCCTCAGCCCTGCACAGAGCGTTTCTCCAGTGTAGTCTCTGGT CCATCTGCATCAAAATCACCTGCAGGACTTTGCTGACAATGCAGTTT[C]A/JTGGATCCCACCCAGGA CTCAAAAACCTAGGAATTGGGAGAAAGAGGACCTGGAATCGGTGTTGCTAGCAAGCCCCCAGGTGG TTTGTAAAGTGGACTAAAGTTGAGGACCAGACATGGAAGGTTGGCTTTGGC
WI-9841	101	A G ---	---	TGGAAAAATAGCTTTTATCAATCTCTGATATGCTACATATGTCATGGAGAAATGCAGAATGGCATGA TATGAAATTCATTTTGAATGAATAAAATATAC[A/G]TGTGTATGTATATATATCTATTAAACACTT AGGATTATACACACAATAAACCGTCTGTAAAGATAAACTAAGGTTCTATCAGTGGGAAATGAGA TTGAAAAGAGGGGGATGTTACTTGATATGCTGTG
WI-9880c	222	G A ---	---	GAACTAACACCTTTCTGCATGGATTTTCTTGATTATTGGCAGTTAACAATAAAATGTTATTAGATC ACTGGTCTTCTGTGTGGGTTGAGTTTTTATGATACTCTCTGTAGACCCATAAGGGAGGCTGTGA GTTGTTTCTACATCCTTGGACTATATAAGATCCTCTTTTAAATATATTTTATAAGCACATGAA AATGGAATGAAATAATGA[G/A]TTGACATAGGAATTACCTACATATTTTG



WI-9880b	157 C A ---	---	---	GAACTAACACCTTTCTGCATGGATTTTCTTGATTATGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTCTTCTGTGTGGGTTGAGTTTATGATATCTCTCTGTAGACCCATAAGGGAGGCTGTGA GTTGTTTCTACATCCTTGGAC/A/TATATAAGATCCTCTTTAAATATATTTTATATAAGCACAT GAAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-9880a	108 C T ---	---	---	GAACTAACACCTTTCTGCATGGATTTTCTTGATTATGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTCTTCTGTGTGGGTTGAGTTTATGATATCTCTGTAGACCCATAAGGGAGGCTG TGAGTTGTTTCTACATCCTTGGACTATATAAGATCCTCTTTAAATATATTTTATATAAGCACAT GAAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-10183	127 C T ---	---	---	ACACTGCAGGCACCTCCAAATCTNACAGACATATGCACCTCGGAATCAACTCAGGCATGCACAGCAT CCCTGTGCTGGAGTTTATTTAAACAAACGCCCCAGTTATCAGAGTTCTNTTTTGTCT/CACCC ATTTCCATAACAAAAGAGCTACACAAAATNNGGGGGAGANACTCTCTTTGGAGACTGCACACATT TGCAGAGGGGTGATGAATAATGATTCCAAA
FB25G10b	109 A G ---	---	---	TCCCTCAATGACAGATGAACATAATTTCTCTTGGGTAGAAATACTTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAATGGAA/A/GTGTATTTAGATCCTCCCCCAG TGACAAAGTAACTGAACCTGACCATAATTTATACATAAAATGGAATGTAAGAACCTATTTTGGATATCC CGGAC
FB25G10	109 A G ---	---	---	TCCCTCAATGACAGATGAACATAATTTCTCTTGGGTAGAAATACTTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAATGGAA/A/GTGTATTTAGATCCTCCCCCAG TGACAAAGTAACTGAACCTGACCATAATTTATACATAAAATGGAATGTAAGAACCTATTTTGGATATCC CGGAC
IB3071	102 C A ---	---	---	ACAAAGCTGAACTTCCATAACAGTCAATGGTACAGTCAACATCACATGTACAGAACACACAAATTTA GATGAACCTGAAATTAAGNTAAATAAAATAAAATC/A/CAATTTAGNAACAAATAAATCAAAAC ATTAAGGNTCCCTGNNATATTTCTTAAACCCTAATGAGATTTCACTGNNCTCAAGTCATTTTGTAGTGA GGCATTACAAATATGACCCTATTAAACCAGTCTAGGGATTCTG
NIB551	161 C T ---	---	---	CGTCTTTCTTTTGTAGATTGCAATTAAGTAGATAATATGAGAGAGAACTGACAAATGGGTTGTCCC TACTGAGCTTGGGCCAGGTGTACTTAGGAACCCCAATCCCACCCAGAGAGACTCATCTATGTTA ACACTAAGGATGCCCTGGAGGAGGTCT/TTTGACCACATACATCGGCCCATTTGGTTGATTTCAGCTTT GCAAGCAGCGTAGTGAGAAACCAAAAGCTTGTC
S72904	51 G T ---	---	---	AGCATAGAAAGTGATTATATTTTAAATGGTTTCAAGTGAAGTCCCTTTG/TTAATTTGTCAGTTT ATTCTGGAAATCTTTTGAAGTTAAATAAGGATCCTAGAGACGACCTCGAACTACAGGCCCTAAA GAGAAATTCCTCAACCCACAAGTGTGTAACCTCTCCCTTTCTGTCAATTTGGTTGCTTTAAATA TTGCAAAAGTCCTGATGCTAAACAGTATTTGGAGTGTCTTTCAGTGTCTGTA

UTR-00481	115	CT	---	---	TATTCTTTTATCCTGGGGCCACAGTCTTGATTATTCCTCTTGTTAAAGACTGAATTTGTAAACC CATTGATAAATGGCAGTACTTTAGGACACACACAAACACACAGAC/CTJACACCTTTTGATATGTA AGCTTGACCTAAAGTCAAAGGGACCTGTGTAGCATTTACAGATTGAGC
ESTC1	33	---	---	---	CCCTGTAGCAGTCTTCAGCCTCCTCTACCCCTACNAGATCTGGAGCAACAGCTAGGAAA
ESTC102	37	---	---	---	GCTACTACCACGGCTGCTTCGTTTGGACAAAAATAACNAGGAGGCATCCACGGGATTAGTTA
ESTC103	21	---	---	---	GCCATCAAAATTTCCCTTCACANTCAATACTGTGGAACAACAAGATAACACATCTTCTTGCTCATCCC ACTTGAA
ESTC107	20	---	---	---	TGCTGGCTCACTTCCCTCACANGCTGTATTACCTTTCAGAGCTGAGTGAGGCTGTGCT
ESTC109	35	---	---	---	AAAACAGGAAGCCCTGCCCGCAGAGGCACATGNACAGGGCAGTGCACAGTGACC
ESTC110	23	---	---	---	AAACCTCACACAGAAAAAGAGGANAACACTCAGAAATGTGATTACAGATTAGGCA
ESTC113	37	---	---	---	AAGGGACACAGTGTGCTGACAAGGTGACACTGAACANAACAGTTTCCTTTAATTGTTAAAGCGGG CATCG
ESTC117	24	---	---	---	AATTGGCTTCTCCACATGATACNTAAGTTCAAGGTCCAAAGTTCCCTATCACAAATTTACAAAAAGC CTCCA
ESTC119	24	---	---	---	TGTCAAGCAGATCTTGAGGGTTATNGTTAAGCCTGATAACACGCCCTCTTT
ESTC122	34	---	---	---	GACAAATAACACAGCTAAGCTACTGACATAAAATATNCAATAAATTTATGAGATATAAGGTACAGATG AGAAAAATCTGAAA
ESTC123	21	---	---	---	GAAGCCAGTATGTTGTGGCAANATTCGAGAAAAACACACTGAAAAA
ESTC128	42	---	---	---	GCAGAGGCATCAGATAAGGCCTCAGAAAGCCCGGCCCATCATNTCCATGGGACCAGGCTGGCTCAA TGTGGAACCTGG
ESTC129	20	---	---	---	AGTCACCATGCCAGCCTAGNATGAGTTTAGTAAGATTGGTTAIGCTGGGGAG
ESTC13	46	---	---	---	GTGTATCTGGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAGNAGCAGGTGCCGAGGGTCTGGA TCAGAAAA
ESTC130	49	---	---	---	GCCTGCTCACAAGGTAGACAAAAACATAAAATCTTCAGGAAAAATGAAACANGAGAAGCTGAAACAAT CTACACCTGAATG

ESTC132	30	---	---	---	GGTAAAGTCTAAATTACTGCCTTAGCAAAACNCATGTTGTCAGGTTTTTCTGCTGCA
ESTC137	21	---	---	---	CCAGTTGGCTCTGTCCTCANAGTCTCTCTCCATGIGGCAACA
ESTC139	45	---	---	---	AGGAGCACAGCCTAAGGACATGAAGTCAGAGTTCTCAGAGAGNGGGCTGGTCCCTGAGCTAG GAGGAGG
ESTC14	20	---	---	---	CCCATTGTGGTCACAGGAAGNAGAGGAGGCCACGTTCTTACTAGTTCCCTTGCATGGTTAGAAAGC TTGCCCCTGGTG
ESTC142	72	---	---	---	CCTAGGCTCATAACAATACAGTCTCAATACAAAAGACGTAATAATCTATTTTATTCATTTTAAATC AAAGANACCATTCACATTCCTAACAAACA
ESTC143	29	---	---	---	GTTTACGAAAAGTACTGAAAATGCTATTANTAGCTGAATTTGTGATTTCCCTTTTG
ESTC144	26	---	---	---	AAATCCATATTTTCTTGACATGAGGNGCTTTTTTAGCAGCATTTCCGG
ESTC146	20	---	---	---	CATGTCAGGATAAGGAGCANACACCAGGATTTATACACGGTGGCAGCG
ESTC148	42	---	---	---	TCCTTGGTGTCTACACAGACACTTAAGTACTGTATCGCTGTNATCAGCGGCTGTGGAGGCCCTG GGGGTGGCTGGGCTGTGTCTCTGAG
ESTC149	28	---	---	---	TCAGTTCATTTATTTGCTTTAAGAGTTANATACCATGAGACACACAGTTCTGG
ESTC15	28	---	---	---	GGATTGTAATATTGCCAGCTTTGTAAAGNCATTAAAGCAGAAGTTTCTCAGTGATCTT
ESTC150	20	---	---	---	CCAGGAAACAAGCAGCACACANACTTATAGAATACTTTGGTTTAAAAATTATTCATAATCAATATT AAACCTGATGTTTAAAGAACCTAATGAGA
ESTC151	49	---	---	---	GAAGCTAAGGCCCCATTTTCTTTTAAATACAAATCTACTGGTGCTNAAAACCTCAGAGCTTAGGA AACACAGCC
ESTC155	37	---	---	---	TTTTTAATTGACAACCTCAATCTCTACATACATACAGTNTTGCACGAATTATAAGTGGATCAACAATT ATATTATTGATACAAACTCATGAGCATTTTACA
ESTC156	32	---	---	---	GCAGCATTTGTGACAGGAGAGCGCAACAAANCCCTGGCTGCCCTGGGATGGAGCGGGGGGCGCTCA CCACCACCTGCAT
ESTC158	35	---	---	---	ACCAAGCCCTGGGATTTACTGTCTTGATGACTACANGGCTTTGCACAGCTGAGATGCTTCAGTGTGC AA
ESTC159	31	---	---	---	AGCTGGCAAGAGACTTCTCTGAGGCACATCAGNTAGTGGTGGTCAATTTAGGGCACGGTCTGGTTCTGCA GCTTTGAAAGG

ESTC16	23	---	---	---	CACTGAATGCTCTGCCATGAGCCNCAAGCAGCAGTATCATACCCACAAGGACAGGTT
ESTC160	38	---	---	---	TTCAGCAATTGCTGGTGAGTGGGGCCCTGAGCTGGGGNGCAGTCGGCAGTGTCACTGGGCCCGTTTG GGACTGGGTTGA
ESTC162	36	---	---	---	CTCTCGTCGGTTTGCAAGTTGCTGTTTGTTCAGNTACACCAGTCAGAGCTCCACAG
ESTC164	31	---	---	---	TCATTCTCCATAGAATAATTGGTTTTGTAACANCGAATACAATCCAATATATAACATTAAACAATCC GATACATACCA
ESTC169	22	---	---	---	GTCTCTGGTGTGCAGGGAATCANTTGCTGGATTAGAGGAAGGTGCCCGCTCTGTTCATGACTT
ESTC176	23	---	---	---	CACCTCCTCCCCCTGAGCTACCCANGTAGTGTCTGGGAGCTGGCA
ESTC177	42	---	---	---	TGGGTGGCTCTTTAAATACCTTCCATTATATTTCAAATTTTNCCTTTATCTATTTAAATACCTTTTAT TCTCTTTATCCCATAAAAAGGCAACCAA
ESTC18	29	---	---	---	TCAGACACTGCGGACATCAGCAATTGCTCCTGTCAGCTCCCTCCCTGCAGGGGCCCTGGGAGAC AACTGGACAAGA
ESTC181	21	---	---	---	TAGGGATTCCAAAGTTGCCTGGNTTAAATATAATACATATTCACAAAATTTACACAGCTCATGCATAC CA
ESTC186	43	---	---	---	GCTTGACTAGCGAGGCTACATCACAAATTTATAAAGTGCCAGATNAGTGTAAATGTCTCAGCTTG ATTTTCACCTCA
ESTC187	24	---	---	---	ACCATGATTGCCTCACACAAGCATNATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGGCTGG
ESTC188	25	---	---	---	TCTATTACAGGGTTATGTCACACCCNTGTCAACCTCAAAACAGATGATCACTCATCTGCTTCCAT CTTGC
ESTC189	27	---	---	---	AAAGTACAATCCAGTATATGCAGAAAGNTACTCAGCATCACACTCGTGATCA
ESTC196	42	---	---	---	TCCTCAATACCACCTTTCCCTAACTTATCAGTCTAGTAAGCNTTTCAAAGGAGGAAAAATGGGTTAC CTTTCAGGGG
ESTC197	26	---	---	---	ATCTCCAGTGTCTGCTGCCCTCCTCCCNCGCAAAGTCTCCACAAGCACA
ESTC20	33	---	---	---	AAGATTAGACAGACCGGTATAGTAAGCTCTGNGGAACTCCAAGATCTAGAGGGGGCTGTGGGAA CGCTGCTTAGATC
ESTC200	44	---	---	---	TTTGGTGAAATCCCAATATATGAGTTTAAAAAATCATTANCATCATTAACAGTACTTTAAAT CAATTACTCCTTTTGCCTGCAACAG

ESTC201	35	---	---	---	TCCTACTTGGGTAGTTAGCAAAACATTTTAAAAACCACATCCAACAGATTGGTT
ESTC202	22	---	---	---	CTGCTGGAGGGAGGACAGACAGCGGCGGCTGGGTGGCGGCCCCAGAAAGCGTGGCGTGGATGTT CGAGATGAGCC
ESTC203	27	---	---	---	ACACTTAACAGGTTAAATATCCAAATNAAATTTACTGCAACTTTTGTAGAAATTTATTGTGCTAC AAGACACGTTGCA
ESTC208	43	---	---	---	TATAGCCCCATCGCTCTCAGTTATTAGAATCTGAGAGGGATAANAGCAATAACTATTGTTTAAAGC CTAAGAGTGAAAA
ESTC210	29	---	---	---	GATGAAGTGGCTTCTCTTGGCGAAAGGATNAAGAAGTGAGTGACGGTGACCTGTG
ESTC212	27	---	---	---	GGGTAACCTGATGAGGAAGCTCTAGTGNAGAAATTCAGGACGGCTCTCAGAGCAGAGGGCTTGGT TCAAGTC
ESTC214	21	---	---	---	CTCAGAGTCCCTCTCTCANACCAGGGGCGAGGAGGAGTTAGGGAAT
ESTC216	49	---	---	---	TGGCAAGAAATTTATTACACTAACAAATTAATTTAATCACAGGTATTNTTAGATTGGTCAGAAAA CAAAAGACCA
ESTC217	28	---	---	---	TTTTGTCAGTAAATGAGCAATACACTGANTGGAATCTGCATGATTAAATAACATTAACAAGTTTCAT AAACACACCCCA
ESTC219	32	---	---	---	GTACACATCTGTGGGGTGAGCACACAGCAAAANGGGTGGGACGTGCAGAGAGGTATAGGGTAAAG GCAAGGAAGC
ESTC22	41	---	---	---	TCATTGAAGAAAAATTATGGGTTTATTCTTATTCTAATTNGAGAAATGCTTAATGTCACAGGCTACA TAAGGGCC
ESTC223	27	---	---	---	CTTCTGAAGCCCAAGAGAGGGGCGAGAANGTAGTTCTTGATTTAAAAAACAGAAAGGGGAGGAGGA
ESTC224	37	---	---	---	CGAAGGTAGATTTCCTCACATATTACAAAAATACACANAACACACACACACACACACACA
ESTC225	20	---	---	---	TGCACTGTTACTCCCCAGACNGAGAGCTTACATACCATATAGAAAGAGCATAAGTGCTTCAGAAAGGA ATGTGATGATCG
ESTC23	27	---	---	---	TTCTACTTTATTTCATATCCCAACCACTAAGCACTCCCTTTAATTTAACTAAAAACCATACAGGGT TCCTGAAAGGG
ESTC230	43	---	---	---	GGCTCTCCACGAATTTGAAAGACATATTGGCTGACCTGATACNTAAGGAGCAGGCCAGAAATTAAGA
ESTC231	24	---	---	---	CAAAAGGGTTAGTCATATTCCTCCCANCAACAGCATGATAAAAATAATTCAAC

ESTC28	23	---	---	---	GAAGAGCTGGGCACGCATCTGACNCTTCTCCTCTATTCTCTATAAAAAATAAAGGAAGCAGAAATCT GC
ESTC3	20	---	---	---	CAGACATGACCTACCGTCGCGCCCTCAATTCATATTTATTCTTGAGCCGCTTGTCAGGTTTGAT TCGCACACTCC
ESTC31	32	---	---	---	ACAGCCCCACAGAACTATTGTAAACAATATNTCAGTCGGTGATCATTTGTAATATACAATAACAAAG CAATTCCTCAGA
ESTC33	25	---	---	---	AGCACTTCAGCTCCTTGACGTTGTNGGACCAGGGAACCTCCGGAA
ESTC39	26	---	---	---	AAGGAAGGGAACCCACCTGGCTTNGGTCACAGAACTCAGACCTGGGCATTA
ESTC4	23	---	---	---	CCACTGAATCACACAACATGGACNAATCTCAATCATTTATGCTGATGGAAGAAACCAATT
ESTC40	22	---	---	---	GGCATGCTAGACAGAGGCATTANTTTGAAGATCTTTTAAAAATATTTTGACTTGTCCCCCTTCAC
ESTC45	37	---	---	---	TTTGGAGGTTTGTGCTGGAGTTTGTCTTTGTACNCCTCATCATCGAGGCTATATATAA
ESTC50	56	---	---	---	CTGTCCGTGTGAGCCCTGCCCTGCTCCATGGCCAGGAGCCACTGGTCCGGANCCGGGCAGATG TTTACCCTGT
ESTC56	45	---	---	---	GTGCCCTGAAGATTAGCAGCAGCAGCAGCAGGTCGCGAGGAAGNAGTGGAGGGAAGGACACCA AGT
ESTC57	20	---	---	---	AAGTGGCCCTCCAGTCCCTCTCTGGGCACAGATCCACCAGTCTGCTC
ESTC59	38	---	---	---	GAAACACAAAAGTGTGAGAAAAAACTTCTCAAAATTTGTTCCAGACTTCAGGAAAAATGATTTCC ACATGGTAAGGCC
ESTC6	27	---	---	---	TCTGCAGCACTTCACTACCAATGAGCNTTAGCTACTTTTCAGAATTGAAGGAGAAAAATGCATTATG TGGACTGAACCG
ESTC61	57	---	---	---	AGTGATTTTGGCTAGGCGTGTCTCATCTGTGAAATTCACAGGCAATGACAGCANCCTCTCTCCC ACCCACTCAAG
ESTC63	20	---	---	---	ACAGACACAGCATCACACCANAGGGCCACGGGAGGGTCGGGAGACGACACTTTTCCCTGGGAAA GGCAGCTCTAATC
ESTC69	20	---	---	---	GAGAGGCTAGTCAGGAGGGANACCCCTCAAGTTTAAATCCCCACACTTACTTACTGCTCATCCGT CACTTCGCTAA
ESTC7	45	---	---	---	AGTTCCCTAGAGCTGTGGGCCAGATAGCTGTCTGAGTTGCANGCACGATGGAGATTGGACACT G

ESTC72	37	---	---	---	GGGCTTCCAAAATGGGTATTGGGGCCAGGAGGCTGGGCTTTGGCGTGACGCTAAAAAGTGTGACC
ESTC74	49	---	---	---	AACAATTCACAGCTACAGGAAATCTAGAACAAAATCAAAATATTCATCACNTTGGGTTGAAAGTTG GAAGA
ESTC77	40	---	---	---	ATGACTTCTGTCCCATCGGAACACAGAGTTTCCCCAGNGAGCCCTTCCTATCTGCGGTTA
ESTC81	20	---	---	---	GGCTACGACAGGATAAGANCCCCACTCCGCATGTCCCCAGAGGGCAGCACTCCAG
ESTC82	25	---	---	---	TTTCAGATGATGGGGTCTGAGATGNTGCTCAGGCTGCATCAGCTGTCTTCAGTCTCCAGAACAGAAA GAGCCTGACCCA
ESTC83	53	---	---	---	CAAAATCAAATACACAGATCCAGATATGTGAACCATATATACATATCTATACANCCATTATTAGAC TTTCACAAAACCT
ESTC85	28	---	---	---	TTTAGCTGTATACCAAGTTTCCATAAANCTGTCTGTCTGGTGGGAGGCTACAGCCTGACCACATTG TTTGC
ESTC89	22	---	---	---	ATTGCAAGGAAGTGAACGTGNTCAAACAGAAAATGGTGACAATGA
ESTC90	33	---	---	---	CTGGTCTCTTCGCTTGGCATTCGCTCCTCTCNGGCCAGTGCTCCACCAAGTGCTTCCCCGATGAT
ESTC93	29	---	---	---	CTCCCCCTCCTCAGTTCACAGTGGAGACTANGGAGATTACAGGCGAGGATCC
ESTC95	32	---	---	---	GCACGTTCTTTGTTCTCCTCTTCCAGAAGTTGNAGACGCTATTATTAGTTTGAATTATCTGTCG
					AAATGACTTGACGAAGCTCATAGAAGATTAGCAGGTAGTAGAATAATGACTGCTGACTCCTAATTCA GTGGATCTTCCCTGGCCACCGTTTGTATTGAGCTGCAATGCTTCTGACTGTTCTCCA/C/TGCCAG ATCTTATCAATGATCTTTACCTAAGAAACAGCAAGAATTCTGGCAAGCACACGATCTAGAGATAC ATCTTATTGGGATTTTTCACAAAATCAAAGAAGAAAGGCTTAGCTG
DWU-100	127	C T	---	---	TTCCATCCTAGATATCTACTCAAAATATTGAGACAAGTTTCAAAACAGAAAGACGCTTGTGCTGAA TGTTCAATGGC/A/GGCCCTATTCACAGTAGCCAAACGATGAAAACACCCCAAGCTATATATTACCA GATGAAGGATAAACAATAATGTGGTCCATCCATACAATGGAGTATTACACAGCCATAAAAAAGGAAT GAAGCAGTGAATCCCTACTACACTGTGGAT
DWU-177	77	A G	---	---	CAAAATCCTGGACTATCAACCTTGTGCTTAATCCCTGCAGCATTCAGGTTAATCCATCTAAGTGAC ATTTTGAATTCACGCGGTGCCACCAATCATGCCAGCTTCTGTATATGATGAGATATACATTT ATGCTGACCTTCCCTCAAGACTGATTTTTCATGTCTGGACTTACAATATCTCAAGGAACAGCAATG TCAACAGGGAATCTGGAAACCAAGCCCTATCTGAGTCTTGGCTCCCTCC
DWU-286	213	A C	---	---	





EST10398 2a	147	C T	---			TGCTGGGGTGCAAGGCTGCAACAAAGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGATGATGTTACATTTGGGGCTTGACTTTCCACACGGAGAAG CATTTGTTTCTTCTGCGCCAAAGAGGTATCTACCAATAGTGCTATAGGCATTG
ESTD-C7	14	G C	---			ATATCGTGGCCTTA[G/CTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD- D4S95	90	T C	---			CTTTTCATGCACGATAGGCTTTCTCTACTAATCACAGAATTTGAGAAGAGCAAAACAACCTTCAAGG ATAATGGGGCAATCATTCTTTT[C/CTCTCTTAGAGTCTACCGG
ESTD- GPPK2L	38	G A	---			AGTCTTCATCTCGGGTGTCAGGTAGATCCCTTTTACC[G/A]CCGAGAACTGCTCGATATC
ESTD- HRASb	82	A G	---			CTGGGCTCGCCCGCAGCAGCTGCTGGCACTGGACGGGGGGCGGCGCAGGCTCACCTCTATAGTGGGGTGG TATTGCTCCACAAA[A/G]TGCATCTGGATCAGCT
ESTD- HRASa	37	C T	---			CTGGGCTCGCCCGCAGCAGCTGCTGGCACTGGACGG[G/CT]GGCGCCAGGCTCACTCTATAGTGGGG TCGTATTCGTCCACAAAATGCATCTGGATCAGCT
ESTD- NRAMP	81	A G	---			GGAGGCAGGAGGTGGGGGGGGTCTGCTGCTCCAGGTCCACAGACCAGAGAGCGGCCTCAGTG TATCCCCACCCCA[A/G]TGGGGCTGGGAGATGAAGAGGAGTTGATGCAGGT
ESTD-OTC	18	A G	---			GTGACCTTCTCAGCTTTAA[A/G]AAACTTTACCGGAGAGAAATTAATATATGCTATGCTATCAGC AGATCTGAAATTTAGGATAAAACAGAAAGAGAGGTATGTAACA
EST36751 7	36	C T	---			CCAGTCTGTTCAATTTAGCTTTGCAGTTTAACT[C/CT]GATTACTTTTCTATTCAAATCTCTGTA AAATTGAATATGAACCTAGTTTCTGATCTATGTTTCAAGTTAAACAG
EST40562	109	A G	---			CACGTGAAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGAACTGTCCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAATTTTCACTGGATGCATTAAACAAAT[A/G]TTTACCTTTTGAAAAATAA ATGAAGGATTTGACCTGCTTCGCTCTGGAAGAGTATCCGTACCGTCTGACGTTTTTGAACAATACA GATGCTTCCCTTTGAGCAGTTTTCAGCCTCCTCTACCCCTA
EST18288 3	121	C T	---			GCTCTATACCCCTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAA GATTGACAGGTTTCATGCAGGCTGTGACAGGATGGAAGACTGGCTGCTCCCTGA[C/CT]GGGAGCCAGT GTGGACAGCACCTGGCTTTCAACACCTACGTCCACTTCCAAGGTAAAGGCAAACTCTCTGCTGGCTC TGGCCCTAGGACTTAGTATCC
ESTD-AK- 168	31	C T	---			GGGAGTGACAGCTAGAGCACCAAGGGGGGCT[C/CT]TACAGCTGTGTTCTCATGGAGGACAGGCTTCT GCTCATTCTGG
ESTD-ALB	180	A/G	---			AATCCAGCAGCTTTAGGAGGCTGAGGCAGGCATATCACAGAGTCAAGAGTTTGAGACCAGTCTGA CCAAACATGGTGAACCCCATCTCTACTAAAAATACAAAAATTAGCCAGGCTGGTGGTGCATGCTGT AATCCAGGAGGCTGAGGCAGGAGAAATCGCTTGAACCTGGGAGGCG[A/G]AGGTTGTGGTGAGCCGA GATGGCACCATTCACCTCCAGCCTGGGCAACAAGAGTAAAACTCTGCTCTC

EST70523 3	182 G T ---	---	---	TTCCGCCAGCCCCCATCTTGGCACCTGGTCCCTCAGGGGCAACCCCGGCACCTCACCGCTCT CGCTCTCGGTACATCGGGGGGGCGCTCTTGGACACATAGCTGGACCGTTCCGTATAGGAGG ACCGTGTAGGCTTCTGTCCCGGGCTTGCAGGGGCCAGCCCTG/TCAGAGAGAGGGGTCCCTGT GGTTGAGCTGAACACAGCTGTGAGTGCTCCACGTG
ESTD- APOA2	101 C T ---	---	---	CCAGGTGTTGTGGCACGTGCCTGTATCCAGCTACTCGGAGACTGAGGCATGAGAATCTTTGAAC CGGGAGGCGGAGGTTGCAGTGAGCTGACATCG/TCGACCTGCACCTCCAGCCTAGGTGACAGAGC AAGACTCC
EST58707 7	112 C T ---	---	---	CAGTGTATCTGGAAGCCTACAGGACACCAAAATTAACCTTAATCATCAATGGTTACAGGAGGCTTT AAGTTACAGCATCTTTGGCTCACATGAAGGCCAAATTCGAGAGAC/CTCTAGAAGATACACGAGAC CGAATGTATCAAAATGGACATTCAGCAGGAACTTCAACGATACCTGTCTCTGGTAGGCCAGGTTTATA GCACACTTGTACCTACATTTCTGATTGGTGGACTCTTGTCTAAGAACCTT
EST74167 6	137 C ---	---	---	AGACATGAAGGAGTTGAAGCCTACAAATCGGAATCGAGGAACTGAGGAACAACCTGACCCCGTGGCGGAGG AGACGGGGACCGGTGTCCAAGAGCTGACGGGGCCAGGGCCGGCTGGCGCGGACATGGAGGA CGTGGGGGGCGCTGTGTCAGTACCGGGGAGGTGCAGGCCATGCTGGCCAGAGCAACCGAGGAGC TGGGGTGGGCTCGCTCCACCTGGCAAGCTGGTAAGCGGCTCCTC
EST43211 8	132 C ---	---	---	CGCTGGTGCAGTACCGGGCGAGGTGCAGGCCATGCTCGGCAGAGCACCGAGGAGCTGCGGGTGCG CCTCGCTCCACCTGCGCAAGCTGCGTAAGCGGCTCTCCGCGATCGCGATGACCTGCAGAAAGCGC TGGCAGTGTACAGGCGGGGCGCGGAGGGCGCGAGCGGCTCAGCGCCATCCGCGAGCGCTG GGCCCTGGTGGAACAGGGCGGCTGGCGGGCGCCACTGTGGGCTC
ESTD- ARSB	126 A ---	---	---	GGAAAGAAATGGAGCCTGTGGGAAGGAGGGCTCCGAGGGTGGCTTTGTGGCAAGCCCTTGCTGA AGCAGAAAGGGCGTGAAGACCGGGAGCTCATCCACATCTCTGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAGCCTCTGGATGGCTCGACGTGGGAAACCATCAGTGAA GGAGCCCATCCCCAGAAATGAGCTGCTGCATAATATTGACCCAAAAC
EST36770 4	144 C ---	---	---	TGTAGCCAAAGTCACCTGCATCATCTTTGGCTGCTGGCAGGCTTGGCCAGTTTGCAGCTATAATCC ATCGAAATGTATTTTTCATTGAGAACACCAATATTACAGTTTGTGCTTTCCATTATGAGTCCCAAAAT TCAACCTCCCGATAGGGCTGGGCTGACCAAAATATACCTGGTTTCTGTTTCTTCTGATCAT TCTTACAAGTTATACCTTATTTTGGAAGGCCCTAAAGAGGCTTATG
EST26021 1	137 A ---	---	---	TAATGTAAGCTCATCCACCAAGAGCCTGCACCATGTTTGGGTTGAGTGAGCATGTTGCAACCTGT CCATAAAGTAATTTGTGAAGAGGAGCAAGAGAACATCTCTGCAGCACTTCACTACCAAAATGA GCATTAGCTACTTTTCAGAAATGAAGGAGAAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGC TCTGAACAAAGCTTTTCTTCTTTTGAACAAGACAAAGCAAAAGCC
ESTD- BA511	29 A G ---	---	---	GGGCAACATAGTGAAACCCCATCTCTACAI/GIAAAATACAAAAATAGCCAGGTGTGGTAGCAAG TGCCTGTAGTCCAGCTACTTGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGAGGTGGAGGCTG CAGTGAGCCAAGATGGTCCACTGCA



[illegible]

ESTD- D17S33a	75 C T ---	---	CATCCCCAGCCCATCCTTAGCCACTGGGCAATTTTGGCCCTCTGACGATACACTCAGGGCCGT CATGCTGCTACACATCCAGGGGGCCCTACCCCTTTGTTAGTCCATGGGAAGGCTCCTCTGGGGCG GTGGGTGTGTGGCTATGTGGTCTGTGTAGACGGGGCTTTGGTTTCAGTTGCACATATTGGGTT ATTGCAGATTGCTTTGCTTTCCACCTGAGCGAGCCTC
ESTD- D18S8	133 A G ---	---	TTTGAGACCACCCTGGCCAAACATGGCGAAATCACATCTCTACCAAAATTAACAAAATTAGCTGGGTGT GGTGTACATGCCTATCGTAATCCAGCTACATCGGGAGGCTGAGGCAGGAGAAATTGCTTGAACCC[A /GJGAGGCAGAGCTTGCACTGAGCAAGATCACACCCTGACCTTACAGCCTGGGTGACACAGTGGA GACTCTGCTCAA
ESTD- D3S11	44 G ---	---	AACTGATTAGAACCTGAAATACATAATTTATCTGAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCATTAANAATCCAATAAAGTACACTGTATAAAGAATTTAACAGAAATATCATTTGT TTATCAAACATATTAACACITATTTTATTGGTAAGCCATACTAAATCTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	37 A G ---	---	AGGTTCCACATTAATGCTGATGTTTGGCTGATGTTTCQJGJGAGCCTTGATGTCATCTGTATCTCCT CAGGTATCCCACTTGAGACGTACTTTTCAAAACTCTCTACAGCCGTTGTTGTTAATTAATCAAGGT TGAACATAAAGTA
ESTD- D3S2b	247 C T ---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTCTGC TGAGTCTTATTCAAACCTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGATTCCC AGAAGTGAAACATACTGCTCCTAGAACCCAGAGTCATCTGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGCTCTTTATTGGAAGGATGCTGTTGGT
ESTD- D3S2a	248 G ---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTCTGC TGAGTCTTATTCAAACCTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGATTCCC AGAAGTGAAACATACTGCTCCTAGAACCCAGAGTCATCTGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGCTCTTTATTGGAAGGATGCTGTTGGT
ESTD- D7S399	83 A G ---	---	TGAATCTTAATTGCTATCTCTACAAATGTATAAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCJAGJGCTCCTCTACATCCTTTTCAAAACATTTTCATCCATGGACTCCATAC TAGAATATTTGAAGAAACAAACATGACAAACATTTTC
ESTD-DMb	146 A C ---	---	GTGGGACACCGAGGGCTCCAGGCTGGGCGCTTGACGCTGTGGCTCAAGCAGCTGCTGGGCTCCACT TCCATGGGTGTGGGCTGGGACCTCACTGTCCTGGGAGAGAGGAGGAGTGGGAGGGAGACA GAATGCTGATTACJCTGTGTGGAGAACCAAGAACTCTGGCCTGTGGGTAGGGGCAGCTGCTTCCAAG ACCTCCTGATTGAGGAAGGGGAGCAGCAGAGCGAAGAGMACAGAT
ESTD-DMa	66 C G ---	---	GTGGGACACCGAGGGCTCCAGGCTGGGCGCTTGACGCTGTGGCTCAAGCAGCTGCTGGGCTCCACJ GJTTCCATGGGTGTGGGCTGGGACCTCACTGTCCCTGGGAGAGAGGAGGAGTGGGAGGGAGA CAGAAATGCTGATTATCTGTGTGAGAACCAAGAACTCTGGCCTGTGGGTAGGGGCAGCTGCTTCCAAGA CCTCCTGATTGAGGAAGGGGAGCAGCAGAGCGAAGAGAACAGAGT

ESTD- DRD1	154 C T ---	---	TCCCAGCCCTATCGGTCAATATGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAACCCATCAC ACAAACGGTCAGCACCCCAACCTGAACCTGCAGATGAATCTGCCACACATGCTCATCCCCAAAAGCT AGAGGAGATTGCTCTGGGGC/TTCGCTATTAGAACTAAGGTAC
ESTD- DRD2	144 C ---	---	TCTGCTTTGGTCAGGAGGTGCCCGGCGAGGCCAGGAGCTGGAGATGGATGCTCTCCAGCACCA GCCACCCGAGAGGACCCGGTAGAGCCCCATCCACCCAGCCACCACTGACTCTCCCCGACCCG TCCCACACGGTCTCCAGAGACTCCGACAGCCCCCGCCCAACACAGAGAAGATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	109 C T ---	---	AAGACGATGCCAGGATGAGCGGACAGTAGGAGGCGCATAGTAGGCATGTGGCGGGCTGGCTGG CACCTGTGGAGTTCTCTGCCACACAGGTGTAGTTACAGTGGC/TACTCAGCTGGCTCAGAGATGCC ATAGCCAGAGGGAGGTGCGTGATGCCAAGGGGCTTCCTGTGAGGAGA
ESTD- ERB2	93 C T ---	---	TCTTCAGGATCCGCATCTCGCCCTGGTTGGGCATCGCTCCGCTAGGTGTACGGCTCCACAGCTGG GGTGAGGGGGTGGTGGTCACTGC/TJGGGGCCGGTGCAGACCCACCGGGCTGGGAGACTTCA CCCCGCTCACTCCGTTCTCGCAGCAGTCTCCGCATCGTGTACT
ESTD- ETS2	43 A G ---	---	ACTCACAGTCTTTTAAGTGAATGTGCGAGAAAGAGGCACCA/GJGGAAGCCGTCCTGGCGCCTG GCAGTCCGTGGGACGGGATGGTCTGGCTGTTGAGATTCTCAAAGGCGGAGCATGTGCTGGACACA CACAGACTATTTTAGATTTCTTTTGCCCTTTGCAACCGAGAACAGCAATGCAAAAACCTTTTGAG AGGTAGGAGGGTGGGAAGAAACCAACATGTCTTTTCAGAAGTTAGTTG
ESTD-F9	111 A G ---	---	AGATCCTGATGATTTTTTCTCTATTTTTTCTAAATGTTTACAGTTTGAAGTTTAGATTTATGCCCA TGCTCCATTTTGAGTTAATATTTGTGTAAGTATGATGTTTA/GJGTCAAACCTTCATTTTTTTTTCC ATAGGTATGTCCAAATTTATCCAGCACAAATTTGTTAAACAAAAAC
EST68787 5	144 A ---	---	CTTCTATGGGATTTGACTTTATTTCTCCATTGCTTACCTTTTACAGGTGTTAATATAGTGAAGAAG GAAGCTTGCACTCATGACAAATTTGAAGCTGACAAATACACAAGAGGAAATAAATTCACAGTCAA AGAATCAAGCACTTTTCGAACATTTGAAGTTGTTTTGAACCTGGTGTCACTTTTAATACAACTAG CAGACGGAACTGAACCTCAGGGTAAGAAT
ESTD- GODH	200 C G ---	---	CGCAGACCGGTCACTGTGGGTCGGGAGTGTGGAGGGAAGGAGGGAACCTGGGGTTTAGGGACT TTCCGGGGTGACTTTCCCGTTCTGTGCTTGACAGAGAAAGGGGGGAGAACACAGAGCAACTGGCTAA GTGAAGGGACCTCTGGTCGCACCGTGTGTTCTGTGCCCCCTGTTTCACTGTCTGTCTGCCGAGT/C/
ESTD-GCK	88 A/G ---	---	GJGACTCTGTCCCGGAAATTCGAGAGCT GTTTTATGCATGGCAGCTCTAATGACAGGATGGTCAAGCCCTGTGAGGCCACTCTCTGGTCACTATGAC AACCACAGGCCCTCTCAGGA/GJACAGTAGCCCTGGCAGGAGAAATCCCCACCCACACCTGGC TGGAGCAGGAAATGCCAGGGGGGCTGAGCCCCAGGGAGCAGGCTAGGATGTGAGAGACACAGTCT ACCTGCAGCCTAATTACTCAAAGCTGTCCCCAGGTACAG

EST34088 2	62 A T ---	---	GTGGGGCAACAGTGGGAGAGAGGGGCCAGGGTATAAAGGGGGCCCAAGAGACCGGGCTC[AT] AGGATCCCAAGGCCCAACTCCCGGAACCACTCAGGGTCTCTGGACAGCTCACCTAGCTGCAATGGCT ACAGGTAAG
ESTD- GNAT2	56 A G ---	---	GACCTGAGTACCTCCCTAGTGAGCAAGATGTGCTCCGATCCAGGTCAAAACCAAC[AG]GGCATCA TTGAAACCAAGTTTCCGTCAAAGACTTGAATTCAGGTAAGTCATGGTTCCTTAGG
ESTD-HT2	154 G ---	---	GGGCTAAATTTCCGAGCAACTTTGCATAGACTGTTTTATTTGACTTGACAGGATTGCTAGAGATAGG CAGGGAGAGGAAGATGTGTACAGTTTGTGAGAGAGATAAAAGGATAACCTGGGGTTTCTGTGC TTTGCTTCTTACATCCCTGGGAGTTAATAGTGCATTTTCAAGAACGGTATACAGGGACAGCA AAGCGCAGTCGTGAAGTTTCAAAACAAGACACACCTT
ESTD-HT5	149 C ---	---	AACACACAAGCCCGAGCAATTTGAATCGGACCCCTGGTTTACAAGACCAGTGCTTAACCCCT GAGCTATGGAGCCCTCGTCTGCTGTTGTTTCTTCTTTCATCTTATAGATTGATGTTATGCTCCTA GCATTCGGGTACCGAATAGGATGTTAGCTTGAGTAAATCCAGGATATTCTCTACAAAATGAAA ACATTTCTGCTCTGTAATCCCTCGAAAAGTTCT
EST37382 5	124 A G ---	---	CTGAGAAACAATTGGCAAAATAAGGAATTTGGCACTCCCAACCCCTCTTCTCTCTCCCTTGGG CTTTGAGTCAAAATTGGCCTGGACTTGAGTCCCTGAACCAAGCAAGAGAAAAGAG[AG]CCCCAGA AATCACAGGTGGGCACGTGCGTCTACCGCATCTCCCTCTCACGGGAATTTACGGGTAAAC! ACCCAGTGGAGCCCGCTCATTCGACGGTCTTTGGCAGGAGGTGC[CT]CTGGGAGAAAGGAAGATG TTCAGGGCACACATAGCTTAGTGGAGACTC
ESTD- IGHV4-6	120 C ---	---	TTTACTATTTCAATGGATACAGAAATTGGGAGTCACTATATTCCTATGAACAAAAATTCAGATTT CAGTGTAAAGTAATGTTGCCTACATTTGTGTGAGTGACGGGCGAGTGGGATCCGAGAGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGGAAGATGAGTATCTATGGATACGAACGTGAAAGT ATGTAATACTTCACAAAATACTAATAAACGGAGTTGAATATAAACCCCA
ESTD-IL1A	110 A G ---	---	CAAAGTAAGCACCCCAATAAATGTTAGCTATTACTATCATATTATTATTATTTATTTTITG AGATGGAGTCTGGCTCTGTCAACCCAGGCTGGAGTGCAGTGGC[AG]CAATCTCGGCTCACTGCAAGCT CTGCCTCTGGGTTTCATGCCATTCTCTGCTCAGCCTCCGAGTAGCTGGGAATACAGGCACCCGCC ACTGTTCCCGGCTAAATTTTGTATTTTGTAGTAGACGGAGTTCACCGT
ESTD-IL1B	99 A G ---	---	CCACTACAGATGGATAAATGGGTACAATGAAGGGCCCAATAGCCCTCCCTGTCTGTATTGAGGTGT GGTCTCTACCTTGGGTGCTGTTCTCTGCTC[AG]GGAGCTCTCTGTCAATTGCAGG
EST74082	134 A T ---	---	TCCAGGTGGCTGGACCCAGGCCAGCTCTGCAGCAGGGAGGAGCTGGCTGGCTCGTGAAGCATG TGGGGGTAGCCAGGGGCCCAAGGAGGACCTGGCTTCAAGCTGCTCAGCCCTGCTGCTGCTGCTG TJCCAGATCACTGTCTTCTGCCATGGCCCTGTGAGTGGCTCTGCTGCTGCTGCTGCTGCTGCTG CTCTGGGACCTGACCCAGCCGAGCCTTTGTGAACCAACACCTGTGGC

EST45311 0	151 C T ---	---	---	GGCCTCCTCTCTCCAAATCTGTCCCTATAGTTTTCCCTCTATTAAAGTGAACATACATGCATCTTTTAGT GGATAGATGCACAAACACACAAAGCCATTATGGGGAAGGATCCACGTGTGTGGCCATATTGTAACA CATTTTCTGCAAAATC/TJACCTCTTTTCATTTAACAGCCCTTATTCAATGGCCTTTTCTTTTTCAGTA GTACATACACATCTGTGTCATTTGTTGAAT
EST65258 8	80 A G ---	---	---	TGCCCATCACGCGCGGAGACATGGCTTGCCACAGCTCTGAGGATGTCAACCAATTAACCAGAAAT CCAGTTATTTTCJ/GJCCCTCAAATGACAGCATGGCGCGGGTGCTCTGGGGGCTCGTCGGG GGACAGCTCCACTCTGACTGGCACAGTCTTGCCATGGAGACTGAGGAGGGGCTTGAGGTTGGT GAGGTTAGTGCGTGTTTCTGTGCAAGTCAGGACATCAGTCTGATTAAA
EST38216 3	26 A T ---	---	---	ATGCAGGATGAAGGTGGACAGGGAGG/TJGAGGGCCAACTGTCTCCAGGGCTGCAGATGTCTG CTGGACTATGGGTTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782 149 G T ---	---	---	---	ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATATTAGCATTTGTTTAGCATTACCTAA TTTTTCTCTGCTCCATGCAGACTGTAGCTTTACCTTAAATGCTTATTTTAAATGACAGTGAAG TTTTTTTCTCTG/TJAAAGTGCCAGTATCCAGAGTTTTGGTTTTTGAACAGCAATGCCTGTGAA AAAGAACTGAATACCTAAGATTTCTGTCTGGGGTTTTTGTGTCATGCA
ESTD- KRT10b	183 C T ---	---	---	CCAAAGTTAAATAGTATGGAGTTATCTGAGAAATTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCAATTTTAAAGTAACTGCTAAGTTTTTCCATTAAACCACATATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGTGTCTTTTAAATAGT CTCTGCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT10a	133 A G ---	---	---	CCAAAGTTAAATAGTATGGAGTTATCTGAGAAATTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCAATTTTAAAGTAACTGCTAAGTTTTTCCATTAAACCACATATTACTTCTAIA/ GJGAGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGTGTCTTTTAAATAGT TCTGCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT8b	231 C T ---	---	---	ACCTCACCCCTCCCTTAGCCGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCTATCTCTCCGCTCAGGTTTACCAIC/TJGTCAACATTGACACA
ESTD- KRT8a	21 C T ---	---	---	ACCTCACCCCTCCCTTAGCC/TJGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATC GGATTGGACACCTTGAGAGTCTTAACAGCAGGGCTGACATGAGACCTCAGACAGAACTTTCTAGAG TTTGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCAT GGCTGCCTATCTCTCCGCTCAGGTTTACCAIC/TJGTCAACATTGACACA
EST75099 6	82 C T ---	---	---	CACCTGTGTGTAGATCTCCTCAGTGGCGGCTCTACTGGTTGACTCCAAACTTCACTCCATCTCA AGCATCGATGTCAA/C/TJGGGGGCAACCGGAAGACCCTCTTGGAGGATGAAAAGAGGCTGGCCCCACC CCTCTCCTTGGCGCTTTTGAGGTGG



ESTD-LF79	142 A G ...	---	GGGTGATTTGAGGCTCAGTTAATATTTCAAAATTTGAACCGTAGCAAACTGCATTGGTATTAGA AAAATAAAAAATTTCCAATATGTAGTGTGTTATACCTGCCTCTGCCATGCAGCATCATAGCCTGT GGGAACC/G/GGGAGGCTTCCCTTACCACCCAGA
EST35879 9	142 A C ...	---	GAGATCGGTGTGTGAGTTATTAGGCATGGTTACTGTGATTCCCAATCTTGGCTTCCACCGATG GAACTGCCGGCAAATCCTGACACGTGTGCACCCAGGCTGTACCCAAATTAGGTGAACATGGCTTCGAG AGAGTTG/CACJACAGATTCTCTGGAAGACAGCAGCGGGATGGGGCAGGAGAGAGCTGCCTGGATGA A
ESTD-LMP2	35 C G ...	---	TACACACTTTCCTTACCCATTCACTGAAAACGACT/C/G/GCAAACTGGAGCCTTGTAGGAATGGAGT TGACCTTCCCCAAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	113 C T ...	---	TGTCAGTGTCCCTAGGGGACCTCACTCCAGCTTCTTCAGCTCTGCCCTGCTCCTGCCTGCA AGGTTTGTCTTAATTCATCAATCAATGTCTCTCATCTTTAG/C/TTAGCTGTGGGTTTTTGTGTG TTCTCTGTTTTTGTCTTAGTATCTGACTACTTTTAAATAAAAAAGAGATGTATCTAAACAAAAATAG AGATTGTATCAGAAGTTCACAACATTTATTAAAAATTTTTCACCTG
ESTD-MCC	45 C T ...	---	TTGTCAGGAGTGTGTGATGCTGCTGCCCTCCAGCTCTGTCCCTAGC/C/TTGAACCTTCAGGACAACGTGC AG
ESTD-METH	118 C T ...	---	CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAACACAGCATGCATCCCCGAA TCTCAGGAAGTCTCTGCTTTCCAGGGTTTGGTCAAGTTGCTGATTACCC/C/TTGGATTTTCTGACG ATCTTCAACTGCTAGAGCATCTGTTCCCTGTTTAGCATGG
ESTD-NF1	25 A G ...	---	ATTATCCAGATGAATTTACAAAACCTA/G/TTACCAGATCCCACAGACTGATATGGCTGGT AACATGGACTTGATATTTGTACAAAAAAGTTTTTATTTTCTAAAAAAGAAAAAAGAAAGAAA AAATTTAAAGGGTGACTTATATCCACACTGCACACTGCC/T/G/GCCCCAAAACGCTTATTGTGGT AGGATCAGCCCTCATTTTGTGCTTTTGTGAACCTTTTGTAGGGGACGAGAAAGATCATTTGAAATTC GAGAAACTTCTTTAAACCTCACCTTTTGGGGTTTTTGGAAGGTTATCA
ESTD-NFKB1	107 A G ...	---	TGTCCTAGGCCCCAGCCCTGCTTGTCTCCCTGGCTGTATCTT/C/G/GTACTGCAAGAGAACACACA GACAT
ESTD-NPPA	45 A G ...	---	GTGTTTCTTAATCTTTCCAGGAACACAGTGACCATAATTTCTTTCTGCAGGCATATAGAATTTGGT GGGTTTCTTTTATGTAGGGTGATTTGGATACTTTTTGTGTGATTATATATTAGCAATTTGAGGG ACAAACCAGATAGGCAGAAATGGGCTTGAATAGTAGATGCTTTATTAACTTTGGCAATAGCATTG/ C/TJATCCCTGIGGTTTTTAATAAAAT
ESTD-NRAS	202 C T ...	---	GCCACCACCCACCACACACCTCCACCTCCAGCCAGACAAAGTTGTTGACACAAGAGAGCCC TCAGGGGCACAGAGAGTCTGGACACGTGGGG/G/GT/CAGCCGTGTATCATCGGAGGCGCGCGG CACATGGCAGGATGAGGGAAAGACCAAGAGTCTCTGTGGGCCCAAGTCTCTAGACAGACAAAAACC TAGACAATCACGTGGCTGGCT
ESTD-PAI1	100 A G ...	---	

ESTD-PAR	120	A	---	---	CTCTTCAGGAACCAACAGCTTCTTACCAAACACGAGCTTATTGCTGTCCGAGAGGTACAAACCCGTAGA ACTTCTTCTTAACGTAAATTTAGTTAAAGGAATCGAAACTGGCTCTGAAGACATGGAGATACTGCCT AATCGACTGGCTTTCATTAGCTCTGTGAGTGTTCCTTCACTTTCTGTGTTCTAGAAGCTTTTCTTAG GACTGGCAGTTTAAAGCTTTCACITTAGGCTTCTGTATACCCATGCC	
ESTD- Per/RDS	74	A	G	---	ACCTACAGACGTCGCTGGATGGTGTGTCCAAACCCGAGGAATCTGAGAGCGAGAGAGGGCTGGCTG CTGGAGA/GAGAGCGTGCCGGAGACCTGGAAGGCTT	
EST68308	5	29	C	T	---	GGAAAGAGATTAAAGAGCTTGATTGGAC/TAATCTCGTTCCTTTGAGTGTGGAAGAGTTTCATGTC TCTGCCCTGAGTTACACAGAAATCCTTTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAAT GGAGAAGTAGACTTTAAAGGTAAAGAAAGTAGTTATTTTTA
EST54045	6	39	A	G	---	GGAAATTTAAAAATATTTAAAAATACCTCCATTTTGCCTTA/GTCTCTTTAGTGAAGATGATACCTGCG AAAAGACATGGCTAAAGTTATGATTGTGATGTGGCAATTTGTTTCTTACAAAAATCGGATGGGAAA TCTGTTAAGTAAGTACTGTTTGCCTTGGAAATGGATTTTAAATGTTGACTTTATCAT
ESTD- PXMP1	88	A	G	---	---	ATGAACATGGTCTTTAATTTATGATAATGTTTGTATAGCTATCTTAAAGGGCTTCTTTTTTTTA ATGCAGAAAGAGGGGAAAAA/A/GJGAGCGAGCTGTGGTGACAAGGTGTTTTTCTCAAGGCTCATAC AGATTCTGAAAATCATGGTCCCTAGAACATTTTGTAAAGAGGTAACTTATGAAATTTATAATCTT
ESTD-RDS	127	A	---	---	---	CCCGAGGAATCTGAGAGCGAGCGAGGGCTGGCTGTGGAGAAGAGCGTCCCGGAGACCTGGAAGG CCTTCTGAGAGTGTGAAGAGCTGGCAAGGCAAGGCAACAGGTGGAAGCGGAGGGCGCAGACGACGAGG CCAGGCCACAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCGAACACTGAGAAATAGTGCAC CCAAGAAACGTGGATCTCCCCCTCATCCAACCTCCGAAAGTCTGAA
ESTD- s14544	94	G	T	---	---	TTGGGAAGTTAGAGCCTATATTAATACGGAATTACTAAGCAGGACACAGAGGCTTAATTGAAAA TATCCCAAAGTTGAAATGCTCAGTTG/TTCTGTGTGGGTAGATGCAGGATTTATATGATCCGTTA ACCTCT
EST52908	0	45	A	C	---	ATCACAGGTCTCTGGTCTCTGGCCATCTTCTCTGGGAGAGATGG/A/CJTGTTGGTCTGCAAGCCCTT TGGCAATGTGAGATTGATG
EST19590	55	C	T	---	---	AGGAGAAGCTGAGGAGGGGAAGAGAGACAAAGAATGACATTGATGAGTGAAGATGT/C/TTGGCTCAG GATGCCGGAAAAATGAC
EST76136	39	C	T	---	---	TGAAGCTTCTGCCAGCTTGCAATGTTTCTAGGAGAAC/C/TTGGGTATACCTTTATCTATAGCCTT CCCTAGGTCTT
ESTD- SPTB	176	C	T	---	---	TGAACACCCCTGTGTCCGGAGCCAGGTGTGTTTCTCTCTGGAGCCCTGAGGAGTTTGTGTGTGTG CAGTCCCCCGCCACCTGCTGTTGAGCCTGGACATACACCTTCACCTCTTGGCCCGGAGAGAC ATTTACCCACCTGGCCATGTCCCTGGCCTGTTGTGCACA/C/TTCCCTGTGGAAGACCCCAACCCCTGC CTCCCCACCCCAAGCCAGTTTCTTAGCAAGGGCAGGAC

ESTD-TAT	224 C	---	---	---	AAATGGTCAGGACCCCTGATCCACAAGAAGTGGTACCAATTCATCAGGGCCATCAGTTCATTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTCAATTCATCTTTAAATGACTTGTGGACAGGATCA ATTTCCCTCACCTAGAACGTTTGTACAACTTTCTTCCAGTATGGATGGGATATGATGGGGGG GAGAAGCAAAATTTAAATAGGACCCATGAGACACATCA
ESTD- THRb	125 A C	---	---	---	TGCGGCTTTCTCCGGCAGGTAGACTCTTACTTGGCTGTGATTTCCAAAGAGAAGAGTCCCAAG CACACGAAACAGCAAGTTGCAGATCCCATGAGGCCAGTCTCAATCACACAGGATC[A/C]TTCAT CCACACTGGATTGGCCCAACAAGTCTGAGTGGCAGCCAGGACTCAACGGTCCCTGTAGATGGG TAGTGAAGTTTTCATCTCCTGTGAGCTTCTGGATTTCTTGTCCACCGCAACAAGAAGTCTATGC CAAGGCAGAAAGCTGGTCTTCATGGGCAAAATCAATGTCTCTCCAGATTTCA[G/T]ATCCCCAA GCAGTGCATCCATTGACACATAATAATGCATCCAGACAAAGAGGTCAATAATATGATGTCGTTAAA CATGGGTGTTGATCCATTTTTCATTTGGCCATAGGTCCCTATGGGATGACA
ESTD-TYR	122 G T	---	---	---	AGTAGTGATGAAGCTAACCAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AAACTCCAGAATCCTAATCAGTCTGGTCTAACAATGCCCTACTCTCTATGCAATAGTATCACAA AACCACCTGGTGAATATAATAGATTGAGTTAATGCTATTTCTTTCACCTTTATACCTTCTTCT AATACAAGCATATGTTAG[A/C]ATTAAGTTCTAGGCATACTT
ESTD- TYRP1	222 A C	---	---	---	AGTAGTGATGAAGCTAACCAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AAACTCCAGAATCCTAATCAGTCTGGTCTAACAATGCCCTACTCTCTATGCAATAGTATCACAA AACCACCTGGTGAATATAATAGATTGAGTTAATGCTATTTCTTTCACCTTTATACCTTCTTCT AATACAAGCATATGTTAG[A/C]ATTAAGTTCTAGGCATACTT
ESTD- TYRP1	222 A C	---	---	---	TTCCCAAGGCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCAGAGCCCAAGACACAAGGTCAAGAGACAGGAACACCCAGTG ACTCTGAGATGTCA[C/T]CAGACTGAGAACCCCGTTATATGTAAGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12	148 C T	---	---	---	TTCCCAAGGCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCAGAGCCCAAGACACAAGGTCAAGAGACAGGAACACCCAGTG ACTCTGAGATGTCA[C/T]CAGACTGAGAACCCCGTTATATGTAAGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12b	148 C T	---	---	---	TTCCCAAGGCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACAC[A/G]TGGATGCTGGAATCACCAGAGCCCAAGACACAAGGTCAAGAGACAGGAACACCA GTGACTCTGAGATGTCAAGACTGAGAACCCCGTTATATGTAAGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12a	74 A G	---	---	---	ATGGGCTGAGGCTGATCCATTACTCATAT

EST58607	105 A G ---	---	CTCTGGATGGGTTACAGGTGGCAGGCAAGCCAGTCCATCTGTAGTCATCATAGTTGTTGGCTCC
0			CAAGTTGCTCTCTCACTGGAGAACAGGACAGCCAC/GJTGCGCGGGATGGCGCGGGAGTTTC
			TGGTTGCGGCCACGGCTGTGGCTCTGTTGTGAACGGTAGCCTTTCGGTTGGATGCCTAAACCTTTGT
			TTCTTGGCCAAAGGAGGGGGTGCATGCCTGAGATGATAGTGGGCC
ESTD-VWF	36 G ---	---	AGGTAGGAAAGCAAGAGTTGATTAGTGAAGGAGAGAAATGGACCTACCTTCCACACTGTCTTTTGG
			TCCCTAGAGTCTG
			AGCACCTCTCAGCTCAAGCCTCAGCACAGATGCTGTTCTATAAGGATGACGTGCTGTTTACAA
EST71770			CATCTCTCCATGAAGAGCACAGAGAGTTATTTTCTGAAGTCCGGATCTATGACTCAGGGACAT
6	189 C G ---	---	ATAATGTACTGTGATTGTGAACAACAAGAGAAACCACTGCAGATCCAG/CJTGTTGGTGGGA
			AGGAGTGCCAGTCCCAGGGTGACACTGGACAAGAAAGAGGCCATCCAAAG
			TTCTGCATCTCTGTGGAAGTTAGAAGGAAACAGACCACAGACTGGTCCCAAAAGAAATGGAGG
ESTD-TNFab	152 A G ---	---	CAATAGGTTTGAAGGCGCATGAGGACGGGTTTCAGCCTCCAGGTCCTACACACAAATCAGTCAGTG
			GCCCAGAAGACCCCTC/GJGAATCGAGCAGGAGGATGGGAGTGTGAGGGGTATCCTTTGATG
			CTTGTTGTCCCAACTTCCAAATCCCGCCCGCGATGG
			TTCTGCATCTCTGTGGAAGTTAGAAGGAAACAGACCACAGACTGGTCCCAAAAGAAATGGAGG
ESTD-TNFa	88 A -- ---	---	CAATAGGTTTGAAGGCGCATGAGGACGGGTTTCAGCCTCCAGGTCCTACACACAAATCAGTCAGTG
			GCCCAGAAGACCCCTCAGAAATCGAGCAGGAGGATGGGAGTGTGAGGGGTATCCTTTGATGCTT
			GTGTGCCCCAACTTCCAAATCCCGCCCGCGATGG
EST52418			CAAATTACAGGGTCAACTGCTATGATGTGTTGGAGCCAGTCACCTTTGGTGGCTACAAGATGTCG
6	113 A G ---	---	GGGAGTGGCCGGAGTTGGCGAGTACGGGCTGCAGGCATACACT/GJAAGTGAAAACTGTGAGTG
			TGG
			CCCACTCTATTTGCCAGCCCCAGGGACAGAGCTGATCCTTGAACCTTAAGTTCCACATTGCCAGGA
EST13586			CCAGTGAGCAGCAACAGGGCC/GJGGGCTGGCTTATCAGCCTCCAGCCAGACCCCTGGCTGCAGA
3	89 A G ---	---	CATAAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGGAGAAAGGAGTGGCTGCTGCTGCC
			CCGGTCACTC
			AGGCAGAACTGGGGCCCCCATCGGGGGACGTGGAAGGCCACTTGAGCTTCCCTGGAGAAGGACCTGA
EST51976			GGGACAAGGTCAACTCTTCTCAGCACCTCAAGGAGAAAGAGAGCCAGGACAAG/JTCTCTCTC
7	123 A T ---	---	CCTCCCTGAGCTGGAGCAACAGCAGGAACAGCAGGAGGAGCAGCAGGAGGATGCGATGCTG
			GCCCCCTTGAGAGCTGAGCTGCCCTGGTGC
			CCACTTTGGTAGTCCAGTGTGACTCATCCACAATGATTTCTCAGTGTCTATCTGTTCTCGAGTTT
			CTCTGCCATGTTGCTATTGCAGGACGGACCTGTCCCAAGCCAGATGATTACCATTTTCCACAGTGGT
EST11458			CCC/GJTTAAAAACATTCATGAGCCAGGAGAGATACGATTCTCTGCAAGCCGGGCTATGTG
6	140 A G ---	---	TCCCGAGGAGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC

ESTD- AT3aa	60 C T	---	AGACCTCAGTTTCTCTCTGTAAAGGGAAGTTTGTCTTGGATCTCCATGGCCACAGC[C/T]AGCA CTGGTCCCTGTGAGTCTGTATCAGGTAGAGAGATGGACAGGTGGAGAGAAATTTGAAAGGGCA TTGGAATTCAGAGCAAGAGACAGATATTAGAGCTGGGAAATGTGG
EST39852 8	106 C G	---	CGGTCTCTCCAGGTATTGTTGCAGAAAGCCGAGATGACCTCTATGTCAGATGCATTCCATAAG GCATTTCTTGAGGTGAGTACACCTTCCCACCTCTCTTA[C/G]GTACAGAAAGGAGATGCATGAACA GCAGGAACACGTTGAAAAGGCCTGTTTCCAGTGTAAAGGCATGCAAAAGGCCTCCACAGGCTGCTAT AATACAGCCCT
EST62448 0	112 A G	---	ACCTGGTTGCTGGTGTGGTGAACCTGGTCTCTTGGCAATTGCCGGCCCTCCTGGGGCCCCGTGG TCCTCTGTGCTGTGGGTAGTCTGGAGTCAACGGTCTCTTA[G/T]GAAGCTGGTCGTGATGGCA ACCTGGGAACGATGGTCCCCAGGTCCGATGGTCAACCCGGACACAAGGGAGAGCGCGGTACCC TGGCAATAT
EST36027 2	120 A C	---	AGTGACTTCCAAAGAAATGGCTACCCAACTTGGCTTCATGCGCTGCTGGCCAACATATGCCTCTCAGA ACATCACCTACCACTGCAAGAACAGCATTGCATACATGGATGAGGAGACTGG[A/C]AACCTGAAAA AGGCTGTCAATCTACAGGGCTCTAATGATGTTGAACCTTGTGCTGAGGGCAACAGAGGTTCACTTAC ACTGTTCTTGTAGATGGCTGCTCTAAAAAGACAAATGAATGGGGAAGACAA
ESTD- COL2A1cc	112 A G	---	AGAATGATATAGTCTCAAACTGGCCATCTCCATTTTCAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTATGCTCTCTTCTCTGTCACCTT[C/A/G]GGGTGTTCAAGGTGAAAA GGTGAACAGGGTCCCGTGGTCTCCAGGCTTCCAGGTAAGTCAACTCAAGCATATACAATACTGCCT TTGGTCAGCCTATTGAGCTGTAATCACCATACCGTACCT
ESTD- COL2A1dd	97 C T	---	TGAGAGAACACCTAGTCTCCATCCTTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGCTGGACCTGGAACA[C/T]TGGACTTCTTCTACTGCAGCAGACAAGACTTA CCCAAGAGAGATTAAATGGCAAGATATACAATACAAATTTTATTGACCAAAACACTATCATGGAACA GCATT
ESTD- CPT2	150 A G	---	GCCGCAATGCCGGGAGTTTCTCCAATGTGTGAGAAGGCCCTTAGAAGACATGTTTGATGCCTTAGAA GGCAAAATCCATCAAAAGTTAACTTCTGGGCAAGTGAAGAGCTACCATCACTTCTCATCATGAAAAAC TGGGAGGCCGGGCAT[A/G]GTGCTCATGCTGCTGTAATCCAGCATTTTGTAGAGGCTGAGCGGGTGGAT CACTTGAGGTGAGGAGTTTGAGACCAACCTGGCCCAACAT
EST12274 0	135 A G	---	CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTCTTGCTTCCAAATAGAGCCTTACCAAAGTGAT TACATAAAGAAAGTCAAGTGTTTACTCTCTCATGACCAAAATATCTTCCCTCCTTAGGATGAGGTG[ A/G]TAGTAAATGACCGATGGGGTCAGAACTGTCTGTCCCATGGAGGATACTATAACTGTGAAGA TAAATCAAGCCACAGAGCTTGCCAGATC
EST76807	91 G	---	ATGCTAAGGGGATCGGACATGAAGGACCTGTGAGCCGATTGTCTATCTCCAGCGGCCCTGTCTATC CAGCTCACTCATCAATGGGGCCAGTCAGGCCAGGCACTGGGCTCCGGAGGACTCACCACTGCCCT GCTGCACTGTGAGCTGGTGCAAGTTGAGGACTTCTTG

ESTD-SSA1	111 C T ---	---	TTCACTTTGTGGATTGTTCTTTTGTGTGCAAGCACCTTTTCAACATGATGTGATCCCATTTGTCCAAGTTTGCTTTGGCTGCCTGTGCTTGTGGGATATTGAAGAGATGCTTTTGGCAGTCCAATGTCCTAGA GAGTTTTCCCAATGTTTTCTTGTAAATAGTTTTCATAGTTGAGGCCTTAGATTTAAGTCTTTAATCCATT TTGATTTGATTTCTGTA
ESTD-RYR1	109 A G ---	---	CTTGACGGGAGGTACGTCCTCCGCCCTCTTCATGGACATATGGATGATGTGTGACCATTTCCCT CTGCTGACAGTGATGACACGCGCAGACTTGTCTACTATAGAGAGGGGAGCTGTGTGCACTCATGCCC CGTCCCTCTGAGGCTGGAGCCACTGAGATCAGCTGGAGTGGAGCCACCTGCGCTGGGGCCAGCC ACTCCGAGTCCGGCATGTCACTACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD-WT1	70 A G ---	---	AAGACCTACGTGAATGTTACATGTGCTTAAAGCCTCCCTTCTCTTACTCTCTGCCTGCAGGATGTG CGIAGTCGTGCTGAGTAGGCCCGACTCTTGTACGGTGGCATCTGAGACCAGTGAGAAACGCC CTTCATGTGTGCTTACCCAGGCTGCAA
ESTD-F2 EST44438 7	100 C ---	---	GATAAGTACACTGAGGCCCCAGGAGGTTATTGCTAGTAGCCCCAACTGTGCATGCACGCTTAACCTCT GCACCAATGGCTCCAAAGGCCCGTAGGGAACTGGGGGATCTAGGGATGGGTGAGGAATGGCCC AGCCAGTCCCGCGGCTGCTGGTCCCAACAGAGGAGGCCGTGGAGGAGACAGAGGATGGGC TGGATGAG
ESTD-PBDA	103 A G ---	---	GCAGCCAGGAGCCGCTGCACCATGCCCCGATAGATCGGACCTCAAGCTCGACTTCAAGGA[C/T]G TCCTGCTCGACCTAAGCGGAGCAGCTCAAGAGCCGAGCCGAGGTGGG
EST12839 3	122 A G ---	---	CCCTCTATGCCAGATGGAATTCAGTCCCTTCCAGTCTCAGGATCGCCTAACCTGTGACAGTCAAGAGT CTGAGCCGTGGCTGGGAAGGGCAGGACTAATCCAA[AG/TC]CTCTACCCGAGCTTGTGCGCATACAG ACGGACAGTGTGGTGGCAACATTGAAAGCCTCGTACC
ESTD-CTLA-4	48 A G ---	---	TGCAAAACACACAAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCTCTTTGCT CCTAACATCTATGTACTGGATTATCTAAATGAACACACAGCAGCTTACTCCAGAG[AG/TC]CAAGTCCA AGGCCATTGGCTATCTCAACACTGGTGAATGATTACTTGAAGGAAACCTTGAATGTTATTCAAC TGGATTTCCAGTAGGTTTCAGTTACTTATGAATATTATGATACTTAGCTTAG
ESTD-ACE	96 C T ---	---	ATGGCTTGCCTTGGATTTACGGGCGCACAAAGGCTCAGCTGAACCTGGCT[AG/CC]AGGACCTGGCCCTG CACTCTCCTGTTTTTCTCTCTTCATCCCTGTCTTCTGCAAGCAATGCACGTGGCCAGCCTGCTGT GGTACTGGCCAGCAGCCGAGGCATCGCCAGCTTGTGTGTGAGTATGCTATCTCCAGGCAAGCCAC
EST54419 8	88 A G ---	---	GATCAAGCAGTGCACACGGGTACAGTGGACCAGCTCTCCACAGTGCACCATGAGATGGGCCATATA CAGTACTACCTGAGTACAGGATCTGCGC[CT/GT]CTCCCTCGCTGGGGGGCCAAACCCGGCTTCCA TGAGGCCATTGGGACGTGCTGGCGCTCTCGGTCTCCACTCTGAACATCTGCACAAAATCGGCCTGC CTTCTGCCTAATTTGAATGATATTGTGCTGTGGGACCTGAGCCTTTTATGGCACAATGATCACTA TTTTCTTGACCCCTACTTAC[AG/AT]CCTGGGAGATGTTATTTGGGTTTAGCGTGTGCTATGTTGTCTA CTATAGTCCAAGTGAA

ESTD-PS-1	99 A G ---	---	GGGAGTAAACCTTGGATTGGGAGATTTCATTTTCTACAGTGTCTGGTTGGTAAAGCCCTCAGCAACA GCCAGTGGAGACTGGAACACACCACTAGCCCTA/GJTTCGTAGCCATAATTAATGGTTTGTGCCTTAC ATTACTACTCTTGCCATTTTCAAGAAAGCATTGCCAGCTCTCCAATCTCCATCACCCTTGGGCTTGT TTTCTACTTTGCCACAGATTATCTTGTA
ESTD-B3AR	104 C T ---	---	GGCTCCAGGGTTCCGTGGAGGGGCCCTAGCCGGGGCCCTGCTGGCGCTGGCGGTCTGGCCACC GTGGGAGGAACCTGCTGGTCACTGTGGCCATGCCCTGAGACTCCGAGACTCCAGACCATTGACCAA CGTGTTCGTGACTTCGTGGCCGAGCCGACCTGGTGATGGGACTCCTGGTGGCGCGCGGGGCCA CCTTGGGCG
WI-567b	48 A G ---	---	TCACACACTGACCCCTTACCTTCATCCTCACCTGCTGCTGCCCTGGTTC/GJAGCCCTCATCTCTTTTA CAGGGATCCGCCACAGCATCCCAACTGATCTGGCCTTAGGCTCTCTCCCAATCCATTCTTCAAAAG GCTGCCACTGTGATCTTCCCAAGGTGATCTGATGCTACCATCTTGCTTCAAGCC
WI-801c	58 GT ---	---	ATGGAACATTTCTCCATAATGAATGAGGTCTCAATCCATTACACATCCCCCTTCTG/JTAGATGG TATTGGAGAAGTAGACAGAGAAGAAATTAAGTAGGCAATGCATGTTTGCAGGGGTGGGGCTGTGC ATCTGTGATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCCCACCAGAGAGTTAA CATTCTGCCACCCCTC
WI-801b	58 GT ---	---	ATGGAACATTTCTCCATAATGAATGAGGTCTCAATCCATTACACATCCCCCTTCTG/JTAGATGG TATTGGAGAAGTAGACAGAGAAGAAATTAAGTAGGCAATGCATGTTTGCAGGGGTGGGGCTGTGC ATCTGTGATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCCCACCAGAGAGTTAA CATTCTGCCACCCCTC
WI-1099b	76 A G ---	---	GAAATTCACCTATACAAGAACATTTTCTCTAATTAATTTACATTAGTCTCATTATTCTGAAATATTAT TTTTTACA/GJTACCCCTTGATTATTTTGTATTCAATTTGTACGAGAGATTACAATATCAGTAACGC TGTTCAATGATAGTGTATCACAAATGTCTAAATACATTTTGGGTCAACATCAAAATTAGAAAGAAA CTTACAAAGTTTATTGTCTTATGTTTA
WI-2529	71 C T ---	---	AGGAAATGGCTGATCTCCTGGTGGCTTATTATAGTAAAGGAGATGTAATGCTTGATGAGCCTCT CAA/CJTTCCTTAAGTGTGCTGCTCAGTCAGTGAACATTTAATGAAGTCTACACAAATTAATTAGTGT AAGTTGTAATGCTGAATAAGCTTGAATAAAGTGAAGAGGTAAAGAGGAGACAACTGTGCTTT TTAAGAAATAGAAGATCATTCTTAGAATGGCTTTGGGGATGACAAGTA
WI-10088	205 C G ---	---	TAAGGGCTGTCTTCCCCAGAGGCCCCACGGGACAGAGAAGCATCTTGATACCCAGGGCCACAAA TGAGCAATCCATAGATACATACATATAAGAGAGACCTGTACCCTATGAGGTAACTGAGGATGAAGGA GTGAGTCATATTGGGTGGCAATTAATGACCCAGCCTCTCTCTCAAGAAGACTTTTACATTTTAGAC AGG/C/GJAGCAGAAAGCAGCAAGGAGAGAAAGGAAGT

WI-2625	98	G A	---				GGCAGTCCTGGCTAGTGGTAGACAGCACTGAAGGATGGAGGAAGAGAGAAACAGGCAGAA GCACTGTGGTAGTTAACAAAGGCTATTTAGGA[G/A]CAAAATGATGATACCTCCCTGAGGACTCGCAG AAATTACCAGCAGTGGACAGGGTTATCTGTGGTGAATTCAGTTATCCACTTGCAGGAGGAAAGCCA GCCAGCAAAG
WI-2924	54	G A	TAGG	GTCTCTCTTA	GCCTAAGTGT	AATCAGAGG	TCTGTTGTCATATTTCCCTCTTTGACTCTGACCTTCTCTTAGTCTTCTTATAGG[G/A]ACCTCTGTGATT ACACTTAGGGCTACCTGGATTATTTAGAACAAATC
WI-2939	72	G T	GTGCCTTT	GGCTTGCTCA	CTTGTTGAGGG	AAGGCTTG	CCATTGTTGAGTTGGTGGGTCACCTTGTCAATCCCTCGCACTCAACAAAGTGGCTTGCTCAGTGC CTTT[G/T]CAAGACCTTCCCTCAACAAGAATGTCTTCCATGCTCCCGTGTCTTTGAAAAATTCGACT TTATCCTGAAAAACICAGCTGCAGTGTATCTCCGGTATAAAGCCACTCCTG
WI-3203	99	G A	AGACGAG	GGTTATGCCGC	TCAAGTATTGC	CTTGTTGG	CTTGCTACATGCATTTACAGCATACAACTCAGTGAATGCCGTAAACCCCATTTATAAACAT CTTGCCATCGAAGGGTTATGCCGACAGCAG[G/A]CCACACAAGGCAATACTTGAAGTGACTTGGA GAATAAAGATTTGGATGGATGAAAGCAGAGGAGATGCTAAAAGTGA
WI-3473	101	A G	GCCTAGGGA	AAGCATTTTA	CCTGATGTCAC	CAACATTTCT	GGAAAAAGAAACCTGAAGGATGAGTAGAAGTTAATTGGGAGATAGTTGGTATAGGCCCTGTTTGGGA GATTGCAGAGAAGGAAGCATTTTAGCCCTAGGGA[G/T]AGAAAAATGTTGGTGACATCAGGGCT ACACACTTTTCTGTATGCTCTTCATCAAA[G/T]GCAGGCGTCATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATTTGCTGGCTCCCC
WI-1796b	29	A G	---		---		ACACACTTTTCTGTATGCTCTTCATCAAA[G/T]GCAGGCGTCATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATTTGCTGGCTCCCC
WI-1796	29	A G	---		---		AGTCGTCCATCTTCAGGGTCTAACTCTGGATCTGGCCTGCAGAGTAGGAAAGAAAGATGGGGTGAGT AGTCACATTAGGTATTTCCAAATAA[C/T]AAATGCCCTCTGAAAAATATCTCTCCCATGTCCCTGTCT TAAATATAACATTTTCCC
WI-4360	93	C T	AAATAA	GTAGTCACATT	GAGAGATATTT	TTT	GCTGAGCTTTTGGCAGAGCCAGGACAATTCAGCTGCCGATTTTAAATAGATTCTGCAGCACTGCAA CAGGAACCAAAAATCAGTC[C/T]GGGTAACCTGAGAGTGGTTTTCACACCCAAA
WI-1959b	87	C T	---		---		GTTGTGCTGTAGCAGACACAGAAAGGCA[G/A]GAGAGAAAAAGCCTTTTTGGTCCAGGGGCTTACAC TGAATCCCTCAAAACAATGCAAGATGAGCTAATGGTCTTAGAGGTATAATCTAAGTGTGAGAAAAACA AAGGTATAGGGTTTG
WI-1973b	28	A G	---		---		CTTGAGTATGCGTGGATTTGGTATACACAGAATGGGAGAGCTGGAACATAATCCCCCATATACCA AGGGACAAAATTGTATCTGTTCTACAATTATACAGTAGGAGACATTATGTTCCATGACAAATGGTAAT TTTTAA[C/T]GACAGTTTTTAATTGAGTGAAATTACCATAAAAAATAATAATAGTAGCAGCTAATTT TACTGAGCTGTTACTAGGTGGCTATAAATAGC
WI-1980b	140	C T	---		---		



WI-2015b	190 A G ---				TGTCAGATAGTCGGTCTCTACCTAGGTGCAGTAGCATGCTAGGAGCTATTAAAGTACACAAATTATGCT ATATATTTATACAATATACAATTACTTTGCAGATAGCATGACCATGCTAGTGAACCCCAAGACTAT GTGTGAATCGTCTATTAGGGTTTGCTATAAACTCTACATGGTGTCTTTTCCAACCTA/GCATATACTT CTAATACCATAGAG
WI-754b	49 C T ---				GAAGGCACAGGGAAGATGGCTGTCACTACCAGCCAGGAGAGAGAGC/TJACATTTATTGGTAA TCCTATAAGTGCACTCTTAAATTTGTTACTTTAGA
WI-754	22 T C ---				GAAGGCACAGGGAAGATGGCT/CJGTCACTACCAGCCAGGAGAGAGAGCCACATTTATTGGTAA TCCTATAAGTGCACTCTTAAATTTGTTACTTTAGA
WIR-1b	56 A G ---				AGGCAATCAGACCTACAGAAAGGAACCCCAATAAACTCTGATGATCGTACATCC/A/GTJGGCTG GAGGGTGATGCTCTCTGAGGACATGGAGCTTCATGTTGGAGCCCTCCCTG
WIR-1	56 A G ---				AGGCAATCAGACCTACAGAAAGGAACCCCAATAAACTCTGATGATCGTACATCC/A/GTJGGCTG GAGGGTGATGCTCTCTGAGGACATGGAGCTTCATGTTGGAGCCCTCCCTG
WIR-3b	72 A G ---				TAATTTAAATGGGGCCAATAACACAGTACTTATCTCACAGCATTTCTTAAAGGCTAAATAAGAA GAAGT/A/GTJCTAAAGTTATTAGCTCAGAGCCTCACACATTCAGTGACTGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-3a	69 A T ---				TAATTTAAATGGGGCCAATAACACAGTACTTATCTCACAGCATTTCTTAAAGGCTAAATAAGAA GA/TJGTATCTAAAGTTATTAGCTCAGAGCCTCACACATTCAGTGACTGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-4	47 T ---				GAGCCTTTCTAAAAATAAGGATTGTGACTAGCAACCTCCTGTACAGATCCCTGCTCACACATGTGCA AGGCAGCAGCAAAATTTGCCAGCTGCC
WIR-5g	209 C ---				CGGCACAGAGAGACAGAGAGAGAGATTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5f	196 C ---				CGGCACAGAGAGACAGAGAGAGATTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5e	194 C ---				CGGCACAGAGACAGAGAGAGATTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG

WIR-5d	191 A	---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTACAAAGAGGTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAAACACCCAGCTGCAGCCAGAGCCTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGTTAAAAAAGACACAGAGAGTGGTGGCTCTATGGAACACACAGG TTTTACGTCAG
WIR-5e	177 C	---	---	CGGGACAGAGACAGAGAGAGTTCTGCAGCATTACAAAGAGGTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAAACACCCAGCTGCAGCCAGAGCCTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGTTAAAAAAGACACAGAGAGTGGTGGCTCTATGGAACACACAGG TTTTACGTCAG
WIR-5b	159 A	---	---	CGGGACAGAGACAGAGAGAGTTCTGCAGCATTACAAAGAGGTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAAACACCCAGCTGCAGCCAGAGCCTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGTTAAAAAAGACACAGAGAGTGGTGGCTCTATGGAACACACAGG TTTTACGTCAG
WIR-5a	37 A	G	---	CGGGACAGAGACAGAGAGAGTTCTGCAGCATTACAAAGAGGTATTAGGACTCAGTTCTGCTG CTGTGAGNCATCCACACTGGAGGATGAGAAACACCCAGCTGCAGCCAGAGCCTGGTCCCACTGTT AGGTTTGAAGGGAAGGCAAGGTTAAAAAAGACACAGAGAGTGGTGGCTCTATGGAACACAC AGGTTTACGTCAG
WIR-6	63 A	C	---	TAACCCCTGAAACTTTGTCTCCTCATCTCAGGGAGAACACAGACTTCATGTTAAGACCCAGAA[AVC] CGCAGCTCTGGGGTGGGGCAG
WIR-7	12 C	T	---	TTGCTGACTATT[C/T]AAGCATCTGTAGAATATTGAATACATAGICTTGAGATTGATC
WIR-8	46 C	T	---	GGCGTCTCTATGACTATCCTGGTCATTGATTGACTAATGATTCCTG[C/T]GCCCTTG
WIR-2	56 C	G	---	AAACAGAAAAATAGAGGTTATAAGGATGGAACATAAAAGTTGTGAGAAAGGATGA[C/G]CTGAAG AAAGAAATTACTCTCTTTGACCAATAAATACAATTGGGAAACACTGGAAACCATGGCTTGATTACT GACAAAC
WI-7069	93 G	A	---	TGTCCTTGCTTATGCCTGCTCTTTCCGCTTGGCAGGATGCTGCTAGTATTTCACAAGAAAGTA GCCTTCAGAGGGTAACCTTAACAGAGT[G/A]TCAGATCTATCTTGCAATCCCAACGTTTACATAAAA TAAGAGATCCTTTAGTGCACCCAGTGACTGACATTAGCAGCATCTTTAACACAGCCGTGTGTTCAAAT GTACAGTGGTCCCTTTTCAGAGTTGGACTCTAGACTCACCCTGTTCTCACTC
WI-18694	41 A	T	---	GGTCATTTCTTTTATCTGTCAGGCAGCCAGCTCTGACTTTA/TCTCTCTGTTTCTGTCATCTCTCCC CCACATACCAACTCTTCCACCATGATGATTATACCAATAATACAGTTCCCTTATATGAGGGGCTCTGGA AAATTAGACAGTGAAG
WI-18612	37 A	G	TGC	CACACTGTTACACACCTATATTTCAAGTTTGGAAATGC[A/G]TATTTGCAAGCAGCAATACAAAAGTA TTCATGAAGAAATGCATAATCTCTGAAAAATTATGAAAACATCCCT

WI-18517	87	C T	CAGCCTGA	CAGGAATCAG	TGTTTGACAA GTGCAACA	TAAATAAACAAGGGCTACCCCTCAACACCCCTCCATTGTCAACCTCTACAGCCTGCATGCC ACAGGAATCAGCAGCCGACGCTGTGTGACCTGTCCAAACACAACTGACTGC
WI-18668	76	C T	TAGGCAAAA GC	GGCGAAAAAC	GC TAAAT TAAA CTGCAC TTTT	CGATTGACAAACCTTTTATTTTCAACTTAGGTAACTAGTCCAAATCAGTGTAGATTGGCGAAAAACT AGGCAAAAACGCTAGGCAAAAAGTGCAGTTTAAATTTAGCAAGGCTCAAGACAGTATGTGGAAAGGAA GGTGAGATTTCCTCTACT
WI-18680	75	T C A	AGCATCTGGA	AGCATCTGGA	CCTCCTGAATA TACAACGGAGC	TAAACATACGAGTACTGTACACGCAAGCATGCATCCCTGAGTCTGAGTGAGGCTGTCACTCTAGC ATCTGGAATTCGCTCCGTTGTATATTCAGGAGGGA
WI-18704	99	A C	GGGTCTCGA	GGGTCTCGA	TGAAGCCCTG CTGG	CACCCAGGCTGTACCCAGGCTTTCTGTGCGAGCACACCAAGGGCAGGTTGGGCTTGAAGGAGCC CTTGAGGAAACACGGGTCTCCGAGGGGTACAC/C/CAGCAGGGCTTCAGCTTAAAGTCG
WI-18673	29	A G	---	---	---	TGTGGCAAAACCTTGTTTAAATTGCAAAAC/A/GIACCTTAAATTTACAGCACATTCAATAATGAACCAAC AGGAGAGTTGCTGACTTTGTAAACATATGAATATATAAAATCCCTTGCAATTCAGGTAGTCAAGGTA AAAAGCGCATACAAGGAAG
WI-18640	121	T C	GCGG	GCGG	GCAAATACCAC TGAAGAGGAC	ACCAGTCATGTTTATTTGGAGGTTAATTCCTATTAGGATATGAAAGGATTTCAGCAACGATTGAGATT GTGTTCTCACGGAGGGCTCGGGCCAAGGTCGTGGGGTGGGGGTGCAGAGTC/C/GTGTCTCTTC
WI-18533b	91	T C	---	---	---	AGTGGATTTCGGGACC GGGAGAGGAGGTAGATTGCCAAATTGAGGCCATTTTTTAACTCCCGAGATTTCTCTTTATTT TATATTTTCATTTTCATCCTAAATTC/TACTGAGCCATTTCTTTGGTTAACTTTAGA
WI-18533a	59	T G	---	---	---	GGGAGAGGAGGTAGATTGCCAAATTGAGGCCATTTTTTAACTCCCGAGATTTCTCTTTATTT TATATTTTCATTTTCATCCTAAATTC/TACTGAGCCATTTCTTTGGTTAACTTTAGA
D11734	83	A C	TTC	TTC	AACCAGGATA AGGCTACAAGT ATTT	GAGCATATGCTGCATGAGGACCTTTCTATCTTACATTATGGCTGGGAATCTTACTCTTTCTATGATA CCTGTTCAGATTTTC/A/C/AAATAGTTGTAGCCTTATCCTGTTTACAGATGTGAAACTTT
D49493	159	A T	TCTGGGAATT	CCTGAAGGAA	ACTTTCAGGCC AGGC	CAGGACTTGTTGGTGCAGTCGACACACAGAGCACAGCTCATGGGCAACATCAGTGGGGCCAGAGAG AGCTGCCGCCAGTGCATCATAGGGGCTTTTCATGCTAGTACTAGCCCTTAAATGCCAGCCTG AGTACCTGAAGGAATCTGGGAATTT/AT/GCCCTGGCCTGAAAGTGGCCCATCATACCCACTGTT CT
EST10030	98	T C	TCTCAAGTCCC	CATTTTGTTC	GCAGTGGTGGT ATGGATGA	TATTTTCATAGAGGAGACCTAGGAGGAGTTGACACAGCACACTGCTCAGCAGATGACTTAAATTTT CCTTAGCCATTTTGTCTCTCAAGTCCCCTTC/TTCATCCATACCACCACTGCTGATTG
EST10052	24	G A	GAGGCTG	GCTCACTCTG	TGTGGAACCTC AATCTTAGACT TC	TATTTGGCTCACTTCTGGAGGCTG/A/GAAGTCTAAGATTGAGGTTCCACATCTTGTGAGGGCTTC CTGTTGAGTCAATCAACCTGGTGGAGTTCATCATGTGGCAAGAGAGAGGGCTACAGAGCAAGAGGAA A

EST10605 2	118 C G ---	CTCTCAAGTAG ATAAGAGGCA TAATCT	---	GCTAAATTTTC AGAAAGAATT TTGTTT	CTTGGTAAATCACAGTTCTGTATTATACAAAAACTTTGTTTTCTCTGACAAACTGTACACATAGA AACAAATTTCCAAATGGACAGGAACTTAAATTTGTGGAGATGCCCATGT[C/G]TTGTGAGACTTAA AAAAAGAAAAAGATCCC
EST11048 0	61 T G	TAATCT			CATGTGTCATCCCATGATTGAAAAAGACATGTTGCTCTCAAGTAGATAAGAGGCATAATCT[T/G]AA ACAAAATCTTTCTGAAAATTTAGCTTATGAACCTCATTACACTGCAAAACCAGAGAGAGGCAC
EST11260 8	101 G T ---			---	TATGGAGGCCAGAGGAAGTGACACTATATGTGGAAAGTGCTGAAAAGAAATGAAGTGTC AACACAAAA TTCTATATCCAGCTAAATATCATTTAAGAAATGAAG[G/T]GGAAATGAAGGCAATATCAGATAAA
EST11349 9	109 C T ---			---	TTGATGGAGAAATCCGAGGCTGCCAGCATCCCAAGTAGATTCTTTGGACGAAGAAATCTCT TCTGTGGATTACAGCTTTACCGCTTTCCCTCATCTGCTGGT[G/C]TTTCCTCAGAGCTTTAATGTCCGT CCTGCTCCGAGTCAG
WI- 16632a	71 A G	CCAACTACTT TGGAGCCT		TCCAGCTTTCT CTAAAACTCC T	GAATCTGGGTATTAAATAGCGGGTGCCACAGGAGCACATAGGAAGAGCATCCAACCTACTTTGGAG CCCT[A/G]AGGAGTTTTTAGAGAAAGCTGGAGCCGGAAGACCATAGTAGGAGGTAGCCAGACCAA AAGGGAGGAAGGAGTGGAA
EST11772 6	74 A G ---			---	CCAGGAATAAAAGAAAAAGAGTCAGAGGAAACAGTCTTTGATGTTATGAGGCTGAGACACTACTC TTCTTCA[A/G]GACTATTTCATTCTGACTATAAGTGAATAAATACATTGAAGACTTCAGGAGCTCA
EST11795 3	82 G A ---			---	CTGTCCATTATTTTGTGCATGTTGTTCTTAAAGGCTGTGAAAAGATAACTTGGAAATGTGGGAAAC ACATAGATCCCAGA[G/A]TATTAAAGGGGCTGAAAAGTAGCCTTAAGAC
WI-16644	42 G A TAC	CAATAAGCAG CTCATTTTGAT	ACTTCATGAAT TTTACTTTCATG TATACC		AGAGCAATGGTGCATCTCAATAAGCAGCTCATTTTGATTAC[G/A]GGTATACATGAAGTAAATTC ATGAAGTAAATTCATTATATACAAAAGCCTCCACAGAACTTCATGCACCCTGAGCTATGTGAAC TGAAAAGTAAACAGTGGAT
EST12005 9	56 A G	TTGTATAATA ACACTCAGTA CAAAAGTCTGT	GGCTGGTCACT TCTGGAT		GCCTAGTAATTTCCAAAAGGAACATGTTTGTAATAACACTCAGTACAAAGTCTG[A/G]ATCCAGG AAGTGACCAGCCCGACGTGTGCTATGACCCCTCTGAACCTCCCATTTCCATAGTTTTTGAATC
EST12055 9	32 T C ---		---		GTGGAAAAATTTTTTATCTGTAGCTTTCC[T/C]ATTATATTATCTTGTCTTGAATTCAGCACCC CACCCGATTTGCAGGCAGTCTTTCTTAAACTGTGCCCTGTGAGCTGTTAAAAAGTCTCT
EST12492 1b	95 A G ---				CCCTAGCAAAATGACTTGGAGTTGTGTCCAATTACCAAGTTACATACTGTGCCAAAATTAAGCTCTC TTCCCCAGAGGCATTAACTGAGATTAT[A/G]GGAAACGCACAGCAAAAATTGACGATGCAGCTTTTAA CCTTTTTA
EST12492 4	25 A G ---			---	ATCTTGAGGTTTCTGGCCTGTCAG[A/G]AAGTGACATCTTTTACTTACCAGGTCAGGAACCCCTAT AAAGAAACTGTGTAGAAAAAGATATCAGGTACAGACTTTTTAAAGGGCTCTTATCAGCTCAATAAA

EST12502 2	52 C G ---			ATACTAGGGAGAAAAACCAACTGGAGGCAAGTCCACAGGTCACACTTGTCAIC/G/CAGCAAGTAT AAACAAAGTGGGTTTCGATGAAGAGAAAAATGCTACGGGGAAATGACCAATTTTAAGGGCCATGTG GTGTCGAGGCAGTTAGAGG
EST12619 8	105 T C ---			CCAGAGAAAAATTAGAATGTATCGGTAAAAAGAAATAGGAATGCATATTTCAACTCACTGTACAAA CAGGTGTTTTATTATCCCAATGACAGTGTTCCTGAGAT/C/GATGCATGTGGCAGACGAG
EST12620 0	67 A G ---			TTTTCTCTCTCTCATTATTCAATTTGTTCAAAACACTGTCTAGTACCAACATTGTCCACCGGC/A /GTTGAGAATACAATATTGAAGAAGAGTCACIGCCCTGCCCTCTGGAAAAATCAGAGTATTGA
EST12817 9a	22 C A ---			TGGGGTTCTCCAGGATTCCAG/C/CTCGTAGCTGATGTGCATGAGGTTCTCATCCATGCTCCACGG GTCTTGGGAGTGACCGGATGGGAATCCATGTTCCTTGGTACTCCATCAGGTCATTGCG
EST12941 8	23 T A ---			TCTCAGCTTCCACCTGACCTGCA/T/A/CAACAGCCCCAGTTATTTACCAGAAATTTGTTGCGTTTCA ATGATGTTTAGCTTTAATACACTGCACCTGTTTG
EST12949 2a	52 A G A T A C T G T T	GGCTTTAATCA TAACCTAATA	TGTTGCTCTGT GGGTCTC	AGGATTCATGAGGCTTTAATCATAACCTAATAATCTGTTAAAAACAACAC/A/GTCTGTCACTTG CAGAGACCCACAGGACACACATCTCTCTCCTCCTCAGACTCTGAGGTAGGAGGTACACTGGCT AAGGAATAA
EST13067 4	104 C T ---			ATTTTTGTTTCTTAAATGAAGCATAATAAACAGTTAAATCTCAGAAAAATCATCTATAGTTGA GTGTAAACTCCCTAAATCAGTCTTCTAGGGCCACA/C/TGGAGCAGAAAGCAGCTCCACCCCAAG CACTCTGAAC
EST13117 6	66 A G ---			TGCTGTCTGCATCAGTCCCTTTAAAAATTTAATCGCTTTATACAAATTGACACCAATAAATGCAC/A /GJTATTTAAAGTTTACAATTTGAGAAGCTGACACGTGTCCATACAGACACACCTCATTTTACTGTGC TTTACTG
EST13121 6	44 C T ---			TCTGCTTTAAAGATTCTTCATAGCTGCTTAGGTTTGTCTTCC/C/TAAGCATAATCAGCTATAATCA CCTAGATCCCTCCACAAATATTCTGTGTGTGCGCAGGCCAGTCTCCTCACTGTCCCATGAATAGCC AGTCTATTCTCCACTCT
EST13226 6	74 T G ---			AACTGTTTACTAACAAAGGTGCTTTAATTTGAAAAGCATTTGAGGAAATAAATTAATGAAATAGTCT GGCCATT/T/G/GACTAACAGTTCTACAAATTTACATATCCGTCACTCAGATGAGCATATACCAAG TCAGAGGAAACAAAACATG
EST13230 6	72 G A A G A C G C	GCTCAGATGTG ACAGAGC	CCGGCTCCTGT ACAGAGA	GCATCATCAGCGGCTTTTACTGAACCTTACAACCAACTTCCGCTCAATATGAGGCTCAGATGTGAGAG ACGC/G/ATCTCTGTACAGGAGCGGTACTGTCTTCAATCCTTTGCATGCAGGTGTTTACCACAGGCA AACAGTTTACTCCACAT
EST13236 9a	70 T C T C A G G C C T	AACAGAGGTT TGACAAAAGA	G	AAAGATATAAAACAACCTCCCATCAGTAGCAATACAGGTTATACATTTTAACCAGATTTTCTCAGG CCTT/C/TTTTGGATACCTTTAGTAGTTAACTCTCTTTTGTCAAAACCCTCTTGTATATAACCA

EST13278 2a	51 A G G	CTTTCACCGAA CAATATTTTAG G	CATATCTTGG GTGGTGAGAA	TTTCGAGAACGTTTACAAGCTCCAAACCTTTTCACCGAACAAATATTTTAGG[A/G]ATTTGAAATTTAT TTCTGTAGTTCTCACCAACCAAGATATGACAGCTTG
EST13282 0	99 A T	CCACACATTTTC AGTCCAAGA	GATGGAAAATT TGAGGAAGGTT	GCTCACTAGATGAGCATTGACCAAATATTTAGATAATACCTGTGGGAAAGTGCTGAATTTACTAGCC TGCCTGAGAATCCACACATTTTCAGTCCAAAG[A/T]AACCTTCCCTCAAAATTTTCCATCTCCCATCAGA GG
EST13290 9		CAATTTTTAGA AGTTGGGTTT	AAATCAGCTTCA TGGAAATTTCA	AGCTCATCTGCAAGCAATTTTGAAGTTTGGGTTCTT[A/G]CTGAAATTTCCATGAAGTGATTTTTT TTTTCTGTGCTTAACCTTCACTTAAAGACCTAAAGACAAAGTGATATCACATACATATTTTTGT ATGTGGGGCTTTTTTG
EST13518 2	45 C G		---	GAAACATCCTCCAGTAGTATTGAGGTTAAATGATTCAGCATT[A/C]GACITTTAAAAATTACCTCA ATGTTCTCGGAGTGGTCCATAGTTTAAATGACTTCTGCACCTTCTTTAACTTGATTG
EST13522 8a	66 A G		---	CAGGTTGGTGATTTCAACTAGGAGCTATTTTGCCCCCATCCCCCAGCGCAGTGCTGGAGAC[A/ G]GTTTTGATTGTCAACAACCTGCGAGAGGTGGTGCTACTGGAATCACTGGGTAGAGGCCA
EST13568 6	69 T C		---	CTTTAAGGAAGTGAGCCAGATGAATCCCAATGACCAACCTGGTTGAGAGCCATTGGTCTAGGAGTAGA AA[T/C]GCACACAAGGAATAAGGAGAAAGGAGGTTGCGTTAGTTGAGGGAGAGAAAGTTGGAAGCA TTTCAAGCTAAGTAAATGGT
EST13785 0	101 C G		---	AAGATTACGGACCAATAAGAACTGCCCCCGACCCATACACACAAATTTATAGCAGGTAAAAACCAA CTGAAAGGAACAAAGTAATGACTTCTTGAACAA[A/C]GTTGATTACGAAAGTGAAAGGCTACAGGG TGATTACTA
EST14038 1	25 A G		---	CCTCAACCATCTGTAACCCGAGCC[A/G]CAGTGACCGGAGCTTGTCTTCCCATCCAGCCCTCT CCTATCAGCATCCGCTAAGCGTCAGTCAGCAGGTG
EST14083 7	23 A G		---	CAATGGTGTCATGTGAACATAT[A/G]ACCTATTATCAAAAGTTAAAAATATCCCTTCTTGCAATCA CAGTGCAAAAGGCATGAGGGTGAAAGTCATCTGCTAAATGACCGAACAGGAGGTAGGAGG
EST14221 5	42 T C	GCATGCTAGA CAGAGGCATT	GGAACAAGTC AAAAATATTTT AAAAGA	AAATCAATGCATTCTTGTGGCATGCTAGACAGAGGCATT[A/T]CTTTTGAAGATCTTTTAAAAAT ATTTTGACTTGTCCCCCTTCACACTCATTTTTAAATTGT
EST14812 2	50 A G	CAAGTCAGCTT CTACATTCTGA ATA	TAAAGATTAC TTAAATCCCAT TATGTACT	TTCCACTTAGTACCAAGGATGCCCTTCAAGTCAGCTTCTACATTCTGAATA[A/G]AGTACATAATGGG ATTTAAGTAAATCTTTAGAAGTCCCGGAGTTTGCCCTTTTCTAACATTTTCATATCAGGTGAAAAACAAT TTTTTCATATGGGTGATT
EST14815 3	128 A T	CATCACCCAC ATACTGGTT	CGGGAACA GTACCGGAA	TTTGCTCGGCAATACATAGTGGCAATGCAGCGTGAGTTCGGCCGCTCCCCACTGAACCCAGTAAT TCACCAGACAATGGCGCACCACTTAAATAAATGCCCCGTATCACCCACCATCTGGTT[A/T]TTCC GGTACTGTTTCCCGTA

EST15420 6	109 C A ---	---	---	TTTAAACCCCAAGACTGTAGATGTCAGGACTCCGATCATTTTCTCGCCTATAGCTTGGATATCTTA ATCTCTCCCTTTTGTCATCATATATCATATAGCCAAGGGACT[C/A]GGAATTTTGGCTGCTTCAAGTCA TTCCAAACCTCTCAGG
EST15700 6	48 G C GGA	---	---	GTCACCAAGCACTTTTATTAAGACGTGAAAGAGACAAAGACACAGAGGA[G/C]AGCAGAGAAATAATA TCTCTGTTTCAGCTATCCAGGATGTTATGCCAATTATCCAGAGTCTTGTATCTGATCTGATGTA
WI-16739	57 G A CACAAGC	---	---	AAGGATTGAAACATACCTAGATCATATAAATTTGTGAAGGTTTGGCCATCACAAAGC[G/A]TTATAG GGAATAATGAACATCAACTATCTACAGCTAAACCTAATGAAGACCAAAATGGCTCCAAGGT
WI-16782	96 C T CACTGTAAGG TC	---	---	CTTCTCCTTCTAGACGTGGAATACACACGGATACAGTATCTGGAGATGTAGCAGCTGGCTCTTGAC CATAATGGTGGGAGTCTCACTGTAAGGA[C/T]GATGGAGGAACAGAAAGATAGAAGAAGTTTGGGGT GCTGATGAAATTTGTGGGG
WI-16783	64 A G G	---	---	AAAAATGTAAACCTTAGAGGTTGCCCTCTTTGTGTCACITTTTCTGAGATGCTTTTACCTGAG[A/G] CTAATAAGGATTGAACCAAGCAGTATTTTAAATGGCAAAAGTCCAGATGTAACCTCGAGT
EST15948 2	58 T C ---	---	---	CAGGACTTAAGGTCATTTTGCCTGGAAGACTTTAACTAAAGTCAAGGCAACATAGGAT[C/T]GTGA CAGCAACACTCGGACCAGGAAGTGTGAAATCGTCACTAGCGTGGCCAGCCCTTTTTCCTGGC TGCTCTGCCTCCAGAGC
EST16088 8	89 G C ---	---	---	GGTTTGAAGACGCAGCTTTATCTCCACCTGCCACTGGGATCTCATTTTGAGAGCTGTTTGTGACGC TTTTCCAGAAAGGCCGCTC[G/C]GGGTTTCTGAACCTCTATGGGCATTTTAGAAT
EST16089 9	96 C T ---	---	---	CGTCTGAAGTTTCTTTTATCACAAGTCACATCAATCCCTCGGGCCCTGCTCAAATGCCACCTCTTC CTGAAAGCCATCCCTAAGTAGTCTC[C/T]AAAGAGCCATCCCTGCCCTTTCTTTGCT
EST16100 1	24 C G ---	---	---	ATCCAGCTGTGAAGGGACAGGAG[C/G]GTAAACACAGTCCATTTATAAGGGGTGTCACATTCCTCA GGGCTCCAATAATGCAACATTTTCACTCGTCCATGCTGCTGATAGTTTCATAGTAAAAAAGTC ACTCCAGACAGGTTGGCTC
EST16104 9a	83 A G ---	---	---	TTCTTTTAAATAACCCACAGACACCCATGACACTTCCAAATTTACAGAGCAAAAAGTGATTTGCAG CTGGTTCTCCAGGGA[A/G]TTGGCCCGAAGCTGGCTCAGTTCACCTCCAGGACCTCAGTC
EST16118 0b	119 T C ---	---	---	ATGGTATAACAAAATCAGTTCAGGTTTTCCTGAAACAAATGATCCTTTGGTCTTTCCCGTGGC CTCCTAAACAACTAAACAAACCCCTCTACGTCTAATCAGTCACCTTAAGATA[T/C]CGAGTGGCAAGT CTTTCACA
EST16118 0a	32 C G ---	---	---	ATGGTATAACAAAATCAGTTCAGGTTTTCCTGAAACAAATGATCCTTTGGTCTTTCCCGTGGC ATGCTCCTAAACAACTAAACAAACCCCTCTACGTCTAATCAGTCACCTTAAGATAATCGAGTGGCAAGT CTTTCACA

EST16151 2	53 C T ...			AGCCAAATCAAACGAACCTATATCAAAACACACAAAGGCCTAGAGGAGATTATC/TJAATGAACGT AAATAATTCAAGGCAATTTTGATCTAAAGCATTTTGTCTAGCTCTACAAAGGCATGAATGAGGTGT GGTCACGTTTTGTATAGGA
EST16182 6	54 G A ...			CATTGGTTGGGTAGGGAAGATAGTAGTGTGCAATAAATGGTAAACAGCAG[G/A]AAATGGAA TTATAGCTTTCTTTTCATATAGGGAATTGAAATTTATTTACTAGGGTGATAGGCAGAGTAGTA
EST16183 2b				GCAGGTAAACTGTGGTTCAACAGTATTGTTCTTTTCATAAAGAAAGAAATATCTAGTTG[A/G]GTAG AGGAAGGCACGTCTTCTCGCCCTTCTCGTTTCATATTTTATGTCACTGTCTAAGTGGGCCGTGT GCAAGAGATCTTTGAGA
EST16198 4a	28 G A ...			AATCTTAGGCTCTTGGCTTTCAAAATCA[G/A]TACAGACAGATAAGAGCTTTAAGTATTTCGCATTT CCCCAGAGGAAAAGTCAGCATATAAACACACATGGGTGCACATGCTCACGCACATGGTGTC
EST16229 2c	52 T C ...			TGTGAACCTCGAATTCGCTTGCCAAAGTCTGAGTCACAGTTTCATTTGGGAGTT/CJCCCTGTGCAGCC CTTGCCAGTTTCCACGAGGAGGATCTCCACTAGCTGATTCAGACAGGAGGCTGCA
EST16229 2b	45 T C ...			TGTGAACCTCGAATTCGCTTGCCAAAGTCTGAGTCACAGTTTCATTT/CJTGAGTCCCTGTGCAGCC CTTGCCAGTTTCCACGAGGAGGATCTCCACTAGCTGATTCAGACAGGAGGCTGCA
WI-16816	124 A G TGGGTTA	GGAGCATTGT	GCCTAGATTTT GTTCAGGACAG	CAGACTTTTCTCACACCTCATTTGGCTGGAAGTGGTGCACATGCACATCCTTGAACATATCATTGGCAA AGGAAATGGGTATCAAAAATTGCTTAAGGCCAAGCAGGAGGCCATTGTTGGGTTA/A/GJACTGTCC TGAACAAAATCTAGGCTC
EST16269 5b	49 G A ...			GCACCTCTCTGTGGCTTGTCTCTGTCCAGCTGTGTCCAGTGCCACAC[A/G]ATGGTCTAGCCTCATGG CAGAAGCATTTTAGCCAACTCCTGGTGTCTCCACTCTCTCTCTTCCGCCGCTGGGCTCACCACC TCTTCTCTCTCAATC
WI-16824b	83 G A ...			GTCACCCAGCCCAATGCTTCAGGAATAAATGATGGTGTGCGAGCTGTTGTTCTTATGAAGAAGTCAG AAGCTGATAAACGTGG[G/A]CTTACACCTTTAGCACGGATAGTTTCTGTTCCCAAGTGGGTGTGGA GCCTTCCATTATGGGAATA
WI-16824a	47 T C CAGCTGT	TGATGGTGTG	CAGCTTCTGAC TTCTTCATAAG AA	GTCACCCAGCCCAATGCTTCAGGAATAAATGATGGTGTGCGAGCTGTT/CJGTTCTTATGAAGAAGTC AGAAAGCTGATAAACGTGGGCTTACACCTTTAGCACGGATAGTTTCTGTTCCCAAGTGGGTGTGAGC CTTCCATTATGGGAATA
EST16445 3	96 T C ...			TTGCTTTTATTAATCCAGACGGCATGCTACAGATACTGTACAGCATGAACATTTATTCATTACAAA AATGGCTTCCAAACCATTAATAATGAACTTT/CJGGAATAAGAGCATAAACGGAAACAGTAACATCA
WI-16857	47 G A A	CAAATAAGCA GCTAATGGCA	TGTGAATTGGG AAGACCACT	TATAATCCATCCTCCAACACACACAAAATAAGCAGCTAATGGCAAT[G/A]CTAGTGGTCTTCCCAA TTCACAAGACCTGTGCTTCAAAATTGTTTCTCTGATAATGTGGAGAAATCTGCTCTTTATGTA



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WI-16879	79	C T	GATACAGCC ATATTCCCA	CAAGGCTTCT AGAACTAGAGT CC	AGACAGGTCAAACTCCTAGGGATAAAGATATAAATCCAGCACAGCATTAATTCAGATACAG GCCATATTCCCA[C/T]ATAGGACTCTAGTTCTAGAAAGCCTTGGGAGAACAGGCACCCAG
WI-16882	99	A G	GAAATGCCA CGTCTCTGAC	GACACATGTCA GGTAAATCGC	ACATGAATGGCAACCTCTTAGGTGGGAGAGACAATCTCCOCTTTCACCCAAAGTTACTCTGAC AAGGCTATGAATGAAATGCCACGTCTCTGAC[A/G]GCGATTACCTGACATGTGTCTATCTCCCT
WI-16888	70	G A	GCTAACTTTGG GCAGGTTC	AATGTTCTGAA TTGACCAAATT TAA	GTAGTAATGTTCACTACTACCCGGGAGAGCAAAAGAACCATGGAACGGTAGCTAACTTTGGGCAGG TTC[G/A]TTAAATTTGGTCAATTCAGAACATTCCAAAT
WI-16905	75	C T	ACTGGCCTGT GTTGTTCA	GTCATACTCT TCTAGGCAGTG GG	TTTGTGTTTGTATTTCCTCCCAACATCAGAACATAAGTTCCATGAAACAGGAACCTTGGCCTGTG TTGTTCA[C/T]CCCACTGCCTAGAGAGTATAGACA
WI-16910	74	G A	AAGAGTAAAG ATGGCGTAG	CAAAATGAAG TATCGTTTCTA TAACAGA	AGTTTTCAGTATGTGCTTAAGGAGGTATATTGCTATGACTTTTCATCTCAGAAGAGTAAAGATGGCG CTAGAA[G/A]GTATCTGTTATAGAAACGATACCTTCAATTTGGGCTGAACCAAGTGAAGGT
WI-16918	93	C T	CAGCCATTAA CACCAGCAC	TCCTGATACAG AAGTGGCATC	GGAAAGAAAATAAACTACCACTTCTCTCTGCTACCACAGAGCACTAAATCTAGGAATTTGAC TTTACTGCAGCCATTAAACACAGCAC[C/T]GATGCCACTCTGTATCAGGAACTTAACGTGACAACC ATGAAAGGTCCTCTGAAAG
WI-16947b	127	A C	GGAAAGCAGA CCTGGGG	ATGTGATTGCC CGTGG	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAATAGGCTGGAG[C/G]ACAGG TGGCTGAGGCTTCAACTGACATCAGACAAGACTGCAATCAAGGAAAGCAGACCTGGGG[A/C]CCA CGGGCAATCAGATGAGATG
WI-16947a	58	C G	CATGGAATA GGCCTGGAG	GCCTCAGCCAA ATCCTGT	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAATAGGCTGGAG[C/G]ACAGG ATTTGGCTGAGGCTTCAACTGACATCAGACAAGACTGCAATCAAGGAAAGCAGACCTGGGGACCA CGGGCAATCAGATGAGATG
WI-16966	43	T C	AAATGCACAC TACATAACAA	TGCAAGTTATC AGTATAAAAA CTCATATT	CATTTGTTTACTTTAAATGCACACTACATAACAACCTAAT[C/C]TTAACTTGGTCCAACATAATT AGTATAACTAATAGATTTTATCTACTGATAACTGCAATGCCATTAAA
WI-16995	55	T C	GAGCAGTAGA GACTGAGGTA	CATGTTGATTT CCAGGCGT	TTAGTGCCAGACATCAAGCATAGAAGAGCAGTAGAGACTGAGGTAAATAGTATT[C/J]ACGGCTGG AAATCAACATGCCTCTTCTCTGTGAAGTTGTCAAGATGGAGCTGAGAAGGCTGAGTCAATCT
WI-16992b	60	T G	---	---	AAATACATGGTGTCAACCTCAGCTAAGCACCCAGAAAGTACACTGTGCGCCTCATCTGAGAT[G/G]TG TAGGACTGAAGGAATGTTTGGGGTTTAGGAA
WI-16992a	46	G A	AAGCACCCAG AAGTACACTG	CACATTCCCTT ACAGTCCCTACA C	AAATACATGGTGTCAACCTCAGCTAAGCACCCAGAAAGTACACTGT[C/G]CCCTCATCTGAGATGTG TAGGACTGAAGGAATGTTTGGGGTTTAGGAA

WI-17010	23 T C	TTCAACAGGA AAAGCCATG	AATAATACGGT GTTTGAATGT CA	ATGTTTCAACAGGAAAAAGCCATGT[C]/JATGACATTTCAAAACACCCGTAATTATTAGAAGCTCATTTAAT TGTTTAAATGCAGACAAAAATCAAGGCTAACTAAAAGCAGATCCAAATGACCCAGTGATCAACCTAGA GGTTOCCACG
EST17127 9b	74 C T	CACCTGGCAC AGACAGAGT	GGGAGGCGAGG GGTG	ATTCCGTCTCCAAACAGCATCCAGGCCGGGCATCTCCCCACGATTTTATAATACACTCGGCACAGA CAGAGT[C]/JTJGGGAGCCATGGGGCACCCCTGCCCTCCCCAGGCTTCTCTAAAGTAAACAAT
WI-17040	94 T C	AATTCTTTAT CATCTCAAGCC	GGACTATGGCT TATTCAGTGAT G	CACGGTTCATTAAATTTGGTACAAAGCATGAACACTCAGGACAGATTTGGCACAATACATGCAGTTTC GAGAATTCCTTATCATCTCAAGCCAGT[C]/CATCACTGAATAAGCCATAGTCCCAAGTCTCGTTTTTCC AAATCTTTCTCATATTGT
WI-17044	47 G T	GCCAAGGGAT TAACGTATAG	GGGATOOOCT TGTTTAAGA	TTGTTTGTGTTTTCTCTCTCTGCCAAGGGATTAAAGTATAGG[G]/JTJCTTAAACAAGGGGATC CCCCACTTATAGCTGACAGCAGCAGCTGCAACCACTGACTCTCTCGAGAATGGCAGGGAATCGAAT CAAAAAGAAAGCAAGTG
WI-17021	62 T A	TGGACTTGTCA GCCTATAACT	TGTAGAGTTAG TGGCAGCTGC	GCATGTGTTGGAGCAGATCTCCATGGTAAAGCCAAAAGTGGACTTGTCAAGCTATAACTACTCTT/AIG CAGCTGCCACTAACTCTACAGGCACAGTAACACTTTATACAGGAGCACATGCCAAAAGTGCTGG GAGGTGCCAATAAAATCAA
WI-17065	90 T C	CCAGAAAGGA AAAGCATAAA CTT	CCCAAGAGAC AATGAAATCCT	TGTAAAAATGTAGACATGGGGGAAAAAACATTCGTAAATCAACATGTGCTGTTTTCTACTTCCGGTA CCAGAAAAGGAAAAGCATAAACTT[C]/AGGATTTTCATTGCTCTTGGGT
WI-17066	32 A C T	TGTACAGCCA ACATCACTGTT	GAGATGTTGAA AATGTTCTGGA A	TTCATAAGGTTGTACAGCCCAACATCACTGTTTT[C]/JATTCAGAAACATTTTCAACATCTCAAAAAGA AACTCTGCACCCATTAGCAGTCATTCCTGTAGCTTCCCTCATAGGCAATGGCAACTGCTGATC
WI-17074	86 T G	---	---	TGCTGACTGTCACTAGTATAGTAAGGCCATCAGAGTTGCCAGAACATCTACTCAACTGTTCCCAAGCAT AACTCTCTACACAGGCCTT[G]/CTACATAGGAGTATATTTGGCCAAAGACTCACCCTAGAAAGTAT
WI-17104b	108 T C	---	---	CAGATGAGAACTCATGCTGGCTCATCTGCAAGCTTCTGATGCTTTCGAGCTTTCCCATTCATCCA AATCAGAAAGCAGTCAGTGGCCCCGTGGTTTCCAGACGGCTT[C]/CTCTTTTGTAAAGAAATTA
WI-17114a	37 T C	TTTCCATCAAG GACTTTGTTT	TTGTATTATAA ATAGCAGAGTG AAGAGAC	AGCGTCCAAACAGAGTITCCATCAAGGACTTTGTTTTT[C]/GJGTCCTTCACCTGCTATTATAATAC AAGCTACCTCCCAAGGCCAGATGCTCTAAGTGCTAAAAGAAAGACTGCAGCCACAATCAGAGTTACAT GGGA
WI-17150	76 T G	GATGAAATTC AGATAGTCTTC	TTCTCAGAATC CTGGAAGATAT G	CGTGGCTGGACTAAGTGCTCTTTCCATGTGGACACATCTCCACTGAACAGGATGAAATTCAGATAGTC TTCTCTTTT[G]/CATATCTCCAGGATCTGAGAAGGGCTCCTTTGCTGCTCTAATTT
WI-17163	43 A G	CATTCTTTGT AAAAAACA TAACGTT	CAGAATCTTGC TTTTGCTT	GAAATCGAATACGTCCATTTCTTTGTAAAAAATAACAATAACGTTT[A]/GJAAGGCAAAAGCAAGATTCTG TAAACCAACATTGGAAGGGGACACAGGGAGGGGCAGAGGGGAAAGGGCCAGATTTTCAACGGTTT CTCCACATCTGCAGACAAA

WI-17178	127	T C	GGACTCCCTCA TGAGGAGC	CCCTCAATTTT CAACTGCTTC	AGCAAATGTCCTCCCAATTCATTAGCTATGATGGAGTTATCAGTTTATCAGTTCATTTCCAGAGCGAAATTACTGG GGCGAGGGGGTTTAATATCTGATGGGTTTAATTCAGTGAGGACTCCCTCATGAGGAGCTTC/JAGAA GCAGTTGAAAATTGAGGG
WI-17180b	81	C G	...	...	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAAATCCTGCACATCCCAAGTCTCGTCGCACAG GCTTCAACAAATTAC/C/G/AACATCTTGCCCATTTTGTTTCATTATCCGACCCACACTGACAGATGAG GGAGTC
WI-17180a	47	T C	CACAAAAATA TAGAGAATCC TGCA	TGGCAGGAGAC TGGG	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAAATCCTGCACATTC/JCCCCAAGTCTCGTCGCA CAGGCTTCAACAATTACCAACATCTTGCCCATTTTGTTTCATTATCCGACCCACACTGACAGATGAG GGAGTC
WI-17156	54	G C	TGTTCTCTAAA CTTTAGATATC TCCCA	CAAGAAATAT ATATTTGATTC TGTGGAA	TGAGGTAGCAGGGCATTCCTTAAAGAAATGTTCTCTAAACTTTAGATATCTCCCATG/CJTCCACAGA ATCAAAATATATTTCTTGTTGGAAATTTAAATGTTCTTAACATATCTGCCTACCATCCACCTCAAT TAATATCTTG
WI-17149b	79	T C	...	...	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAAACATCTCATGCACGTGCGTGGAA ACCCAATTGTCA/T/CIGTGTATGAACACTACAAAAGGATGGGGAAAAAGAACACATTTCTCTCACA
WI-17149a	48	C G	CAAGTTTGA AGGAGGAACA	CCACGCAOCTG CATGA	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAAACATG/CJTATGCACGTGCGTG GAAACCCAAATTGTCATGTGTATGAACACTACAAAAGGATGGGGAAAAAGAACACATTTCTCTCACA
WI-17197	67	G A	GCAGAAGTAG CTGGGGCTAC	GGTGAGTGGT GCATACC	ATTTGCTATGTTGCCTGGGCTGGACTCCAGCAATCTCTGCCTCAGCAGAAAGTAGCTGGGGCTAC/G /AJGGTATGCACCACTCACCCTGCTTATCAGTTTCGTTTAAATAGAAATATTTGACTTTTAGATGCGCA
WI-17198	38	A C	TCCCCTTGTC CCTAGTTT	TCCATTTGTCC ACTGAGAAAT	TGATTTTCAGTACTTTTCTCCCTGCTCCCTAGTTT/CJTAATTTCTCAGTGGGACAAATGGACAA ACCATCTCTGTTTGAATTTGAATACACAGATACATGCAAGATATCTTACAAGAAACAATGCACATCC TTC
EST18753	27	C T	CTACCCAGGCT GGTCTCAT	GGATCGCATGA GCCTGA	TCGCTATGCTACCCAGGCTGGTCTCAT/CJTACGGCTCATGCGATCCTCCTGCCTCTGCAGTGGCTGG GATAAGACACAACCTGCCACCCAGGCTGCCCTAGGAGTAGTCTTAATGCCTGATGGTGGG
WI-17108b	74	C T	GCCATTCAGTC TCAAAGTAAA CA	AACTACGATTT ATCATATGCTC CC	TTATTTTAAACATAACCCAGATGCACCTTGGTTTTTACATCTCTGTTGCCATTCAGTCTCAAAGT AAACAC/CJTGGGAGCATATGATAAATCGTAGTTTAAAGGAAGCCATAGCACCTTACAGAGT
EST19067	41	A G	...	...	ACACAAAATTTACCATCGTGACCATTTAAGGGTATAGTTCA/JGJGTGGCATTAAAGTACATTCAACT TTTTGAGCAACCCGCCATCACCATTATCATCCCACTCCGTT
EST19067	40	A C	CGTGACCATT AAGGGTATAG TTC	AAAAGTTGAA TGACTTTAATG CCA	ACACAAAATTTACCATCGTGACCATTTAAGGGTATAGTTCA/JAGTGGCATTAAAGTACATTCAACT TTTTGAGCAACCCGCCATCACCATTATCATCCATCTCCGTT
EST19125	28	A G	...	...	CTGTTTCTCAGAGATGACACTGCCAACAA/JGJTCACAGATTTGCATACAATACAGTTATGTATTGGC TATTCACAAATTACAGTAGTGTTTTTTCTCTGAAAAA

EST20824 8	115 T G	AGTCGGGAGT GCTGATTG	AAGATTTTATC TTGGACCCGA	GTGTGGAGCGGAGTTTATTATTAAATCAGTCTCTCTGAAAACTCAGGGATTGAGGTTTTTA AGGATAACTGGTGAGTAGAGGGCCAGTAAGTCGGGAGTGCTGATTG[T/G]TCGGGTCCAAGATAAA ATCTTAGG
WI-17347	50 A G	ATCCTCAGAA CTTCTCAGCCT	TCAAGCATCCA CTTGTGCTA	TTGGTTAAATGATGCCAGATGGGGTCACATCTCAGAACTTCAGCCCT[A/G]GTAGCACAAGTGG ATGCTTGAAGAAACTAGTCTTGGAACTCAGACAGCAATGGAGCGGATGTGAGTGGGACCA
EST21904 b	128 G A	TTCATATGGCC ATTTTAATAA GTG	GGCAGGTGTTT AGAAAGCAT	TGATTGTGGTCTGGGAGCAGGTGGGCGAGTTTCACTGAGGAGCAGAGGAAAGTAGACGAGTAGAAAT GAGACTGGAATCAATAGAACAGAAAAATGTACTAGGCTTTCATATGGCCATTTTAATAAGTG[G/A]TA TGCTTTCTGAACACCTGCC
EST22111 3	82 T C T	GAAGATCTGT CTGGCATTTCT	TGGAATAACA GCCCCAC	CAACAATGTAGACATAAGGGAACAAATTCAGAGAGCTCAAGTCACCATGTTTGTAAAGAGAAGAT CTGCTGGCATCTTTT[C/G]GTGGGGCTGTTTTCCAAAGGCACA
EST22197 2	78 T C	AATTATTCTGC TATTCCTGCGA	ACCATGAAGG ATGCGGT	GTTTAAATGATCACTACCCAAATCCACAGAGAGATCTTAAATGTTTACAAGCACCAATTAATCTGCT ATTCTGCCAATTCACCCGCATCCTTCATGTTAGAGTATCACAAAGTAAAGTTTCTGGTTGTTTCATC TACTTAAACCA
EST22311 9c	92 T C	---	---	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATATACATAAAAAATCCACCACCTGTAAACAG TAGCATTCAATGGTTTTTACTCTA[T/C]GTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22311 9b	54 A G	---	---	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATATACATAAAAAATCC[A/G]CCACTGTAAA CAGTAGCATTCATGTTTACTCTATTGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22311 9a	41 T C	GGATTAGATC ATCTTTTATT GAGTTATAA	TTGAATGCTAC TGTTTACAGTG G	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATAT[C/J]ACATAAAAAATCCACCACCTGTAAA CAGTAGCATTCATGTTTACTCTATTGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22319	19 A C	---	---	TCGAGGAGCTCTGAGGAGC[C/J]CACCAAGGGACGTGTGCCAGGGCCACCCGTGCAGGCAAGTGTG GTCCAACTCCTTCTCCTTTTACAAAACCTCCAGCCTCACCCACACAAACACTGGCTGACAGGGCCTTCT TAAGCCTTTTAACTGT
EST22433 c	103 A G A A	AAGACATGTT CACCAAGTGA	CAGCTTCAGCT TAAC TGACAGA AGTTTCAGTTT	GATGTTAATGACTTTCTTTGAGATATGATGGAAAAATATCCAGGTACACATGGAAGACATGTT CACCAAGTGAACCAATCTAACCCAGAAAGCTTTACC[A/G]TCTGTCAAGTTAAGCTGAAGCTGAAAT CTGGGAGCTTGACATGCTG
EST22657 9	71 A G	AAATGGATCC TTATCTGCACA	GCATGAATTT T	TATCCATTTCAAGAAAAAAATGACTTAAAAAATACAATTTCTATCCAGAAATGGATCCTTATCTG CACA[A/G]CCATTGAAGAAAAAAATTCATGCAAACTGAAACTATGCTTT

EST22993 5b	71 T C	ATCCTTTGTT TG	TTGCCTGTAA TTTGACTGTAA TG	GCCTTTTATTGCTCTTTTAAACATCAAAATGTTTATAACACACTTGATCCTTTTGTCTACCCCA ATTC/CATTACAGTCAAAATTAACAGGCAATATAATAGGTCTACAGAAATGCTTGCAATTT TTATTTCTCAGCTTACCATTGTTGACTTATCTCTGTACAAGGTGTTTTTCTCCATGGAGAAATG TTAAATCTTTGTGAGGTTAATTTTATTAATCTTTGCCCTTTT/AJATGGTTTTGACAGTTTGTGCTCTTCT T
EST23021 0	108 T A	---	---	T
WI-17387	55 C G	CCTTTGCAGAT TGAAGAAAAA	GCITTTGCCTA AGATTAATAGT AACTACT	ACAGAAATTTAACATGCAAGTTTCATTTACATTACCTTTGCAGATTGAAGAAAAA/C/GJAATATTAG TAGTTACTATTAACTCTTAGGCAAAAGCCATTTCTTTG
EST23669 1	101 A C	AATGTAAGCT CCAGAGGCAG	CCTTCCCTCC TGTAAGC	TTTTTGGCTTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACCTTTGCTCCTCTCCCA AGTGCACACTAGGCAATGTAAAGCTCCAGAGGCAG/C/GCTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGTGCTGCTCACTG
EST23733 9	31 T G	GGCTGTTAGTT TTGTTTTGTTT	TGCACCTTTAAA TCCCATCAAT	AAAGGCTGTTAGTTTTGTTTTGTTTTTCCCTTT/GJATTGATGGGATTAAAGTGCATATAACTGAAG GCAAAGTCCAAGGCTAGAGAAAGATATAGGCGCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA
WI-17470	83 A G	GTCCGTOCCG CCAG	CCAGTGAAGAG GOOGA	CTGACAGTCCCTGTGTGCGGGGTGTCATGTGGCGTGTGTGAGTGAGACTTTTTTACTGCGTCCC GTCCCGCCAGGCCCTA/GJTCGGCCTCGTCACTGGCCTTGGTCACTTTGTATTTCTGCTTGGTTGAAA TACCATCAGCCTCC
WI-17519	55 T C A	GTGTCCTAGC TAATGAATGC	AATTATTATT TGCAGGCAATA CTC	TTTTTAACGAAATCTCACTACTGCAAAATGCATTGTTGCTCTAGCTAATGAATGCAT/CJAGAGTATTG CCTGCAAAATAATAATTGAGATTCTATTTTTAAGAAGCTTAGAACAGTACATGGTGATAG
EST25356 3b	95 C G	---	---	TCCTTGATACAGGTAACCAAGTTTGTAAACATTATTCAGAACTTCACTGTATCTTCAAGTTTTGATAT CAGCATCTCTGTGGAGAAAGCAGTGTG/C/GJTATAATGTCAACATCAGGATTTCTTTTT
EST25356 3a	26 A C	---	---	TCCTTGATACAGGTAACCAAGTTTGTAAACATTATTCAGAACTTCACTGTATCTTCAAGTTTTGAT TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAATGTCAACATCAGGATTTCTTTTT
WI-17581c	99 C T	---	---	GGGTGACGCTCCAGAAATGGGAGACAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCATTCAACATT ACTACCAGTTATTTGATAATGATAGAACCCAA/C/JTAGGGCGCAATTTACATTGACGCGTCAATGC
WI-17581b	86 T C	ATTCAACATT ACTACCAGTT ATTGCGCT	CGTCAATGTAA ATTGCGCT	GGGTGACGCTCCAGAAATGGGAGACAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCATTCAACATT ACTACCAGTTATTTGATAAT/C/GATAGAACCCAACTAGGCGCAATTTACATTGACGCGTCAATGC
WI-17596	86 A G C	ACTTCCCTGTG TAAACACTCC	CATCTTATAG CTAGAAATCGA CAATAT	GTGTGCTGTTAAATGGATAATAGCAGTCTCTCATCTCTGAAGGTTGGAGTAGGAGAGGCGCTACT TCCTTGTGTAAACACTCCC/C/GJATATTGTCGATTTCGATTCTAGCTATAAGAATGGGCGCACTAAGTGGGTC

WI-17623	46 T C ---			---	TGTGGTTTAAATTTCCATATAAATTAATGTTGGGCACATTTC/GCATGTGCTTACTGGGTC ATTTCATATATCTTTTGTGAAGCATCTGCTCCAATCTTTTGCCTGACTTTGGAGTTTITGGT
EST26419 1b	46 T C ---			---	ATTTTCATACAGAGATACAAAGGCAACTATGTGCAGCAACAATCTGA/TTC/GGGCAGTCCAACTTCT TGGGAGGAAGTAAATTCATGTTAAATGTCATGATGGCTGTTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAATG
EST26419 1a	35 C A AG	ATACAAAGGC AACTATGTGC		CAAGAAGTTTG GACTGCCC	ATTTTCATACAGAGATACAAAGGCAACTATGTGCAGC/AJACAATCTGATGGCAGTCCAACTTCT TGGGAGGAAGTAAATTCATGTTAAATGTCATGATGGCTGTTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAATG
EST26780 5	69 G C ---			---	TCAGCTTTAAATTTAAGGGACATGTAATAAATAAAGATGCATTTGACAGGACAGCAGACTAGTTC AAGC AG/GC/JAGGTTAGACCAGTAACAACAACCAAGAAAGCAAAGTGCTCGTTTCCATCTTGGCTTTACCA CACTTACAAACTGATACCC
EST26900 7	39 A G ---			---	TACTTCAGTTTAAGGCAATTTCCACACAGAGACTGTCTC/JAG/GAGACGGGCACAGAACCCAGACACC GTAGAAACACCACCACCACCATGCATGACGGGGAAGCAGAG
EST27152 1	101 C T ---			---	CAAAGGATTTATTTTGTCCCTAATAAAGTAAATCTAGAAAAATAGCAACCCACTGCAAGAAGAGTT CTACTAAACATTTTCAATCATCTCTCTCTC/TJTTACATGGTGACTCTTTTCATGTACACAT CATCGGAAACAGACTGA
EST27504 0a	33 G A ATTT	GCACTTTGCAA CAATTTAATA		GCTGGTGTGAT GCTACTGTAAAT G	TTTTTGCACTTTGCAACAATTTAATAATTTATC/GA/CATTACAGTAGCATCACACCAGAGTCAAT AATGCCACTTTAGGCAAAAGCTTTTCAGTATTTCTGTACACATCTGTTAACAAAGAACCCCATACATT GGTAAATTCATTTCT
EST27662 4	51 C T CTCCAGTCTTG C	CACATTCTGTT CTCCAGTCTTG		TTATGGAAATG GCTTATGTAAAC C	ATCTTAAAGGACCATTAGAAAAGGCCAGTCACATTTCTGTTCTCCAGTCTTGCT/JAGGTTACATAAG CCATTTCCATAAATTTCTATAGCTTCTTCTTAGAGTAACACACACTCTTTGTTAGGAATGTTTC
EST27788 3	100 A G ---			---	ATTTTATTAGGCGGTACAATTTCCAAAGGTGTAAGGTTGAAGGAAAGGCGAAGGCGAGGCAAAATACAT TATTGAGCTGAAAACAACATTTACATTTCAAGGAC/JAG/GCTTCCAGACAAGCCCATGTAGAACCAGCAT GCCTTGGGACTGTGGAT
EST27828 4	58 G A AGAACCCAC	GGAAGTCATC AGAACCCAC		GTGCAGAGAGG TACTCCAAGTA C	TCCTTAAAACTTTCTTCTGTTGGATCCAGTGACGTGGAAGTCATCAGAACCCACAC/GA/JGTACTT GGAGTACCTCTCTGCACCAAGATAGCTGGCTGATTTTCTGCTCAGTCACAATTTTACTTGAA
WI-18369	58 G A ACAATC	AATAAATTC AATCTGTCAC ACAATC		TCAAGAAGGCC TTATCCATT	TAAAAATTTGAGATACATTTCCCAATGTAAACAATAAATTTCAATCTGTACACAATC/GA/JAATG GATAAGGCTTCTTGACAAATTTTGCCACCTCCGTTTAAACGCATCAGAACTCAATCTTATCTC
EST28036 4	37 T C ---			---	TCCGCTTCCAAAAGCTTTATTGGCAATATGCTCTA/TTC/JAAGAATGATCAATCTGTTGCCCT AAGTCAATGGAATGAAGAGCTGTGTCAGGGACACACCCCGTGTCTGAAGGAGACTGCTGTTGTG TCCACTCTTATTCATAG

EST28483 7	31	T A	GGAGTAAAG GTGTTCTCT T TAA	TTTCTGCAAT TAATTTATAC CA	CATTGGAGTAAAGGTGTTCTCTTTAAAT/AJATGGTATAAAATAAATCGAGAAACATTAAAC GGAGAAATGTACAGACAACAGACAGACATGATGTTCTGACTGTGACACATTGGTGAAA
WI-17724	50	T C	TGGGCGCTCC TGTC	TGGGTGGCAG TGTC	AGAAATGGTCTAGTAATCGTTGAGGATTCGGTGATGGCCCTCCCTGTCT/CJGGACACTGCCAACCC CACAGCTGGAGGGGCACTTAAGGCACGTCATTTGTGATTAGA
WI-17730b	68	T C	---	---	TGAGCCTGGGAGAAAGACACAGAGTGAAGTGCTATTAGTTACATCATACCAAGTGTACATACTG TT/CJACATGATTTATGGCTGTGTTGATGTTGACCTCAATAACCTGGCTGATGATGATGTGTCA
WI-17730a	39	A C	GACCACAGAA GTGAAGTGCT ATT	TCAACAGCCAT AAATCATGTG	TGAGCCTGGGAGAAAGACACAGAGTGAAGTGCTATT/CJGTTACATCATACCAAGTGTACATA CTGTTACATGATTTATGGCTGTGTTGATGTTGACCTCAATAACCTGGCTGATGATGATGTGTCA
EST29041 5b	53	G A	GGAACAAACA CATTAAAGCAT CA	GGTATTGTTGA TTTGAGGAGTT AGC	TACTCAGAAATGTGAGTTCATGAGGAACAACACATTAAGCATCATTGTCACTG/AJGCTAACTCCT CAAATCAACAATACCCCTTTATTTTAGCCATGAAAAC
EST29128 4	58	A G	---	---	CTTTAGAAAGGACACCACTGTTGTTGGACTTAGGGCTACCCCTATTCACGAGGTGCCJ/AJGTTATTT TCACCTTGGTTACGTCTGTAGGACCGTTTCCAATGAGGTTACAGTCACAGGTTCTGAGCAGACATGA GTTTTGCTGGGGACACT
EST29912 3	103	C T	TCTGCCAGCTT ACAGGCT	GCGTAAGTGTC TCATTCCTCTG T	ATTATTAGGTATCGCTGTGGGGTGGGGTGGGAGATTGTTGAGATACTGCAACAGACACACAAA AGCAAGAAAGAAACATTTCTGCCAGCTTACAGGCTC/TJACAGAAGAATGAGACACTTACGCGCATG GCCATGATACACAGCAGTGA
EST29936 8	121	G C	---	---	TATTGGTATGCTTAGGGAAGATTCTGATTTAGAGATATTAAATCTTAAAGTTAACTCACCATGAAA TTTAAACCTTCTGTACTGGCTTCACTGATGAGGCGAGTAACTACATAGGGATAAA/GCJAGCTCAGTA TCTGGAATCATGCTTCCCTG
EST30223 2	99	A G	---	---	AAATAATACATCATGGGAATGGGATATCCATCCCTCAAGCATTTATCTTTGAGTTACAAGCAA TCCAAATTACACTCTAAGTTATTTAATATCC/AJGGATTTAATTTCTTCTAGTTCAATCTTTGGGA GG
WI-16260b	86	G A	---	---	CTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAAAGACCCAGA GTTTCACAATATAGGTAGC/GA/ATAACCAGGCTCACTTCCCTTCCGTGAGAACTTCGTGGGAC
WI-16260a	59	G T	TGAGGTGGATT CAAGAAGAAA A	CTACCTATATT GTGAAACTCTG GGT	CTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAAAGTTACCCC AGAGTTTCACAATATAGGTAGCGAATACCAAGGCTCACCTTCCCTTCCGTGAGAACTTCGTGGGAC
WI-17835	30	G A	ACAGGAATA TTGCTTTCT TG	TGGGGTATAGG AAACAGGC	AAGAGAAACAGGAAATATTGTGCTTTCTG/AJGCTGTTTCTATACCCCAATATCATAAGAATT GTTGTGCTTCTATAATGTTCAAGCTTCAAAATCTTTTGTAAATCAATCCAAATGAATTACCTGAATT TTCTCCTTGTTCAAAA

EST31951 4	87	C T	GGGTTGTCAG C CAAACA	CCCAACAAAT CACCTCC	ACAGCCATTATTATGTTTACTTGGTAATATCAGAGACTGAAACATTTTCACTCTTTTAGCAATGACA TCGGGTGTCAGCCAAACAC/CTGGAGGTGATTTTGGTGGGAATTTCTTATCACAATTATTCT
EST31968 8b	95	T G	---	---	CGAATTTGTCCTCTTATTTTGTGATTCTAGTAATCCTAAAAGATTGGGGGGGGTACTATAAGT GCATTTT/CJATAATGGGATTTTCTGCTTAAC TGCCCACTGATTCTTACATGGGAAAGGTGCAAAG ACAGTGGTACTGCTCCC
EST31968 8a	75	T C T	GCGGGTTACTA TAAGTGCAATTT G T C T	TGTAAGAATCA GTGGCAGTT	CGAATTTGTCCTCTTATTTTGTGATTCTAGTAATCCTAAAAGATTGGGGGGGGTACTATAAGT GCATTTT/CJATAATGGGATTTTCTGCTTAAC TGCCCACTGATTCTTACATGGGAAAGGTGCAAAG ACAGTGGTACTGCTCCC
EST32063 2	103	C T	---	---	TCCATGGATGAACAGACAGCTACCATGCCACATCCCACCTCCCTCCGACCAGATGTCGTGGCCAGAGC TGGCTTCCCTTCCAGACCTAGCTGGCTTTGTAGT[C/T]GTTTCAGGCCCATTTGAAATAGCAAACGCAC AGTCATGTAGCACTCGG
WI-16303	65	A G	---	---	AAGGCTTCCAAAGCATTCAAAGGCATTGGGTGTTGTGCTCTAAGTTTCTGGTCACTGCAGCCCC[AG T]CTGTATTAGGGAGACCCCAAGCCAGTAACAATATGGTCTTGCAG
WI-17800	29	C G	GGGAGCACAA GAGAACTCA	TTTCCCTACAAT TAATCCCAGTC TT	TGGACATGGGAGCACAAAGAGAACTCACTC/G/AAGACTGGGATTAAATGTAGGAAATATTTACACAG TTTCCACAAGTCAGAAGAGCTAATCCAAACCCCTGTGTATCTGGAACATACACTGCTGCCATTTCTGCG CCATGAAGGGAAATACCC
WI-17857	34	T G C	CCTAAAGCTG GGATGACTTTC	TTGGCTTAGGT TCTACTTGATG T	AAACTGTCATTCTCTAAAGTCTGGGATGACTTTCCT[G/A]TTCTACATCAAGTAGAACCTAAGCCAAAT TCAGAATCAGAAATCCCTTTTGTCCATCAAAATCCAGCTAACTCCAAAGCTGAATTAATGTTCAATTCT
WI-17860	121	T A	TTGCCAGCAA AGCAAATA	ACTAAGGAGC AGTCAGTCGG	GTATCTGATGTAGTTAACCATGGCCTGTCATGATTATTTGCTATAAGGAAGGGAACAAATCTTTA TAGTGTCCAAAGATAAATTAATCTTGGTTTAAATCTTTGCCAGCAAAGCAAATAT[A]CCGACTGAC TGCTCCTTAGTCTGTGATC
WI-17866	43	A T	TTTATAGCCT ACTTCTCAA	CCGTTGTCACT AATCACACAA A	CAGCAACCTTTTTTTTGTATAGCCTACTTCTCAAAATTTGTT[A/T]TTTGTGTGATTAGTGACAACG GGGGAATCTACAATGCTACATCACATCACAGTAAACTACCA
EST33301 4c	80	G A	---	---	GAAAAAAAAGTCAAAATGTTCCCTTTATGGGTGATGCCACCATGATTGCTCACACAAGCATGATC AATCGCCACGAGA[G/A]ACTGGATGCCAAAGAGTATGG
EST33301 4b	63	G A	---	---	GAAAAAAAAGTCAAAATGTTCCCTTTATGGGTGATGCCACCATGATTGCTCACACAAGCAT[G/A] ATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGG
EST33460 1	44	G A C A	AGCGTGGTTTT CAATACTAAA	CTGTATTATT GTTAAATATTT GCATTGTT	CTATCCAAAGATATTTATTGTCAGCGTGGTTTCAATACTAAACA[G/A]TGTAACAATGCAAATATT TAACAATAAATACAGTGAATTAATAAAGCCATGGCATATCCAGTTGATGTAATACTTTTGCAA



WI-17904	50 A G	AAAGCATGAC AATAAAATGA ACAC	CGGTATGTTA ATAGTAATTCC CG	CAAGTGAATATTGATACATGGCTGACAAAGCATGACAAATAAATGAACAC(A/G)TACGGGAATTAC TATTAACATAAGCGATAACATCAAAACATCTGGTAAATGCAGTTAAACACAAACACAAATGA
EST34149 5	69 A G A T	TGCCAAATAC TCAAGTGTGA GAT	AAGTACTAGCG AGAACAACTA ATAAAATC	GTTTTTCTTTGAGTGACACAAGCTTGTTCAATTTTGAGAAAATGTGTGCCAAATACTCAAGTGTGAA T(A/G)GATTTTATTAGTTGTTCTCGTAGTAGTTTGGTATCTATGAAAAAAGCAGCTAGTTTCAGC TTACAAATCACACAAGT
EST34343 8	95 C A	---	---	TGGGAAACATAAGTTAACTCAAGAAATATATCCAGTCTTTATGTTACTAAAACATTTGTAATAGTGT TTTTATCAATGATGCCGAGGTCACTGCT(C/A)TACAAAGATTAAAGAACTTACCATCAAAACACTTC CAGTGCATCAA
WI-17982	98 C T	GGACCATATG ATATATAACT CCTAAAGC	CAGAAATTATG TGATAATACT CCTTCC	GGTACACAAATTTTAAATGGAAGGAACACACAGGTATGTTGAAAGAACATCAGTACAGCTGGAGACAGG GAGGGACCATATGATATATAACTCTTAAAGC(C/T)GGAAAGGAGTTATTATCACATAATTTCTGGGC GCTACAGAAGTTTTTCATCA
WI-17993	118 A C	---	---	CTCAGTAACCTCCGGTGATAATCTGOCATTTATTGATTTATTATGATAAAACACCTCTCATTTGTGA AAACACAGCTAAGGGTGACATCTCCAGACCCAAACCACTGTCCCTGTAAATGT(A/C)CTGCTGAGAGTCC ACATTTTGGAAATCCAAAT
WI-17996	84 A G	GTAGAGCGA AGGGAACAG	AGGCACATGGG CAGC	CCCATCCAGAAACCCCAAGTGTGATGGTGAAGCAGCATGAAACAAACATCTCCCAGGCCTCGCAGT AGAGGCGAAGGGAACAG(A/G)GCTGCCCATGTGCCCTGTCTTAAAGACGCCACCCCTCAGGTTGATGT CACCTGTGGGAGACCGGGT
WI-17136	33 C G	---	---	ATTCTTTATAAAACACCACTGTCCCTAAAATGT(C/G)ATTCAACATATATGCACACCTTCGATGTAT AGGACACTGATCAAAAAGACAGAGAAATGTGCCCT
WI-18041	24 A C	---	---	GCCACTGAAAAAGGTGCTCTTCC(A/C)GTTTCTAACTCCCTGGACTCCCTCATTTGGAACCTGAAGCTC ACAGATGTTTCAGCTGGACTAGTTAGACTTTGCTGTATTTTAAAGGCAGTGTGATGCTCCAGGAT TCAAACTACTTAATCA
EST35164 8a	57 A G C C C C	CACAGCCCTGC C C C C	CCCTCTGGATT CTGAATCTCAA	TTGAACCAAGGCCCTAACAGATGACTCAGCAGGGCCCTCAAGCACAGCCCTGCCCC(C/A/G)TCTTGA GATTCAGAAATCCAGAGGGTGCTCAGTCCCTGGTTTAGGTCTTCTGTGACATTTCCCTCTTG
WI-18052b	67 A G	---	---	AGCGAATGAAAAATGCTACATAGGCTCCCTGAGTTCCTTATGACGAATCTTTCATGTACACATCTTAGI AGJACAGCAGAGCTGCCCTGAGGGAGGGTGTGTTAATGCTGATGCATGCTCAGGCACAGTGTGGC ATGGCCCATCCATGCTTT
WI-18052a	50 T C A T C	CCTGAGTTCTT TCATGTACGA ATC	CTCAGGCAGCT CTGCTGT	AGCGAATGAAAAATGCTACATAGGCTCCCTGAGTTCCTTATGACGAATCTTTCATGTACACATCTT AGAACAGCAGAGCTGCCCTGAGGGAGGGTGTGTTAATGCTGATGCATGCTCAGGCACAGTGTGGC ATGGCCCATCCATGCTTT
WI-18054	46 G A G A T A A A	GGGAGTGGGG G A G A T A A A	CGTCACCTGC TTCCA	CTGTTGTGCTGAGAACAGAGGGGTCAAGGGAGTGGGGAGTAAAA(A/G)ATGGAAGCAGGGTGACG CATGCAGGAGTCCAGACAAAAGACGGGTGATTTGCTCAGGTTGTAGCAACAGAGGTAATG

WI-18064	54 G A	GTAGTGCTA AGCTGTATTTC	CCAGTGGTATG ATTGTGACATT C	CAGTGCCCAATCATCTCTCAAAACCCGTGGGTAGCTGCTAAGCTGTATTTCAGA[G/A]GAATGTCAC AATCATACCACCTGGGGAGAAAGAGTAGACACAGTCTTATTAGGTGCCAAACTGGGGTACCTGGGAG GCAGAA
EST35347 2	97 T C A A	GCATAAAATT TTCAGTTGGT	CCCTGGGCACC TGCT	TTTAGCACCATTCTTAGTGGAGCAGGATTCTTGATCATGGGTGGAAATTTGTGTATCGGGCTTCAT GGGATGCATAAAATTTTCCAGTTGGTAAGT[C/J]AGCAGGTGCCGAGGTCTGGATCAGAAAAAAGG CAGGA
WI-18070	28 A C	AACCCACTAC TACTCAGAGT	AAAACATAA AGAACTGGA GGTTTT	AAACCCACTACTACTCAGAGTGTGTAT[AC/J]ATATTAAACACATGAAAGATAATACTTAGAAAAA ACCTCCAGTTCTTATTAGTTTGATATTTCTGTACTCAGAGCATTTTAGGTTGCAAGGATATAA
WI-18080c	80 C T	---	---	TGGCATAAAGTTTGCAAAATATCAATATCAAACTAGTCTCTCTTTGTAATTAATACTACTATGCCGTG TTTGACTTTTAT[C/T]TCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGTAT
WI-18080b	65 G A	---	---	TGGCATAAAGTTTGCAAAATATCAATATCAAACTAGTCTCTCTTTGTAATTAATACTACTATGCC[G/ A]TGTTTGACTTTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGTAT
WI-18080a	41 T C	GCAATATCA ATATCAAACT AGTCTCTC	CAATTTACATA AGAGATAAAA GTCAAACA	TGGCATAAAGTTTGCAAAATATCAATATCAAACTAGTCTCTCTTTGTAATTAATACTACTATGC CGTGTGTGACTTTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGTAT
WI-18086	63 G A	---	---	GTGGGCATCCTATAAAAGCAGCCATGTGTGAAACAAATGATATGCACAGAAAGCATACTTCT[G/A] TGGCTTTGTTACACGGGTTTCTTCAAGAGGAAGATGACTCAGCCCTCCAGCTTCTGCAGTCTAGC TTAGGAGAGGGTTTGAA
WI-18115b	71 C T	---	---	AACTACATAGTATGGTGCCCTGGCTTAGAATCAATGGGTAAAGCCCTTAGTGTACCTTTGGTATCC TTC[C/T]TTTGGTATGAAAGACAGACCTCTGCTGGAGGACTCATACAATGTAAAGAAAGGGTGAG TCAGT
WI-18115a	70 C T	TTAGTGTAACCT TTGGTATCCC TT	AGAGGTCTGTC TTTCATACCAA A	AACTACATAGTATGGTGCCCTGGCTTAGAATCAATGGGTAAAGCCCTTAGTGTACCTTTGGTATCC TT[C/T]CTTTGGTATGAAAGACAGACCTCTGCTGGAGGACTCATACAATGTAAAGAAAGGGTGAG TCAGT
WI-18136	78 A G	---	---	TTTTGAGAAGCACTCTGTAGGCAAGGATGCATTCAAAAATGGCTTTGAGGATTAATCTTCTCTTTA GGTAATTTGC[G/A]GTAAAGAACATAAAAGCATTTTAAAGTCCACTGCCGCTTAGAAACT
WI-18169	115 A G	CCATCTTCCG	GAGTCTGCTT GTGCTCCA	GGCAAAATATTTTACATCACACCTGGAATCTGCCAAGTCTTCCACTATGAAGGCAATCGTAGAG TGTCAGGAGGAAGGTGTTATCCAGCAGCCATCTTCCGGAAGCTC[G/G]TGGAGCACAAGCAGA ACTCGGTGGTAGAGTGGG
WI-18190b	26 G A	---	---	TGAAAGAAAGTCGACACAGCGGACACT[G/A]TCATAAGTGGAAACAAAGGATGAAGCTAATCATGGAG GCAAGCTCCCTGGAGAGACAGGACAAATCAAGATGAGCTGGAGACATTAATCCTGGCGA

WI-18190	62 G A	...	...	TGAAAGAAGTCGACACAGCGGACACTGTCATAAGTGAACAAAGGATGAAGCTAATCATCGGA[G/A] GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGATGAGCTGGAGACATTAAATCCTGGCGA
WI-18181	100 A C	AAATATATAC AACACTCCCTT CAGATC	CGTTTACCAT TTGTTAAGCTT TTG	GACAGTGAAAACATTGAAAACACAAAATACAAACAAAACATTAGGAACAAGAAATGTGTAATCCAA TGTTGAAAAAATATATACAACTCCCTTCAGATC[A/C]CAAAAGCTTAAACAAATGGTAAAAACGTA TGTTGTTCTTGAAC ATTACATAAGCAATTCCTGAGTACAACTAGGGGACAGGTATTTACAAAAACAAATAGAGCAGA GTTCCCTGCCCTC[G/A]GTGTGCGGGGAGAGAGGGGATTTCAGCATTTGGTGAGTATGTTAATT CCCTCAAGTTAATTCCTTC
WI-18215	78 G A	AGCAGAGTTC CTGCCCTC	OCTCCCTCTCT OCCC	CATTTCCGAAAATCTGATAGTTAAATATCCCGTCTGGTGTGATTGTGATACACTTAAGT[A/G]AA CCCTGAAAACCTTTATTTGAAATTTGAAGTTTTCCTCAGAACTGGCAGAACTTTTCACATTCTG AC
WI-18232	60 T A A	GGAAACTTG AGTTTGAGATC ACA	CACAGAAGTG AATAGACTAGT GAGACA	TTTAAAAATGCTTAGATTTTCTCAGTATTTTATCAATAGTGTGAAGCTGGAAAACCTTGAGTTTGAG ATCACATAT[C/C]TGTCCTCACTAGTCTATTCACCTCTGTGGGCATTTGGCAGAAAGTGGC AATATCCCCAAATGTTAATCGTAACATACTG[A/G]AAAGCTGTACAGTAGAAGTGTAGCAAAAAAT TGGATGCCACAACCTTATCTCACCATTCTTCAAGCAAGTGAGGGTCAGAAATGTTTCTTGCCTATATC TGCAAAAAGATCGAACAAG
WI-18242	30 G A	AATCGTAACA	CTTTC	GCATCAGACATCACCACCTCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATC[C/T]ACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18266c	119 C T	...	...	GCATCAGACATCACCACCTCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACAT[C/C]TGAGAC CCGCAACTCCGAGGTACCT
WI-18266b	124 T C	...	...	GCATCAGACATCACCACCTCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[C/C]TGACAAATGATGCATGAATCCACATTTTGAGAC CCGCAACTCCGAGGTACCT
WI-18266a	97 C T	AAATAGGAAA TATGGACTATC TTCAAA	TTTCATGCATCA TTTGTGCA	GCATCAGACATCACCACCTCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[C/C]TGACAAATGATGCATGAATCCACATTTTGAGAC CCGCAACTCCGAGGTACCT
WI-18312	73 A G A A	GCTGTCAGCTA TTGTTATTCA	GGAGAAAAGG GAGCAGAAGA	CTGAGCCTCTTGATATGTGGTTTAGTGTCTATCATTAAATTTTGGAAAGCTGCAGCTATTGTTATTTC AAAT[A/G]TATCTCTGCTCCCTTTCTCCTTTTCTGGGATTCCTATCTGCATGTGTTATA
WI-18330b	66 A G	...	...	AAACATCTACAGCTGTCTTAGGCCATCCTGTAGAAATCAGGGAATAGAGCTGAGGAACAAGAGGG[ A/G]TATGTAGGCAGTGAGTCAGGACTATGCAAAACCATAAAATAAAGAACATAAATTTTTTTTGTGAT TCACA

WI-18330a	49	G A A G A	TCCTGTAAGA AATCAGGGAT	AGTCCTGACTC ACTGCCCTACA	AAACATCTACAGCTGCTTAGGCCATCCTGTGAAGAAATCAGGGATAAGAG[G/A]CTGAGGAACAAGA GGGATATGTAGGCAGTGAAGTACAGGACTATGCAAAACCATAAAATAAGAACATAATTTTTTTTGTGAT TCACA
EST37564 5	85	T C A G A	AAATTCAAAGC CATCTACAAA	CTATGGAGGCC TCAATGAGA	AAATTAGTTAGCCATAACAGGCTGGAATTGCTGGTTAGAATACTGCATGTTATTTAAGCTAAATTC AAGCCATCTACAAAAGAT[T/C]CTCATTGAGGCCCTCCATAGGCTGCAACACATCAAAAGGCATTAC TGTAAGTGGAGAGGACTGAG
WI-18327	104	G A T T	AACAGCTTT CGTTAGGCTAG	CGCATACAATG GCTCAGC	CAAAAGGATTTTATTACCTACAACAAGTAAGGAGGACAGCTGGGGCAGTTTCCCAAAGCAGTACCTC CCAAACAATGGTGAAACACAGCTTTCGTTAGGCTAGTT[G/A]GCTGAGCCATTGTATCGGAGGCAGA GT
EST37624 6b	102	G A ---		---	GTGGCAAGAGCAGCTAAACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGCA[CT]GCTGA CCTGCAGTCTCTGCCGTGCTTGGCTCTCTGGACG[G/A]TTCATTCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCATTC
EST37624 6a	58	C T ---		---	GTGGCAAGAGCAGCTAAACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGCA[CT]GCTGA TGGCTGCAGTCTCTGCCGTGCTTGGCTCTCTGGACGTTTCATTCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCATTC
WI-18357	89	C G G C A T C A A	CCCAGCCCTTA GCATCAA	AAGGACTCAA AGACTGAAGAT GA	AATGTTTTAAAGTCTACCGTGTGAGGTGGCCATGAAGCCAAAGCCCATGGAGAGACATTTTCAGA TAATCCAGCCCTTAGCATCA[C/G]TCATCTTCAGTCTTTGAGTCTTCCAGCCAGGTCCAAAGCTT GTGGACCAGAGACAAGCC
WI-18012g	117	A G ---		---	TTTTATCTGGTCAGCTCTCTTAATGGCTGAAGGTCACTCTCTTTCAACTTTCCAGACTTGGAAAG ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTTCTGTA[G/A]GTGTTTCCCTGATACA CGCTGACGTTTCGAGGG
WI-18012f	113	G A ---		---	TTTTATCTGGTCAGCTCTCTTAATGGCTGAAGGTCACTCTCTTTCAACTTTCCAGACTTGGAAAG ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTTCTGTA[G/A]GTGAAAGTGTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012e	112	C T C C C T	GCCACTTTTGC CCCT	TCAGCGTGTAT CAGGAACA	TTTTATCTGGTCAGCTCTCTTAATGGCTGAAGGTCACTCTCTTTCAACTTTCCAGACTTGGAAAG AGATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTTCTGTA[G/A]GTGAAAGTGTTCCTGATACA GCTGACGTTTCGAGGG
WI-18012b	46	T C ---		---	TTTTATCTGGTCAGCTCTCTTAATGGCTGAAGGTCACTCTCTTTCAACTTTCCAGACTTGGAAAG AGATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTTCTGTA[G/A]GTGAAAGTGTTCCTGATACA GCTGACGTTTCGAGGG
EST38390 4	75	A G C T C T G C A T T G	GCAAAAAGGA CTGATTAATAA	GCTAAAGTCAG CTGATTAATAA	CATATCATAGCCAGATCTACAACCCAGAGTAATCCCATGGTTATGTTACATGGCAAAAAGGACTC TGCATTGTA[G/A]TTAAGTTTATTAAATCAGCTGACTTTAGCATTTGGAGATTATTCTGGAT

EST38512 7	91 T	TAATAAACTGACCCCAATTGGTAACTGTGTCTGGACTGAGAGAAACAATGAAAAATCTGTAAAT ACCTGATGACGATGCCAATACTCGT/GJGCTCCAGAGTGCAGTGATAACTGTTATAGCC	CACTGCACTCT GGGAAGC	TGACGATGCC GAATACTTCG	CACTGCACTCT GGGAAGC	TAATAAACTGACCCCAATTGGTAACTGTGTCTGGACTGAGAGAAACAATGAAAAATCTGTAAAT ACCTGATGACGATGCCAATACTCGT/GJGCTCCAGAGTGCAGTGATAACTGTTATAGCC
EST38519 0	24 C T T	CCTGCACTCTCTAAAGATCTTTTC/TJCCCCCAAGTCTCAACAGAATGGTATATCTCTCTGGAAAA AGATGAACGTCATCAATGGATTGTGCTGCTCTGTTTCAGCTTTGATTTTTTTTGCTCTGAGAACCTTG TCTGCTCTGCTGATTT	TCTGTTAGGAC TTGGGGA	CCTGCACTCT TAAAGATCT	TCTGTTAGGAC TTGGGGA	CCTGCACTCTCTCTAAAGATCTTTTC/TJCCCCCAAGTCTCAACAGAATGGTATATCTCTCTGGAAAA AGATGAACGTCATCAATGGATTGTGCTGCTCTGTTTCAGCTTTGATTTTTTTTGCTCTGAGAACCTTG TCTGCTCTGCTGATTT
EST38575 1	66 T C A A	AGTGGTCAATGTAAACTAATGGGACACCAAGCCTCAGGAAGAACAATCCCATGTTTCTGTTTAA T/CJCTCTTATGTGTATACCTTCCCTTCTCTTCTTATACACATAGATTTTCCCTTAATTGCAGC CCA	AGGGAAGTA GTATAACACAT AAGAGA	GAACATCCCA TGTTCTGTTT	AGGGAAGTA GTATAACACAT AAGAGA	AGTGGTCAATGTAAACTAATGGGACACCAAGCCTCAGGAAGAACAATCCCATGTTTCTGTTTAA T/CJCTCTTATGTGTATACCTTCCCTTCTCTTCTTATACACATAGATTTTCCCTTAATTGCAGC CCA
EST38616 9	101 C G C T T C	CCATAGGAGGCTACCTAGCTCTCTGTGCTCCAGAGTGGTGCTCAGCCCGGGGGCCCCGCTGG AGTCTCCGGGGCCCCGCCCTGCTCCGCCCTTC/GJGCCAOCATCCATTCCTCCAGGGG	GAGGAATGGAT GGTGGC	CCTGCTCCGCC CTTC	GAGGAATGGAT GGTGGC	CCATAGGAGGCTACCTAGCTCTCTGTGCTCCAGAGTGGTGCTCAGCCCGGGGGCCCCGCTGG AGTCTCCGGGGCCCCGCCCTGCTCCGCCCTTC/GJGCCAOCATCCATTCCTCCAGGGG
EST38652 8	59 T C C A T T T C A A	TATAGTAGGTACTTTCTGCTGTCAGCAGGAATTTATTCAGTCTGAACCTGGGCAATTCAA/T/CJGCGTG GTATTTTTTCTTTTCAATTTTGCAAGTAAAAAATCAT	TTGCAAAAATG AAAGGAAAAA	TCTGAACTGGG CAATTC A A	TTGCAAAAATG AAAGGAAAAA	TATAGTAGGTACTTTCTGCTGTCAGCAGGAATTTATTCAGTCTGAACCTGGGCAATTCAA/T/CJGCGTG GTATTTTTTCTTTTCAATTTTGCAAGTAAAAAATCAT
EST38654 5	42 T C G T T T A C A	CTCAAGCTGAGAATGGTCATTTTAAATATATCAGTTTTACATA/T/CJAGATAGAAGATTAAAGGACCAT CACTGAGGTACATAGCTCAGAGGAGAGTTAAGATTGGACCCAGGAGTTGGTTCCAGCATATA	CAGTGATGGTC CTTAATCTTCT ATC	AATGGTCAATTT TAATATATCA	CAGTGATGGTC CTTAATCTTCT ATC	CTCAAGCTGAGAATGGTCATTTTAAATATATCAGTTTTACATA/T/CJAGATAGAAGATTAAAGGACCAT CACTGAGGTACATAGCTCAGAGGAGAGTTAAGATTGGACCCAGGAGTTGGTTCCAGCATATA
EST38707 9	75 A G ...	GGATCCTCACTACCTGGAGACCTGAGAAGGACATCCACCAAGACCTACTGATCTGGAGTCCCA CGTTCCTT/CJAGGCCAGCGGGATGTGTGCCCTCTCTCCCAACTCATCTTTTCAGGAACACGAGG ATTCTGCTTTCTGGAAA	...		...	GGATCCTCACTACCTGGAGACCTGAGAAGGACATCCACCAAGACCTACTGATCTGGAGTCCCA CGTTCCTT/CJAGGCCAGCGGGATGTGTGCCCTCTCTCCCAACTCATCTTTTCAGGAACACGAGG ATTCTGCTTTCTGGAAA
EST38759 2	86 A G G G T A T G G	TGACCTTGATTTCTTCACTAGAGGGGAGAAGAAATCACTACCTTTTGATGCCCTCCCACTCTACTTGT CTCCCTGAGGTGATATGG/A/GJCTTAAGTCCACGATGGTGACCTAAACTCAGTTTAAATCTTTGCC TAGCAGCACC	TCACCATCGTG GACTTAAGG	TGCTCCCTGA GGTGATATGG	TCACCATCGTG GACTTAAGG	TGACCTTGATTTCTTCACTAGAGGGGAGAAGAAATCACTACCTTTTGATGCCCTCCCACTCTACTTGT CTCCCTGAGGTGATATGG/A/GJCTTAAGTCCACGATGGTGACCTAAACTCAGTTTAAATCTTTGCC TAGCAGCACC
EST38775 1	40 T A C	GACTCTCAACCAAGAGAAATCAATAGGAGAGGATTGGCT/AJTTTGAATTCAGAGCAAAAGCCCT CTTACTGAGAGGTGAGCCCCAGCCCCCTCCAAATGCCCTTTTCATGAGTTAGGATCTCCTAAGTGGTAC AAACAACCAACAATGGTGG	GGCTTTGCTCT GAATTC A A A	AATCAATAGG AGAGGATTGG	GGCTTTGCTCT GAATTC A A A	GACTCTCAACCAAGAGAGAAATCAATAGGAGAGGATTGGCT/AJTTTGAATTCAGAGCAAAAGCCCT CTTACTGAGAGGTGAGCCCCAGCCCCCTCCAAATGCCCTTTTCATGAGTTAGGATCTCCTAAGTGGTAC AAACAACCAACAATGGTGG
EST38815 4	91 C A C A	CACCCATATTTGACCAAGGGATGAAGCCTAGCCATGCTCTTCACTTAATGTTGTTTCAACAAG TGTTTATGAGAACCCATTACACA/C/AJAAAGCATGTGCCAGTCAGCAGATTCTGTAATAA	GCTGACTGGCA CATGCTTT	TGTTTATGAGA ACCCATTACA	GCTGACTGGCA CATGCTTT	CACCCATATTTGACCAAGGGATGAAGCCTAGCCATGCTCTTCACTTAATGTTGTTTCAACAAG TGTTTATGAGAACCCATTACACA/C/AJAAAGCATGTGCCAGTCAGCAGATTCTGTAATAA
EST38858 4	98 C T T G A C	TCCTTACTGTGCTTACAACCTTTCTCTCCAAAGTTTGGGGTTCCTCATATTTGTTATTTGTTATTA TTCAACACGAGTAAAAAGAACTCATGAC/C/TJCTCCTTGGACTCGCTCTCTCCCCAATCTCGAT ACCGACTGCACCTGTTG	GGAGCGAGTCC AAGGAGAA	CACGAGTAAA AAGAACTCA	GGAGCGAGTCC AAGGAGAA	TCCTTACTGTGCTTACAACCTTTCTCTCCAAAGTTTGGGGTTCCTCATATTTGTTATTTGTTATTA TTCAACACGAGTAAAAAGAACTCATGAC/C/TJCTCCTTGGACTCGCTCTCTCCCCAATCTCGAT ACCGACTGCACCTGTTG
EST38865 2	72 T C T G T C G A T G C	CCCTAATGGATTTTACAGCTCATCTGAGTCTGCTGTGTTCTCTGAGGAGCTGTAGAAATTTGTTGTCG ATGCT/CJCTGTGCTCTCCGCTCTCCCCAATGAGCACATATGCAGGGCAGGCAAGAGCATGCTGGA TTTGCTTAGTTGTTAA	GGAAGGACGG AGGACACAG	GCTGTAGAATT TGTTGCTAGTGC	GGAAGGACGG AGGACACAG	CCCTAATGGATTTTACAGCTCATCTGAGTCTGCTGTGTTCTCTGAGGAGCTGTAGAAATTTGTTGTCG ATGCT/CJCTGTGCTCTCCGCTCTCCCCAATGAGCACATATGCAGGGCAGGCAAGAGCATGCTGGA TTTGCTTAGTTGTTAA

EST38878 9	47 T C	AAACATCATT ACTAGCCTAG ATCCTAA	CCTTCAATAAA TCTCATGTCCT CA	CCAATGAGAACCAAGTAATTAACATCAATTACTAGCCTAGATCCTAAAT/CJTGAGGACATGAGATTT ATTGAAGGGAATCCTCAATTAATATGAACATTTCTTGAGAAATGGGAAATTTGAAACACATTCCC TTATCAATGTCATCTCACACATCTTTATTTTATTTGTTTTCACATTTCTCAAATATCGGATTGTTC TCATGAGAAATAATGGCTGAGGGAGCTGGCAGGCTCTCTCA/CJGCTCCCTGGATAGCTAAAT TTA
EST38882 6b	113 GC	---	---	TTATCAATGTCATCTCACACATCTTTATTTTAT/CJTTGTTTTTCACTTTCTCAAATATCGGATTGT TGCTCATGAGAAATAATGGCTGAGGGAGCTGGCAGGCTCTCTCAGGCTCCCTGGATAGCTAAAT TA
EST38882 6a	35 T C	TTTT	CAA	
EST38909 5	47 A G	GCTAAAACG	GGTATTTGTTG ATTCCCATCTT T	GCACTAACTAACTTTCAITTTGTGGATTGCACAGCATGGCTAAAACG/A/GTAAAGATGGGAATCAA CAAATACCATTAAGATATGGAGCAAGAGAACTCTCACATACTGCTGGAGGGAATATAAAT AACTGAATGGCAGTGAACACACTACACATCAAAACTTAGGGAAATGTGGTAGTGTGGTACGTTGAG GGAAACTTATAACCTCAC/A/GJCGCTTGTTCACAAAAACACAGACACAGAGATTTCCAACTC CAGCAATGACAGGCTAGGG
EST38911 9	85 A G	CAC	GAACAAGCG	TAAACATCCCATTTGAATCCCTTGTGGG/CJGGGGGGGGTGAGATTGCAGTGTCAAGATAAA TATCACAATATATCAAAAACCTTCAAATTTGTCTATGCATTACACACTGACATGAGCCACAAACATT CCTTTACAGGGACTGTAC
EST38955 5	30 GC	GGTGG	CACTGCAATCT CACCCC	CCTGCTATGATGCCTGGGAGATCCGGACCTTCGGTGAC/CJAGGGCTCCCTGCCAGGGCTTGG CCCCTGACCGGGCTCCCGAGCTCGGCCCTGACTGTGGAGGAGCTGAAATACGCTGACATCCGCAACCT C
EST39002 0	42 G A	TGACC	CTGGCAGGGAG CCTG	CACGTGGCCCTAAGTTTCCGGGTCTTCTCAGTCTGGATGGCTGTGTGGAAGAAAGCTTGGTGGTAAG GCCTAAGGAAT/GJAGGGGCGAGGGGGCGATGCCGCCAGCCGAGATGGTCTGTAAAGCCTGTGGGTC AAAGACCTAACTCTGGA
EST39004 8	79 T G	CCTAAGGAAT	ATCTCGGCTGG O88C	AAAGATAATGTCAATCACAACGCAACATATAGAAACATAAAAGAAAAATAAAGTATCCACCCCTAAAAT CCCTATTATTCCATGATATTTTCA/CJAGCAACTAGTATATATCAATATATTTTTCACAAACCAT TCAGTTACAC
WI-16398	90 T C	TCA	TTGATAT	
			TAAGGGCTAAT TCCCTATATAA AAAG	GGTTGCTTTTCATGATTTTCTCATTTTCTATCAGGTTTCTGGTCTTGTCTCTCAATTTTAAACATT T/CJCTTTTATATAGGGAATTAGCCCTTAAACTGTGTACATGCTGCCAAAAATTTCTCTCCAGTT
WI-16403	69 T C	ACT	CCAGAACCCAG ATGTGTTTAA	GCTTTAATGGCTACAGAAAGAGG/CJGGGTTTTATTTTCTTTTTTAAACACATCTGGTTCTGGCAGC TACAGAAAGA
WI-16406	24 C T	AGG	AA	AAGTTATATTATGCAITTTAGAGCAATAGGTGCCCTGAA

EST39236 0b	57 C G	TCATCTGAGA ATAAACTTCCT GTCT	CATTATAGGTA CTGAGTCATAC ATTAAACA	TCCTTTTATTTCATGATTTGTTTCATCTGAGAAATAAACTTCCTGTCTAAATTTTCCAA[C/G]ACTATGTT TAATGTATGACTCAGTACCTATAATGAGACTGGAATAATATTACCTGGCAATGAATGAGGTGTCTC TTT
EST39294 4	63 G T	CCTGAAACAG GGATGOC	GCACAATTAA ACATAGTACCG AGAA	CAAAACAGACCTTTGGTTGAGCTCACCTGGTGACAGAGACTCCTACCTGAAACAGGGATGCC[G/T] TTCTCGGTACTATGTTTAAATTGTCTGAGCCAGCAACCTCGAGTTACCGGCCCTTTACCCCAAGGCC AGCTCTGCTTGTCTGCAT
EST39366 2	72 T C	---	---	AGAAAACATTCTGTCTGATCAGAGGAAGATGTATGTAGAAAATCAGAATCTGACTGAATTCCTAAA ATCTATT[C/J]ACACTGAGAGGAAAATGGAAGAAAATGTTTGATATAAGCTTTTCCCTGACTCTCA GAGGGTTCAGA
EST39371 9	86 A G	CATTGGATTA GGTGAGAGG TT	TGATTTGAGAC ATTTCACATTT TT	AAAAGCTGTAGCTGGCAAGTCAAAGTTTATTTTATGTGTGTAATTTCCAGTTGAGCAATTTTTCAT TTGGATTAGCGTGAGAGG[A/G]AAAAATGTGAATGTCTCAAAATCAAAATGCTTCTCTAAAGATTA GACATTGCCCAACCCCTGC
WI-17177	23 A G	---	---	ACAAAGTGACATATCCAAACCAAC[A/G]TCCATCCCCACCTGTGCCCTATTCTTCTTGTGTTCTTT AGAGCCTTTTTCAGCTATTTCTGTGAAGCAAACTGCACGAAGGCCCTCCCCGTACTCTCCCCCTGGAA G
EST39428 8	31 C T	GCTCCCCACA ATTITGATT	GGTCCCTTATG AAGCCACC	AGGTTCTTGGTTGCTCCCCACAATTTTGATT[C/T]GGTGGCTTCATAAGGGACCCAGGATTTCTGCATT TTCTGGGTGGGCCCTAGGTAATTTCTGTGCTCTTTGGTCCACAGACACAATTTAAAGAAGATCAGGTCT GGCTGTTC
EST39430 2	45 A C	GGCAGAGGAA TAACTGATGTT C	CAGGGGTGGG GTATTG	AATTTAGCAGAAACAATGAAGTTGGCAGAGGAATAAAGTATGTT[C/A/C]CAATACCCCGACCCCTGA CCAGTACCTTTCCCTCAGGCCCCAGGCTCCGGTGGAGGATGCTCGGG
EST39446 7b	117 C T	CTACTGACAT AGGACTTCA	TCTGGAAAAC TGACATAAAC	AAAGCCCTGTAAACTGAAGCTAGACAACGTCAACTTTTGGAAAGAAATACAGGAACCTATTTATAT ACGTAATACACTTTTATACCTGCTTACTGACATAGGACTTCAGAGTAAT[C/T]GGTTTATGTCAGT TTCCAGGATTGTTCTCC
EST39465 2	80 A G	AATGCAGGAG GGTGGC	CAATCTCGGC CCTCT	ATGGTGTCAATTAGAGGGCCACAGGGGATGGGGAGTAAAAAATAACATAAACGAACGAACAGAAA TGCAGGAGGGTGG[C/A/G]AGAGGGGCCGAGATTGGGTGTTTCAGGGCAGAGAGGTGGAAGACCAG
EST39501 0	81 A G	AAAGATTCTT GTAGACATCT AACATTAG	CACITGCAATT CTGAAGGCT	TGCTTACAACCCATAACCATAGGCCATGTGTTTCAGACATTCTTGACCAAGCCTAAAGATTCTGTAG ACATCTAACATTAG[A/G]TAGCCTTCAGAAATTGCAAGTGAAGTTCAAGTCAAAACCAATTC
WI- 18387b	84 A C	---	---	CACAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCCATACATTTTGGTCA CATGCTTAGCCATAC[A/C]CATGGTAACATTGACTATGGAGTCTTGTGAAAAGTGAATGTGCGGATG GCTATGTAGACATAAAGA

WI-18387a	57 A G	CCTTACTTTGG TGACCCCAT	GCTAAAGCATG TGACCACAAA	CACAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCCATAC[AG]TTTGTG GTCACATGCTTTAGCCATACACATGGTAACATTGACTATGGAGTCTTGTGAAAGTGTAAATGTGCGATG GCTATGTAGACATAAAGA
EST40601 9	78 A G	GCGTGGAAACCT GAAACAC	TTCTTTGGAAGA AAGGGTC	TCCCAGGATGGTTTATCCAAAGCTGTGGACGGTGAACATTAAAGACGAAAGAGGTGACTCGCGTGGA ACCTGAAACAC[AG]GACGCTTTCTTCCAAAGAGGGCTGTGGCGATCAGGCCACTCAAGG
EST41935	32 A G	AGTGATCAC ATCTTCAGGAT AGGT	GCACACCTTC ACACTGTTA	TCCATTCAAGTATCACATCTTCAGGATAGGT[AG]ATAACAGTGTGAAGGGTGTGCTCATTTTCTTC AGCTGTAGTAGGAGTCTCCCGAGAGTAGCAGTTGTTGA
EST43091	28 C T	CATTCTGGTCT TTATTTTGGG CA	AAACTGATTT GTTAAACATG CTAC	ATGTCATTTCTGGTCTTTATTTTGGACA[CT]GTAGCATGTTTAAACAAATCAGTTTTTCATAGGCAA CCTTTTGAACATCAAAAGAAATACAATATAATTTTCAAAATTTCTCATCACTGTAAATCA
WI-18420c	108 T C	TTCCATTAAAC AGGAAGTTTC C	AAATTCAGC ATTGCTATAAG C	AGAGACACAACAAGAAGTAAGGGGAAATGGGAAGAACAGAGTGAATTAAGCAAAATCTTGA TTCAGATTCCATTAAACAGGAAGTTCTCAAAAAAATCAAA[CT]GCTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
WI-18420a	38 C T	GAATAAGGGA AAATGGGAAG AA	CCAAGATTTGC TTTAATTTTAC TC	AGAGAGACAACAAGAAGTAAGGGGAAATGGGAAGAA[CT]AGAGTGAATTAAGCAAAATCTT GGATTTCAGATTCATTAAACAGGAAGTTCTCAAAAAAATCAAAATGCTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
WI-18425b	101 T C	CACCTGTCT AGACAGATT C	--- OCTCCTGTTGT TGTTGCA	AGCTGATCAGCTGCTGTTACTGTTTATGTGGCCAGGGAAGCCAAAGATCAGACACCTGTG CTAGACAGATTCAATGCACACAACAACAGGAGGT[CT]GGGGGTACACGGGCGGAGAGCCAAAGAC TAGGGC
WI-18425	81 A C	AAGTGGGACT CTTTTGGCTCT AAGTGGGACT	CTCCCCTGACT GTATCCAGA	AAATTGAGGTCGGGTGGAACATAAAAAGGAAGGAAGAGTAATCAAGGGAGGCCAAAGTG GGAAGCTGATTGCTGATCTAACGTGCTGTCCAGTTCTTTTGGCTTAAGTGGGACTA[CT]TTC TGATACAGTCAGGGGAG
WI-18449	129 C T	---	---	ATCGCTTCATTGAAGCCTGCTTAATTTCTCAGTCAACTGGTCCCCCAAGACATTATTTTATCTT AAATGTCCAATATCTGCCCTGATGCTGTGTTTGTGCACATTGGGGCCACAG[CT]AAATAGGCTAAA AGGCAGTCCCACCTGCT
WI-18457	120 T C	CCACAATGGC AGAGGTGA	TTTAGGCTTTG AGATGGTTTCT	GGTGCTATAGCTGCTGTACACCACAATGGCAGAGGTGA[AG]TAGAAACCATCTCAAGCCCTAAAA TATTTACCATACATCCCCCTCACAGCAAAAGTTTCTAATCTCGGTTTAGGACTCCATTGAG
WI-18462	39 A G	GGTGGGGTGC	GCACGATGGGA GTGACC	TGAGACGTGTGACAAGTCCACAGGGGTGGGGCCGGCTGAGGGTGGGGTGGCGAGG[CT]GGT CACTCCCATCGTGCCCTGGCCGCTCCCTCCACTCACCCACACCTGGCCAGTCCACGTTGAGGT



WI-18491	109	G A	AACAAATGGT AGTGGTATT	CGTGTGCATT TCITGTAATCC	CTAATGAGATGAATACATGGAAGCGGTTTAGCACAGTGCCTAAACACACAGTAAGTAACCAACAAAT GGTAGGTGGTATTAAATACTATTATTAAATCCAGAATGAC[G/A]GGATTACAAGAAATGCACA CGT
EST50757 b	79	C T	GAGCTCGAGG CTGCTTCT	ACCTTTCACCC GCCC	AGCCCCCTCCACTCCACTCTGCTTCCACAAAGTCGGCTCCGAGAGCTCGAGGCTGCTCTCTTTTATAT GTGAGGGCC[C/T]GGGCGGGTGAAGGGTCACAGA
WI-17675	103	T C	GGACATTTGG ATGGTGACTT	GGGGAACCAAC CAGG	GATCTTGAAAGCACTAGAACTAAACATCTTCACCAGGTGCTGAAGAAAGTGTCTCTGTTTTAAT TGCCAAGCAGGATGGACATTTGGATGGTGACTT[C/C]CTGGTGGTCCCATAGATTACCAT TGCTCTAATGGTGCTA
WI-16543	67	G T	AGATAAACTA CATTTGGTTT	GATTCATCAT ACAGGGGACTT	GATCCATTACCTAGGGTAAAAATTCCTGAATGTCAACAAAGAGATAAACTACATTTGGGTTTTGG G/TJAAGTCCCTGTAAATGAATCAAGAAATCCTCAAGTCTGCTTCCCACCCATTTAATACGTATT TTTGTAAAGGCTGAAGT
WI-17687	107	C G	GCCAAAAAGG TTGGGGAA	TTACTTTTGT CCGACCAGCA	ATCTGAGATGGAAGAGTTTCATCCCAAAACCATCTCCCCCTGACCCCAAGTCCATGGAATAATGTC TTCCACAAAACCGGTCCCTGGTGCCAAAAAGGTTGGGAA[C/G]TGCTGGTCCGTACAAAAAGTAAT G
WI-17690b	79	A G	AGGCATTTTC TAGCTGTGTT	...	ACAACATGTGAAGAAGATATGTTGCTTTACTACAGTGGAGGCATTTTCTAGCTGTGTTGATT GGCTTCCCTAT[G/G]ATTACAGGACCCATAACTCTTGTCTCACTCATCTGCTATGCTGCTG
WI-17690a	63	G A	AGGCATTTTC TAGCTGTGTT	CAAGAGTTATG GGTCTGAATC	ACAACATGTGAAGAAGATATGTTGCTTTACTACAGTGGAGGCATTTTCTAGCTGTGTT[G/A]A TTGGCTTCCCTATAGATTACAGGCCCAATAACTCTTGTCTCACTCATCTGCTATGCTGCTG
EST51717 b	128	C T	GCGGAAGACA GTGAGCTGTT	TTGAGGCAATA ATCCAGCTC	GATCCAAATCTCAGTGTCTAACTCATCATCCAGATTATTCTGAAGTGGAAACCCCTCCGACCCAA TGGCAACATCACCCACTACCTGGTTTCTGGGAGAGGCGGGAAGACAGTGAGCTGT[C/T]GAG CTGGATTATTGCCCTCAAA
EST51717 a	39	C T	...	...	GATCCAAATCTCAGTGTCTAACTCATCATCCAGATTATT[C/T]GAAGTGGAAACCCCTCCGACCC CAATGGCAACATCACCCACTACCTGGTTTCTGGGAGAGGCGGGAAGACAGTGAGCTGTTCGAG CTGGATTATTGCCCTCAAA
EST53012	97	C T	TGGTCACTTTG GGGCC	GGCTCTGOCCA CGCC	TTTCCAGGTTGACAGGTTTATCCACCCCTTCCATCCCCATGGCCACCCAGGCAAGGAGGAGACAG GTGTGCTGGAGTCTGGTCACTTTGGGGCC[C/T]GGCGTGGCAGAGCCCACTGGGTTTACATTTCTGT GGGCAGGTGTGGACAC
EST53349	96	A G	TGTTGAAGC AGTCACAATG TAC	CATCTGGATAT CTTGTCACTT TT	AACTGCAATAAACAACAAAAACAGAAGTCCAAGAGGCTAAAGTCTAAGCTATAATTACACATG AAGTATATGTTGAAAGCAGTCACTATGTAC[G/A]AAATGTGACAAGATATCCAGATGTTTAA
EST53389	74	A G	GGAGACCTGC AGAACTTAAA GCA	GGCCTTTCTAA CAATAAATGCT C	TTTGAATGTCTCCATGACTTGACAGACTGAGAGCCAGCCAGCCAGGAGACCTGCAGAACT TAAACAC[G/GAGCATTTATTGTTAGAAAGGGCAAGTCTTACACTCAAAATAGTTTTAACATGAAC ACATTAAAGGGAGATGGCC

[illegible]

[illegible]

TIGR- A003P30	117 C G	---	---	ACAAAGTTCAAAGGAGAACCTCCCTTTGTTTAAATGACAGCTGTGCTCAGAAAGCCTGTGATTTCCTAGGA AACCATCTGGGTTAGCCCATAGAAAAATGCAGTTTAAAGCAGTGTCA[C/G]ACTGGCTGCCTGAA GGTACCCCTGGAGATACT
TIGR- A004S34	156 C T A	CCAAACCTCCT CATTCTATAA	TGTAACACAGCT AACTGTTTTG TTAAA	GCTTGCTTTTATGTTAGGTCGGGGGAAAGGAGGCTGACAAACCGCAGACATCTGGACACCAGC AAGGGTCCAGGGAGGTTTGCAGAACTCTTTGCTTGGCTAAGAGTCTGTATGTGACAATAGCCA AACCTCCTCATTCCTATAAA[C/T]CTTTAACAAAAACAGTTAGTGTTTACAAAAACAGTTAGCTGTT TACATG
TIGR- A004T44b	97 A C	---	---	AACAACAGTGTAACTTTAACAGGGGATGTTAAAGGTAAAGTCAAGAAAGTAAACCCAAAATGAT TGAGTATGATAAAGAAATTTGCATGGCGATT[C/G]AAATAGAAAACTTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAGAAACAATATAG
TIGR- A004T44a	69 G A TGA	GGAAGATAAA CCAAAATGAT	GCCATGCAAAA TTCTTTATCA	AACAACAGTGTAACTTTAACAGGGGATGTTAAAGTAAAGTCAAGAAAGTAAACCCAAAATGAT TGA[G/A]TATGATAAAGAAATTTGCATGGCGATTAAATAGAAAACTTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAGAAACAATATAG
TIGR- A004V08	60 T C GGCATTCTCT	CAGGAAAAACA	TCCTCCACACA AAAGGC	CCTACAATCCTATAATTTCAAGGGTTGGGAGGATGCAGGAAACAGGCACTTCTTAT[C/G]GCC TTTTGGGAGGATCAATTTGGTGCATGCACCTTAGGGGACAAATTTGGCAGTAGCTGTCAAAATTC AGTAGCTGTCAAAATTTCAAA
TIGR- A004V26	125 A G	---	---	TCTAGCTATAAGACCAGATTTTAAATTTCTAGATATAGAATTATCCAGAATAATTTCTATTGAATTGA CTGATTACAAAATGTTAACAGCTGGATAAACCGTAAATATATGATTATCTTCACATGA[G/A]AAGGT TTCAGTTTATAAATGCTTAAATCTGTATCTATTGCTTAAATACTGTATCTATTGG
TIGR- A004V28 a	29 A G CGATCTC	TGTTGTGGTG	CGGAGGTTGCA GTGAGC	CCAGGCTATAATGTTGTGGTGGATCT[C/G]GCTCACTGCAACCTCCGCCCTCCAGGTTCAAGCAA TCTCCTCGCTCAGCCTCTTGAGTAGCCGGGACTACAGGCACCCGCCACCGCACCTAACTAATTTTG TATTTTITAGTAGAGACATTGTATTTTTAGTAGAGACAGG
TIGR- A004X20	25 T C GA	AAGTTTTCCCT CTCTTCTGTAG	TTTTATAGTTG ACTGTAACATG GAGAC	TAAGTTTTCTCTCTCTGTAGGAT[C/G]GTCTCCATGTTACAGTCAACTATAAACATGGCTCATGT TCACTCTGGGCTTGGCTTCAGAGGAGTTTGATATTTTGGAAAGTGGTACCTTTGTTCTGTGTCTTTCA GACCAACCGCTCTCTTTCATTTCTTCAAGGCTTCTTCCAAAGGAGTTAAATCATCATGTCCCAATC ATCATCATGTGCTCT
TIGR- A004X30	26 T C CCAC	TTTGAATCTT AGAGTAGAAC	TTCTTTATGGA AGTGTTTAAA CTATTTT	TTTTGAATCTTAGAGTAGAACCCAC[C/G]ACTCTAGTAATACTTGTAAATAAAATTAATAAGTTTTT AAACACTTCCATAAAGAAATTAGGGGTGCCAGCTCTTGATTTCCTCCCTAGGGATAAAGATATCCAT GTTAGGGATAAAGATATCCATGTAC
TIGR- A004Z04	102 T G ATGCAAAACT	TTCAATTTGGGT	CTTATAATTAG AAATTTTCATGA	CACGGTATATGCCCTTATATATAGGTATATATACAGATCGTACACAATATATTTAACAGTTTGACATG GGGTCCACAGTACCTTCATTTGGGTATGCAAAACTT[G/TT]GCTTTCATGAAATTTCTAATTATAAGG ACTGTGCTTCTCTCATATTCATTTCAATGGACATTATACAAAAATACAGTCTCTTTAGTGATTTAAGACGTC TCTTTAGTGATTAAAGACTG

TIGR-A004Z19	85 C	GAGAACAACT GAGCATTTT	AAGATGGTCA CGGGAAGA	TAAGTGGAGACAAGTTATTGGAGGAGCTTGACACCCCTCTTCTGCCCTAGCTTGTGAGAGACAACACTGC AGCATTTTTTCTTTTTC/TTCCTCCGATGACCATCTTTTGGCTGGCGGCCAGGCCCTGGGTGTC TCCCATATCGCTGTCTTATGTGAGACTGAGGATCTGGTATTAAGGAACAGATC
TIGR-A004Z42c	89 C	TTGGGGAGGT AGGAGACT	CAGGGCTGCG GTCC	GTCTTAGCAGAGGATAACTTTGAGGACAGCCCCCAAGCGCCAGGTAGCCTTCAGGGGCGGGCA GGGTGGGGAGGTAGGAGACTCTGGACCGGCAGCCCTGGCTCCAGCTTCATCATCTGTGTCTCTT CATCATCTGTGTCTTC
TIGR-A005D17c	81 T	---	---	TATGGACTGTGAGAAATATGATTTGGACAAAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGCT/C/GCTAGATCTCTTGGCTCTCTGTGAGGATCTCTCTTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGGTATCTTACGACAGTCAAACCTTACGACAGTCAAACAC
TIGR-A005D17b	79 G	GGGAAACCC AGCAAG	GAGAGGCCAA GAAGAATCTAG AC	TATGGACTGTGAGAAATATGATTTGGACAAAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAG[G/C]CTGCTAGATCTCTTGGCTCTCTGTGAGGATCTCTCTTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGGTATCTTACGACAGTCAAACCTTACGACAGTCAAACAC
TIGR-A005D44	97 G	TTAACAATTAT GAACCTTAAA CTGTACAC	TTGTCTATTAT TTAAAGCCAAC AAAA	CATCAGTAACATATACACAATTGGTCATCAACTGAACCTTGCCCTCCAATATATTTCTATACAATCTT AACATTATTGAACCTTAAACCTGTACACTTG/TTTTTTGGCTTTAAATAATAGACAATGATTTTTT TCTATTACTTAGTGATAGACAAAGTGATTACTTTGTAGACAAAGTGATTACTTTGTTC
TIGR-A005E31b	27 G	---	---	GGAGTTCAAATTTATACCAGGCTCT[G/A]CTCACAGCTGTACTGGCTAGGCAAGCTTTCCAGAC ACAAAGCCACCTGCCTGCCATGTGGATAGTACTCTTTGCCCTGTGCCCTTACAAAGCCACCTTCTAT TTCATACCAATACCTTCTATTTCATACCAATAAG
TIGR-A005E39	182 G	---	---	CTCAGTGTAAAAACCTTTGTTAGGGAAAAAATAAATCCAAATGGATATATGGGAAGAGAAGTG CCAGGCTGGATGGTCTGAGACAGATGACCCCTGGGCTCTTTATTTTGTCTTTCAACAGGACC CCACAGATATTTGGGTATGTATGAGGACTGGGATGCTCTATTTG/C/GGATGCTTCTATTT
TIGR-A005E42a	42 A	AGTAAGGTTA CTGCACCTTAC AGAG	CCTAAATCAGG GGAAATTGAG	GCTGAGTTTTGTATCTTTAGTAAGGTTACTGCACCTTACAGAG/GTCTCAAATTTCCCTGATTTAGGA AGCGCATGCTAATGGGTATTGCATAGGTGAAGTATATAAAATGTGTATTAAAGAGAATCCCAAG CTTGGTATAAGGCAGAAAAATAATGGTATAAGGCAGAAAAATAATAG
TIGR-A005E46	76 A	CACCTGACTCG GTGCTTTAC	COCTGGCTGTG AGGTAATGT	ATGACAATGATGATAGTATTAGCCTACCGTTTGTAAAGCACCTACTGCGTATCAGGCACCTGACTCGG TGCCTTAC/GTACATTACCTCACAGCCAGGGTTGGCAATGGTCAATTTTGACAAATGGTCAATTTG ACAC
TIGR-A005E46	76 A	GCAGGGGTGA CGTATGTAGA	GGGGAGGACAC CCTAAGC	AGAGCAGGGGTGACGTATGTAGAA/C/TGGCTTAGGGTGTCTCCCCACAGAGCAGATACTTGAACCG ACTCAATCTGTGTAAAGAGCACTTTGTCTGCTTACAGGACCTCCCCAAGGTGTCAGAGTTCTAT ATAGGATGCTGGATTAGTTCCTTTGATATTTGTAAAAATTTCCCCAAGAGCCGCATATGAATCTGCC

X57830	106 G C T	AGTGAACCA ACGATCATAT	CATTGACAGAA TAAATGAGGC A	GTGGCAACTGTGGAAGGCACACTGAGCAAGTTTTCACCTATCTCGAAAAAATATGAGATTGGA AAAAATTAGACAAGTCTAGTGGAAACCAACGATCATATCTG/CJATGCCTCATTTTATTCTGTCAAT GAAAAGCGGGTTCAATGCTACAAAATGTGCTTGGAAAATGTTCTGACAGCATTTTCAGCTGTGAG CTTTC
X74070b	72 T G TGGATC	CTTTTAAGAA ATTTTGTITA	GGGCTTAAAAA TATTAGAGATC TAGATTT	AACCTGAAGAAGTTACTGGGAGCTGCTATTTTATATTATGACTGCTTTTAAAGAAATTTTGTATTG GATC/TGJGATAAAATCTAGATCTCTAATAATTTTAAAGCCCAAGCCCCCTTGGACACTGCAGCTCTTT CAGTTTTCCTTATACACAATTCATTCTTTCAGCTAATTAAGCCGAAGAGCCTGGGAATCAAGTTT GAA
Z48804	44 C T ---		---	ACTGCCGAAGTGTAGCGGCCCAAAACCTTGCTCTCATCACCAG/C/TJTAGAGCTTCTCCCGAAGGG CCTTTAGGATAGGAGAAAGGGTTTCATGCACACACGTTGTGAGATGGAAGAGCCCCCTCCAGACCACT CTACAGCTGCTAGCCTTAGTTGCCACTAGGAAGTTTCTGAGGCTGGCTGTAAAGTAAGTGAAGG TCCA
D28513b	133 A G ---		---	ATGACCAAAGCCACCACATTTAGAACTTTGGCTGCCCTTTGGAAGTCCAGAGCTGGATCTCTCAGCTCC CGCCOCAGAGGGTCAGCACTTTGGACATGGCTCACAAGCAGTTTTTATTGACTGCATGAATGC/JA GJTGCGTGCAAGCATGAACCTTGTTTAAATCAAGAGGCTTACATAATTTTAAACGATTCTGTCTTC AGCTGTACATA
D29833b	85 A G ---		---	CCACTCCATCCTGATGCCCCCAAGTTATCCACAGCCTCCTTCCCGACCAAGACCCTATCCACTGGACC TCCATTTTCCCTGTAA/JGJTTCTCCAAGTATCCTACCCCTCCCTACTCCTGCACCCCAATATGAA CAACTGCAGCAGGTGCCACCACCACCAACCAAAAGACACCACTACCCCTTGTAACCTACTGCTTCTGCTAC
D29833a	21 A G ---		---	CTCCCTGCCTCCTCCTCCTGCCTGTGATGCTCCGTCTCAACACAGCCGAAACCTGTCTTGCAATGGGG GAGGGGGCGTTT[G/A]CTTTCTCTCTCTTGGCTTCTCTTATTTCCACAAACCATTTCTCAATAAA GCCAAAAATCTTCTCTTCTCCCTCAGGCCACCTCCTGTCTCCTGCTGCTGCTGCTTTT CTGGA
D31762	82 G A ---		---	ATTATCGCGAGTGGTTGACCTTACACTTACTCCTTAAATAGCAGTGAGTAATGCATTTGAGCTG/T/CJ CCCAGGCTCTGTCTCCTCAGCTCATTTCTCTACTCTTTTCTCTATATACTCATCTTATTAATACATT GCACCAAGAGATATGGAGACATAAACCTGTAAATGAGGCTGGGCTTTTCTGTAAATAGCTTCC TTT
D37931	64 T C ---		---	TTT

D63807	101	C T	---				CAGGCAGGACTTCAGTGTACGTATCCCTGCCCTTCAGTCTCTTTAGAAATCACATCTGTGTTCAATCC ATTGTTTAGAGGGAGTGTATTTTCTGTTCCAC/C/JGAGAGGAGACTTTTGTTCACAAATGGATCAC AATGCAGAGGAGTGTCTCTCCCGCTCGCTCTCGGTGCTGGAGGGTGACCTGTCCAGATGAC
D90145	21	T C	---				TGGGAACATGCGTGTGACCTC/C/JACAGCTACCTCTCTATGGACTGGTTATTGCCAAACAGCCACA CTGTGGAGCTCTCTTAACCTAAATTTAAATTTATATACTATTAGTTTTTATAATTTATTTTGAT TTCACAGTGTGTTGTGATTGTTGCTCTGAGAGTTCCTCTGCTCCCTCCACCTTCCCTCACAGTGTG TCTGGTG
EST14035 1a	59	T C	---				ATTATCACTCTCAAAAATTTTGGTGTGTGTTTAAAGTACTTCTTATTTATGAGCCCCQ/C/JGAGGA CCAGACATGTTATTATCAAGCCCCCTATATACCATCTAAAT
EST16668 5	71	C T	---				GCATTTTAAATTCACATTGAATCATTTTACTATTATGATGTTTACATAACAAATTCAGTATCATTT ATG/C/JTGTAGATTTTCAGATGTAGGTGTCGTCATACTGAGCATTATCT
EST16904 7	57	C T	---				ACAGACTATCGCCAACTTATAATGCTTAACTTTATGATCAATAGTAATAATAATTACA/C/JTGAGATA TTCACACTTTATTATAAATAGGGTTTGTGAAGATGATTTTCCCAACTGTAGGTTAACAT
EST21863 9	49	A G	---				TTTTAAGTACCAGAGGCACTGCTGGAACAGGATGAAAACGTGATACACC/C/JGTTACTACTTACTC TTCACCTCTTCAAACTGATCCCTAAAGACTTCTACTTAGCAAA
EST21885 6	80	G A	---				GGCTGTAAGTAGAATCAAGGTTAAGAACAATTTATGCCTTATTCACAAACATTTTACTGAGCATA CTAGGTGCTGGGA/G/JGTGACAGTGTGAGCAAAAACACAA
EST22623 8a	26	A G	---				ATTTAGTGCAAAATGACAAAGCCCAA/G/JGAGAACAGAGGATCAATAAGATTGAAATGTATTACC TTCTCATAAGTATACGAAGTTTAAACACAAGTATGGGAGT
EST22644 2	98	A G	---				AAAATGATTGAATTCAGCAAGTACATTTATGATCTATCTACATTTGTTAAACAGCACTAAAAATAA AAATTTTAAATGATTATCCATTATTACAG/C/JGAAATGTGGAAGATGGCTTTTAAACCC
EST23587 1	31	T A	---				CCTCATTATTAAAAAGACGGACATAAAAAT/JATATACAACAAAAAACCCCAAGTCACATTTTCAG GAGGTAAAACTAAAAAGTCTGATATGAAAAATATGGTGG
EST24246 7	106	T C	---				AAAGATCTGGCATTATTCACATCATTTCTAAATATTTTGTAAATACTTTTCCATGAGTATTTTTTCA TGTCAGGCAATTTAACTATCATTTTAGCGTAAATACC/C/JGAAATAACCCATAGTTACAGAATTGG GTCTGTGAACCTCAATT
EST24308 3	45	A G	---				TAGTTTAAATTTCTGAACCTTTGGCTTATAAAATTTTCTCAACTT/C/JCATTTAAAAATGTATCAAT GCACCTCTTCAGTAGTACCACATGAAAATATAAACCTCGTTC
EST24435 6	73	G A	---				CTTGAACCTCTGGTCAAGTGGTACGTCGCTCAACCTCCCAAAATGATGCGATTACAGGCATAAG CAGCC/G/JGCGCTGACCCACATTTCTTTATCCGATCTGTGATGGACATTCAGGTTGTTTC
EST25089 6	25	T C	---				TATTGTTGCATTATCAAAATGGTTAT/C/JAGTTTTCAATTAACACTGTAATGATTCTCTATGTATAAA ACAGCTTTGAAGTTGTAATGTAGTTTCCAACTGTTAGTTAATGCTACATT

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EST25476 9	33 G A ---	---	---	AATGATCTTTATTTTCAGACCTGCTCCTAAA[G/A]CTTTTCCTCCTCTAAACCAACACACA AGAGGCTCTCTTGCTGCTTTTCCATGGACTGTGGCGCTGTGGACTTGGACCGTCTGCTGA
EST26183 2	70 T A ---	---	---	AGATAATGCATTAGAGCCTGCCCTCATTGTATCTTGATTAACTTTGTAAAGATTGATCTCTAAATAAG ATT[A]ACATTCGGGGTACTGGGAGTTAGAACAAAC
EST27231 1a	28 T C ---	---	---	AGAAATAAGGTGCTACCGAACTCATGT[C]GATAGCGCTTTCTTTAGGCACATATTATAGCAAT CAGATGAAAGTCTGTAAATCACACACACACTGTGCCTTAACAACAACACCGTGACTCTGA
EST27816 5a	26 T C ---	---	---	CAACTCAAGGTACAAAGACAATTGCATT[C]TAACATTGTTATAATAAAAGGAACATCAGATCAAT CATTAAAGGCTCCAGAGTGAACAGCATCTTCATAACTCCATGTT
EST28588 0	78 A T ---	---	---	GTTTAATTGGCGTATGGTCCACAGGCTGTACAGAAAGCATGATGGCTCTGGGAGGTCTCAGGAA ACTTACAATCA[A/T]GGTAGAAGGCCAAAGAGAGCAGGCATCTCTCCATGACCACAGCAGGAGG AACAGACAGAGGAGGGGGAT
EST30226 5	25 A C ---	---	---	TACTCACACCGACATACATATCTCA[A/C]GTAGAATTAGCTATAGCTACTACTAACTTCAATTGATG AGGGAATATAAATACTACTGAACAAGACAGACTTGTCTAACTTAAACAAGACAGACTCATTTCCITTTGA G
EST30935 9a	59 C G ---	---	---	AGCTATGGTAGAGCAAAATCCAGTGGTGGTAAATCAAGAACTCTAAAGTTTCAGTAGAG[A/C]GAGGT GTTTGAATGTCAAGGAAATCACTGAGGTAGATTGGGATTACAATAAGACAGCTGCCCTGTGAGGT CATAAGAGCTTTTGTGAGG
EST32515 7	25 G A ---	---	---	CCGAATATAAGGAAAAAATGGTGGC[G/A]TGCTCTAAACCTGTTGAATAGAATAATGGCCAAAT ATTACAGTTTCTCACTTCTCTATGAATACTGGCAGCTGTTTATTTTATGTTATATGTGAGTTTCTATGC ATAAAAAATCCCAGTAAGA
EST33274 4	27 T C ---	---	---	TGCTTTGTTCCCTCCAAATCCTAAAAT[C]GTGTGCTCTCAAAGAAATTCGTGGAAGGACTTTGAA TACGAGTTTGTACCATATTCAGTATTCCTGAATACAGGTTTCAGATAACTATGGAGATGATACCATTT GGACTAGGTA
EST33352 7b	75 C G ---	---	---	TACACATTATCAAGAGACCCTGACATGCATCTCCTCCGCGAGAATACATTCGTCTCTCTTAGAGA AGTTTAA[C/G]GCACATAGTATTTTACTAAGAGAAATATCTCTTGGTGTCATATCTAGGGG
EST33424 1	126 A C ---	---	---	ATTTTCCCACAGCAGAAGTATATTATTGTGCTGAAATCAGGTAGCAGGGAATGAATAGCTCTTGG GAACCAGTACAGAATGTTCAAAAAGATTTACAAATCTCAGTCATTACACACTGAGCAAC[A/C]AAA CAAAGGTGTTGAATCCTCTT
EST33488 7	90 A G ---	---	---	CCTTTGGGGGAGTTTAAAGCCAGAATGTACAAAAGTCACCTACAGGAAGACTGGAATGTAGCCATAG TTGAACCTCAACATCGTCTATAG[A/G]ACCATTTCCCGTCTCCAGTTAGGTTCTAGGCATACTAAGCT GCTC
EST33508 1b	45 C T ---	---	---	AAAAACATGCTATTTTGAACAAACTTTTTTATAAAGAATAAGTTG[A/C]TTGAAAAAGCAGTTTTAAAT AACATCAACTCAAAATGACTTTTAGAAGCCAAATAA



EST33508 1a	36 A G ---	---	AAAAACATGCTATTTGAACAAACCTTTTATAAAGA[A/G]TAAGTTGACTGAAAAAGCAGTTTTAAAT AACATCAACTCACAATGACTTTTAGAAGCCAAATAA
EST33863 4	77 C T ---	---	ACAACATAGGACTGGTTATCTTGGTTTGAAGAAATATATGTTGCCACTTCCTATTGTTTTAAAAATGA TCATTTAA[C/T]CTTTGAACACAGCCTGAATCCCC
EST34739 3	97 T A ---	---	GAAGTATCCTTCCAGTGGCAGGAAGTGAAGACTCCAGATCAACCAGGTGGACCTTTTCGTTGATGA GCTGATAGCTTCTAGGCTGTGGGAACCTC[T/A]GGTGCCTTACAACCTCAACTGACGAGAAATTCCT TGTTGTGCCTCATAAACA
EST34792 6b	104 A G ---	---	ACCTGACTGCTTTAAAAGCTCTTTGTAAAGCTGACCGTAGCACAGATCACGTGGCATCCACTATCAATA CTCATAAGTCTAATTTATCCTCAGGATGTTCCCTGA[A/G]GATTCAGGAATTCCTTAGTCTATTATACA AAGATTTTGTGCTGTG
EST34835 9b	93 T G ---	---	GGAAATGTTCCCTTTGCAACAAGGTACGTTTATCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGGAGTCTATGTTGCTTCTGCTT[G/G]GCCCTTAAAGAAACAGACAAATTTGTGCTAAAGAT
EST34835 9a	82 G A ---	---	GGAAATGTTCCCTTTGCAACAAGGTACGTTTATCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGGAGTCTATGTT[G/A]TGCTTCTGGTGCCCTTAAAGAAACAGACAAATTTGTGCTAAAGAT
EST35230 0	93 G T ---	---	CACAAAGGTCCACTTTACTTACATGAAGGAACATAAAGGCATGAGAAACAGTCATCTCAATAAATG CAAGACATGAGCATAAAAGAGGTTCTC[G/T]GCCCTTCCAGCGTTGTTATTACAGAGAGAAACCT
EST35337 9	33 C T ---	---	TCTTTCAAATTTTGTAGTGGCATTTAATG[C/T]TATAAAATTTCCCTGCTTAGGAATGTATCTGCT ATATCTCAGAAGTTTGGGCATGTTGTTTCCATTTTACTTAGTTCAGAACTTTTTCATTTTCATCT
EST35708 9	32 C T ---	---	CTGCCCCAAATTAACTTTTAGGCAATGGAA[C/T]TAGACTTACTGTATGGGACATTTTAAAAAG ACAGCTTAGTAATATGTTTCATATGCAGCGTGTGCTTCCCTCTCTGAGGTGGCACCTTTCCTGTTGTG ATGTGCAAGTGTGGCT
EST35747 9	51 C G ---	---	ATCCAGTGCAGAGTTGTAGCTGGAGACATATTTCAACCCACAAAGGCTCCA[C/G]ATGTTAAAAAGT TTCCCAACATCAACCTAATAACAGTGACAGCAACACCTCCCTCCTGCCCTTCCAGTAGGGTTGAGATT G
EST35751 9	89 C A ---	---	TGGTCCATTATATTAACCTGAGGGAACAAACGGTGTGACATGGCAGACATTTATTCAATGGAGA AGTTCCCTCCCATGAACCAAGA[C/A]CTTGCTCTCATGATAAAGTGGAGACAATAAGAAAGCCAGGT ATATAATTAAAGCCTGTGA
EST36301 4	93 C T ---	---	CACCTGTTCAATTGTTCACTGGGCTGCTATCTGTGGGCTGATGCTCTACCAAGTGTGACGCTACAGC AGTCAGGAGGAGCCATGGCCCTG[C/T]GCTGATGGAGCTTGTAATTTAGCCCCAAACTGATCTTCA GAAAGAGGTACAACAA
EST36519 0a	33 G T ---	---	GCCATCAGCCACAAAGACATGACTACCAACGC[G/T]GGCCCCCTTGACCCCATACTGGCCCTCAGCAG CTAAGACTGGACAACCTTTGTACCTAATGACCGCCACCTGGCATATACTGGCTGGGCTCTTCTCTGT CACAGGGTCTTAGTCGT

EST36620 6	50 GA ---	---	GAC TTATTAGATAAGGGTTTCGGCTACCCCTCAAAGCTCAGGACTGG[A]GCTAGGGTTTAAGG AAGGCTTATTAAATATGGGAAATAAAATACAAAGGGCCACACCCGATGCAAAAGACTTT
EST36690 0a	89 CG ---	---	CCTGTGATGTGCATGGTGCCTGAGCAGTCTACTACTATCGTCAGACAGCTCACGTATGTCAGGA AAGGAAGTCTGGGGATTCTC[A]C/GJAGGGGACATATCACACATATTCTAAGTCACTGTGTGACTCGG CTTGAGCAAGTCAITTTCA
EST36729 9	62 CT ---	---	GAGACAGAAAGCCATCAGTTAAATGAGGTTAGGCCTCTCCTCCTAATATACTGATTGACAATG[C]TJA TATTAGCCAGGTAATGCACCTTAGCTACCCCTGGACAATGCTATCAAGTGTGCTGGGAAGGGAG
EST36823 6	103 AT ---	---	ACTGTCTGGCCGATGATTGGAGCTTGAAAAAACTACCATGCCAGATCTCCACCCAGACCAATTAG GTCAGTATCTCTGGGGTGTCTATTCAAGCAACAATTJA/TJCTTTTATGTTCTTAAGCTCATCATGAG TTAA
EST36987 4	126 CG ---	---	ATGATCGCTTATGTAATTTGAGGGCGACATGGGTAATGGAGATACCCACAGGACCTGTAAATAIT TAAATAATATTTAACAGCTGATCAGAGGCTAAATTACAAGTACATTTTGTATGCAGTTT[C]GTTA GGGAATTAAGACAATGCAG
EST37054 3	88 TC ---	---	GGTCTCACTCTCTTGGCCAGGACGGTTTGAACCTCCTGAGCTCAAGTGACCCCTCCCACCTTGGCTTCC GAAAGTGTAGGATTACAGG[T]C/GTGAGCCACCCACACCTGGTCTTGGTTTAAAGTAACCACTGAA C
EST37269 3b	105 TG ---	---	AATAGTCTATGGCTACGGGCCCCGTGGGATGTTAAAAATGGGATTTTAAATTAAGATTGTGAACATG CAAAACCCAGCAATTTCTCAGCTTATATTTTGAAGTCT[G]CAGGAGAAAAATGGGGTCC
EST37284 2	93 GT ---	---	AAAAACCTTCTCAAGCAGTAAACTTTGAGCAGAGACTCAGATGAAGTAAGGGATGAACCCAGGAA GCTCTCTGGATAATGTCACTCTAGGAA[G]TJAGTAAACAGGTGTAAAACCCCTGAGATAGCAACCCCT CTTGGCTTGCTTGAGGAATA
EST37315 2a	90 AG ---	---	AGATGGGGTCTTGCTAGCTTGCTCGGGCTGAACATAAGATATCCTCCTGCTCAGCCTCCCAGGTAGT TGGAACCTATAGTAGGAGTATCTJA/GJCCCTGCCCTGCTAGAACTTCAAGTTTTGATGGGCAAAATCCA CCCCAGAGGACAGGACAA
EST37374 1	45 CT ---	---	CCTGCCATGATAATGTTAAACATATCAAGATCCTCCTCAAACTT[C]TJAAGGGTGAAAAGCATACC ATTCCATTTAGTTGAATATTCCTTCACATAGCCCAACACATTTTTTCAAGGCACCTCTAGCTACTACA GGA
EST37376 8b	101 GC ---	---	GTGACATCATGTCTCTTCAATGCCCTTTCAATTAATAGTAGT[C]TGAGCGCTGGGGCTGAAGTCAGACT CTCTGGGTTCAAATCACAGTGTGTGCTCTGCA[G]C/GCTGTCTCAGGCAAGTTGCTGACTTCTCTG TGCCAGG
EST37376 8a	41 TC ---	---	GTGACATCATGTCTCTTCAATGCCCTTTCAATTAATAGTAGT[C]TGAGCGCTGGGGCTGAAGTCAG ACTCTCTGGGTTCAAATCACAGTGTGTGCTCTGAGGCTGTCTCAGGCAAGTTGCTGACTTCTCTGT GTCCAGG

EST37378 9	63	T G	---			ACACACAAAAAATGGTGGCAGAAAAATCTGGAAGATTCTAATAACCTCAATTCTGTGAAAAAC[T/G JAACATGCCTCAAAAAAGAGGGGAAAAAATTTAACAGAAAAACACTGTGCTGACATGATTAGCTT
EST37452 4	46	G A	---			AAGACATAAATCTGCAATGAAATCAGTTATGAATATTAACCTCT[G/A]CTTCTCAGGAGTGACAC TAATCATGGTCTGGAAGCTAGCCTATCGCATTTTAAACACCCCTTAATCAATGACGTAGAA
EST37613 6	34	A G	---			CTAGGCATGGGGCTTTACAGTCATTTATTACCTA[G/G]TCATGAATTCATTAAAAACCCACAGCGAT ATAGCAATGAGCAAAACAGACCCCTCCCAAAATCACCCCTGCGTTTCATGGATCTTCCATTCTAA
EST38025 4	56	T G	---			TTATTGAGTAGCTACACTGTGGCCAGAACTAAGCTTTACATGTTTTATATCACCTA[T/G]TTATCTCA ACAATCTTGAAAGGGTGGTATTATTTCCCGTCTTATAGGGAAGACTCTGAGGTTTCAGAA
EST38068 6	57	C T	---			TCTACCAGGTCAACAAAGTATCTGTATATGCTTTAAGTGGCATTTTCATGTCACCTA[C/T]CGCATGG AAGAACGCTCTCCTTTTAAATCCCTAACCTCTCTCTCTGGGAAGACAGAACGTGCACAA
EST38420 6a	100	T C	---			TAAATCAAGGCCCTCTTTCATTACCAAAACAAACAAAAAGGGAACAAAAATACGATGGGAGAGG GAAGAGATGATGCCGAAGTGTATCCTGACTGAC[T/C]GTCCCTGCAGTGCCCATGGTCCCGTGCCT TATTCATTCTCCTCTCTCA
EST38950 5	25	T C	---			TTTATTTGCAAAAGTAAGCAGCCGGT[C/T]GGTCCCTGGATTGAGGCTGAGGAAGACATTACTTCCTG CTGGAATACTTGGGACTTACATTTGACACAGGCTAAAAGTATGGGATGAGAGAGGAACAAAAAGCTT ACAAACAAAGACAGCCCA
EST39053 6	90	T C	---			TTTTTTGTTACTCTGTAGCCAGTCATTAATCTGAAGTTTAAATATATCATTTTATTGGGATGAGATCA TAGTCTTTACACAAATGCTATGT[C/J]AACAAAGTTACTGAATATTTTACCTCTCGTGAGTTG
EST39331 1	70	G C	---			TCCTTCTGCTCTCTAGCACTCAGACCACCAAGAAAGCCCTGGAAGACCAGCCATGGAAGGAAAGTA TG[C/G]GTGTTTAGGGAGAGCTGGCACCTGGCCTCTAATCTTCCCTCTGCCATTGACCAGATGGGT GCCTTTGGATACATCACT
EST40544 7	31	C A	---			GTCAACATTGACCTTACATAGTGCCTCTAGT[C/A]ACCTATGAGGCACCTAGAACTCTATTGTACTTCT CACTTTATCACATTAGCTATCGAAGTTTGAAATTT
EST40548 4	37	T C	---			TTCTAATAGCATGCCCTGTGACAGGGAACTAAGCTCT[C/J]TCAAAATAACTGAAACTAAATCTGTA AGATAAATGCTGGAATTTGAGAAGGCACATGCCCTTTGTAGTTTTCTCCAGAAGGCTCAAGGTGTTG AATAATCTGTGGGACTCA
EST40549 1	42	A G	---			TGTTTCTCTAGAGAACCCCTGTGTGATACACTACGCATGCACA[G/J]ATAAAGTCACATCAAGACTAA TAATCTAAATGTTAGTTTGTACCACCATTTCTCACTTTTGAACCTAGCTCCCTGCAAAAGCACCTTCTA CCCTGCACCTTTGGGGAG
EST40579 1	81	A C	---			TGTGAATTCACATCAGTAAGGCAGTTTACAGAATTTTCACTCTCTTACCTAAAGTCTGTGCTATCTG AGCTGGTGGAAA[A/C]GGACTTGGAGACAGCGATTAAATACGGAACAAGGCTTCCAGGAAG
EST40584 3	68	A G	---			TTGATGGTTGTAGGAATTTGGGAAGAAATATCTGTGAAGGAAATTTGCCACTGTAAATGCACACCC A[A/G]TCTGTACTCCCAATATCCTATGTTTAAAGCT

EST51340	51 G A ---				GATCAAACTGATTGCCAGGCCAGCTCCTGAAGAACTGTGAACATGAAAC[G/AT]CTCAGCCTAGA AGGATAATGTGACCTTCAAATTTGCACACCATTGCTCTTTCAAACTAAGAGCCTCTCTAAGCTA GATAGGCCAAGGATTATT
J04162	134 T C ---				CATGGAGTAATAAGACGAGTGGCAGCAGCATCTCTGAACATTTCTCTGGATTTCGAACCCCATCAT CCTCAGGCCCTCTCTACAAGCAGCAGGAACATAGAAGCTCAGAGCCAGATCCTTTATCCAACCTCTCGA[ T/C]TTTTCCTTGGTCTCCAGTGGGAAGGGAAAGCCCATGATCTCAAGCAGGGAAGCCCGCAGTGAGT AGCTG
K01506	63 T C ---				CTGAACTCAGCTGCCCTACAACTCCATCTCAGCTTTTCTCTCACTTCATGTGAAAACACTAGT[C/C] CAGTGGCTGACTGAATTTGCTGACCCCTTCAAGCTCTGCTTATCCATTACCTCAAGCAGTCATTCCT TAGTAAAGTTTCCAAACAATAGAAATTAATGACACTTTGGTAGCACTAATATGGAGATTATCCTTTT ATTGAGCCTTTTATCCT
L18877	69 T C ---				TGAGTCTGAGCACGAGTTGCAGCCAGGCCAGTGGGAGGAGTCTGGCCAGTGCACCTTCCAAGGCC CT[C]ATCCATTAGTTTCCACTGCCCTCGTGTGACATGAGGCCCATTCCTCACTCTTTGAAGAGAGCAG TCAGATTGTTAGTAGTGAGTTTCTGTTCTATTGGATGACTTTGAGATTATCTTTTGTCTCTGTTGGA ATTGTTCAAATGTT
L31848	36 T C ---				GCATTTTACATATCCCAAGCCCTTTAGGGCTACAGT[C/C]CTCTTGTCTGGACCCCTGTAGGGTGCCA TTTGGAGTTCACAGCCTAGAAAGAAAGGCTTTGGCCCTGGTGTGGTGGCATAGGCCCTGTAATCGT AGCGCTTTGAGAGGCTGAGGCCAGGAAGATAGCTTGAGCTCAGGAAGTTTCGAGACAAACCTGGGCAAT GT
L38517	137 G C ---				GGGTCCAGAAGCCTCTCAGCCAGGAGGAGCTGGCCCTGGAAGGACCTGAGCTGGGGGACACTGGC TCCTGCCATCTCCTCTGCCATGAAGATACACCATTGAGACTTGAAGCTGGGCAACACCGGTCCTCCAC CC[G/C]GTGCTGGTGTAGTCATAGAGCTCAAGCTGAGCTGGCAGGGGATGTTGTTGACCCCTCT CTCCTAGAGACCTTGAG
L39059	123 T G ---				ACTTGAGAAGCAGAGCTGCCACCTTCTGGAGGCCACTGTGTATGATGAGCCAAGCAATTTGGAGCCA AGTTGAAGGGACAGGGCAACAAAATACAGTAGTTTCTTTTGTATTGTATAT[G/C]GCTGTA AGATCATCCCGCAAGCAGGCTGGAGGTGCCGTTGGCCCTGTGTGCTGGGATTTTAGTCTGTGCTGG GAG
41268d	173 G A ---				CAAAAGTTGTCTCTGCCATGAGCACCAAGTCAGGCCCTTGAGGGGATCTCTAGGGAGACAACAGC CCTGTCTCAAAACTGGGTTGCCAGCTCCAAATGTACCAGCAGCTGGAATCTGAAGCGGTGAGTCTGCAT CTTAGGGCATCGCTCTTCTCTACACCAACAAATCTGAAC[G/AT]GCCTCTCCCTTCTTACAAAATGTCT AAGGT

L48728b	111 T C ---	---	AAGTGAACAGAAAGCATGGATTGTTCTATATAAAGCACATAGTTATGTTTACTGGTATCGT AAGAAGCTGGAAGAAGAGCTCAAGTTTTGGTTTACTTTTCTCAGAA[T/C]GAAGAACTTATTCAGAAAG CAGAAATAATCAATGAGCGATTTTAGCCCAATGCTCCAAAACATCATCCTGTACCTTGGAGATCCA GTC
M18079	52 G A ---	---	GCGCACAGTCCAAAAATACAAATTGGACAGAAGATCTATATTGTACCAGAACT[G/A]TTTTTTCACC CCATCAAGTATAAGGTTACTGATTGATGGTCCCTTTTATAAACATTGGTATATTCCATTTCATGCCAA AGCAAAAGAAAGTAAAGCTAA
M19169	113 T C ---	---	TAGGATCTGTGCCAGGCCATTGCGACAGCCACCCACTCCACCCCTGTAGTGTCTCCACCCC TGACTGTGGCCCCACCTCGGGAGGCTCCCCATGTGCTGT[C/G]GCCAAGAGACAGACAGAG AAGGCTGCAGGAGTCCCTTTGTTGCTCAGAGGGGCTCCGCCCTCCCTCCTTCTCTCGCTTCTAATA GC
M21539	114 T G ---	---	TCACCTCGTTCACAGCTCCACCTGCATCTTCTCATCAAGGATCCAGGATACACAGGGAGCTTCT TTCCCTTAGCCTGTGATCTGCCCATGATGATCCCGACAGCAAAAT[G/G]TTTCTCTGAGGCTG CCATGCTGCCACTGTCCAGGTGGAGACTGAGCAAAAGGAAGTCTCAGCTGTACCGGCTTTCAGAGCT TCTCTTTGGGTGC
M26041c	173 A G ---	---	OCTAGCATTATTTCTGGCCCCATTTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCTCACCTCT TCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATTTTCCCTGACTTC CTGATTTTCTTTCTCAAGTGTACCTACTAAG[G/G]GATGCTGGAGTAAGCCACCCAGCTACC TAATCCTCAGTAA
M26041b	157 A G ---	---	CCTAGCATTATTTCTGGCCCCATTTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCTCACCTCT TCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATTTTCCCTGACTTC CTGATTTTCTTTCTCTCA[G/G]GTGTTACCTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATCCTCAGTAA
M26041a	45 C G ---	---	CCTAGCATTATTTCTGGCCCCATTTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCTCACCC TCTTCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATTTTCCCTGAC TTCTGATTTTCTTTCTCAAGTGTACCTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATCCTCAGTAA
M63967	57 G C ---	---	TAAGGAGCTGTGAGGAGGCCAGTCACAGTCCAGCAATTCACACCCCTTGAC[G/C]AATGCT TGCCAAAGCTGTTTTAAAGCCCAAGAACACCCCTTTCTTTGTCCAAATTACTCTTAGAAGAAACCCCA CAATAAAGCAATCAATC
M81695	34 G A ---	---	ACTTACTTACCCTCACCTGTGAGGCTGACGGGA[G/A]GAACCACTGCACACCCAGAGAGGCTGGG ATGGGCTGCTTCTGCTTTGGGAGAAACGCTGTCTGGGAGGGGCTTTGTCTGTCAAGGTTTC CAACTGGAAACCCCTTAGGACAGGGTCCCTGCTGTGTTCCCCAAAGGACTTGACTTGCAATTTCTACC T

U06641d	166 C T ---	---	CTCCTCCTTTATTTTCAGCATGGAGGTTTAAATGGAGGATCTCCTTTTCTGTGACAAAACATCTTTC ACAACTTACCTTTGTTAAGACAAATTTAAAAAAGATCTTTTTCACAACTTACCTTTGTTAAGACAAAATTT TATTTCCAGGCTATTTAATACGTACTTTAG[C]/TGGAAATATTCTATGTCAATGATTTTAAAGCTA TGAAATACAAATGGGGGA
U09607	39 T C ---	---	GAGGCTTATGAGGGTCTCTACTTCAGGAACACCCCAIT/C/GACATTGCATTTGGGGGGGCTCCCG TGGCCTGTAGAAATAGCCTGTGGCCTTTGCAATTTGTTAAGGTTCAAGACAGATGGGCATATGTGTGAG TGGGGCTCTCTGAGTCTCTGGCCCAAGCAAGCAAGCAATTTAAGACTCTCGCATCTTCCCAAC CCCTTA
U09608	82 T C ---	---	GAGCAGAAGCAAGAGCGGCAAGATGAGTTTGAGCGTTGTATCCAAAGGCCCTCATCTGGAGCCTC GGGAAAGTCTGGTCC[C]/ACATCTGCCCGCCCTTCCAGCCCTTCCCCAGCCCCCTCTTGTCTTCTTC ATTCATTCAACAAAATTTGGC
U10694	20 C G ---	---	GTGACATGAGGCCCATTTCT[C]/G/GCTCTGTGTTTGAAGAGAGCAATCAGTGTCTCAGTGGCAGTGG GTGGAAGTGAGCACACTGTATGTCTCTGCTGGGTTCTTGTCTATTTGGGTGATTTGGAGATTTATCCTT GCTCCCTTTTGGAAATGTTCAAAATGTTCTTTTAAATGTCAGTTTAAATGAACCTTCAACATCGAAGTTAA TGAATGACAGTA
U13877b	162 T C ---	---	AAAAGGACTCTGTTCAATCCAGGTTCCATTTTGTCTATCTTTGTGACCTTGACAAAGTTGTTTAAAC CTCTTTTGTTCAGAAATTTCTCCATGGAGTAACAATATCTAGGTTGGAGGATTAGTGAAGTTACATGT AAGCACAGAGGAACAGCCAAAGAGAT[C]/TACCCTGGTCTTACTAAAGTACATATCCTAACCTTGG GGTTACCTTCAGCA
U15555	187 T C ---	---	TTTCTGTCCACTTTCACCTGGTTTTAATAGCCAGCCAGTCAATAATAGTAGAGGAATCAGTCAAGCAA AAATGCTTTTGGAGAAATTAATAAGCAATGCTGAACATCAGGAATTTAGATATCCGTACAGAGAGT TCCAGTAAATTTTATGAGTCCACGACCCCTTTTCTAAGCAGTCTGGTCCATG[C]/TGGTCTCATAC CTCATATGCAGGATTTCATTCA
U17077	122 T C ---	---	TCCAATTATTGGTCCCCAAAGCAGCTTCCAACGTTTGCCATCTGGATGACAAACGGAAGATCCACT AAAACGTCCACGGGATTACAGAAACGTCCTTGACAGCTGAGCGATGACACCACT/C/JTTGTTTGG ACATTTAAATTCACCTCTGCTGAATAGGAGGAAGCTTTCTTTTCTGGGAAACAACTGTCTCTTGG AATTA
U18543	58 T C ---	---	GCACATGCAGAAATAGACTCAGCCTATGTCTCTGATTCAGCTGGGTAGTTCTAGAATTT/C/JAGAAG CTCCATCTTTTAAATGTTTTTATTTGTTATGTCCCCCTCCCGGCTCCCACTAAATTTAGAGCTTTAAA AGATGCACTGCCCAATAGGACACACGATGGTGTAGCTGAAGTTTGTAGCAATTAGGCACTTCC AAGCCTTTAGTAGAGAGAGCC

U25975b	164 C A ---	---	TCACGTGCTGGCCTACTCTCTTTTCCATTTTCTACAAGAAGCCCTTTAGTATATGAAAAATTAT ACTCTTTTGGGGTTAAAGAAATGGCTGCAACCTGAATGAAAGAAGCAATGACTATTCTCTG AAGACAACCAAGAGAAAAATTGCAAAAAGAC/C/AAGATGACTTTTATATGAACCCCTTCTTTAGG GTCAGAAGGAATGTGGACTGA
U25975a	143 C G ---	---	TCACGTGCTGGCCTCATACCTCTTTTCCATTTTCTACAAGAAGCCCTTTAGTATATGAAAAATTAT ACTCTTTTGGGGTTAAAGAAATGGCTGCAACCTGAATGAAAGAAGCAATGACTATTCTCTG AAGACAAC/C/G/AAGAGAAAAATTGCAAAAAGACAGTATGACTTTTATATGAACCCCTTCTTTAGG GTCAGAAGGAATGTGGACTGA
U25997	61 A G ---	---	CAGGGAGAGGTTATTCACAACCTCACCAAACTAGTATCATTTAGGGGTGTTGACACACCA/C/GJTT TTGAGTGTACTGTGCCGTGGTTGATTTTAAAGTAGTTCCTATTTCTATCCCCCTTAAAGAAAAAT GCATGAAACTAGGCTTCTGTAAATCAATATCCCAACATTCGCAATGGCAGCATTCGCCAACAAAA TOC
U28413	29 C T ---	---	ATTCTGACAGCTAAATTAGCCCTAAATG/C/TGGGTAATATTTTCTCATGTTTAAATGAGGTT AATATTTGCATAAAATCCTAAACAGACTTCTGTATAGTTTATTTAGTCAAAATGTGTTCTTGATCC CAGATGTTGGCCTGGGAAAGCCCTCATTGCTACAGTACAAGTAACACAAAGTCGTTGACCTCAGTT G
U30884c	89 A G ---	---	TAGGGTAGCATTTAAGATTCAGGAGTCATTAGCAGTGATGATTTTGGGACCTGCCGTATAATCTGT CTTCTATCCCACGTTAGCCA/C/GJTTGTTCTTGATGAATCTATAGTACATAGAACACAAAACTAT TGACGGAAGTCATTAGAAATGGCTTGTGATATCTGATGGCTTGAACCTGCCACAGTTGAACACAAGT GCTGTCA
U30884a	34 A G ---	---	TAGGGTAGCATTTAAGATTCAGGAGTCATTAGC/C/GJTGATGATTTTGGGACCTGCCGTATAATCT GTTCTTCTATTCCACGTTAGCCAATGTTCTTGATGAATCTATATGAGTCATAGAACACAAAACTAT TGACGGAAGTCATTAGAAATGGCTTGTGATATCTGATGGCTTGAACCTGCCACAGTTGAACACAAGT GCTGTCA
U31216b	78 A G ---	---	GGGACAGCATATGTGGCACCGCCTCTCTGTGCACGTGAAGACCAATGAGACGGCCTGCAACCAACA GCCGTATCA/C/A/GJCCCTCACTAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGACCAAGACCCCTTACAACGTAGAGGAGGAGGATGCCAGCGGATTGCTTTAGCCCGCC TGGTAGCCCTTCCAT
U31216a	70 G A ---	---	GGGACAGCATATGTGGCACCGCCTCTCTGTGCACGTGAAGACCAATGAGACGGCCTGCAACCAACA GCC/G/AJTCATCAAAACCCCTCACTAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGACCAAGACCCCTTACAACGTAGAGGAGGAGGATGCCAGCGGATTGCTTTAGCCCGCC TGGTAGCCCTTCCAT

U31416c	76 G A ---	---	AGTTGCCAGCTCCATGTACCAGCAGCTGGAATCTGAAGCGTGAGTCTTCATCTTAGGGCATCGCTC CTCCTAC[G]CCACAAATCTGGTGCCTCTCTCTTGTACAAATGCTAGTCCCACTGCCTGCT GGAAGAAACACACACTCCTTTGCTTAGCCACAGTCTCCATTCTACCTGACCCCTGCCACCTCTCC AACCTAACTGGCTTACTTCCT
U31416b	68 C T ---	---	AGTTGCCAGCTCCATGTACCAGCAGCTGGAATCTGAAGCGTGAGTCTTCATCTTAGGGCATCGCTC [C]TTCCTCAGCCACAAATCTGGTGCCTCTCTCTTGTACAAATGCTAGTCCCACTGCCTGCTG GAAAGAAACACACACTCCTTTGCTTAGCCACAGTCTCCATTCTACCTGACCCCTGCCACCTCTCCA ACCTAACTGGCTTACTTCCT
U37519a	78 C T ---	---	ACGGGTACACACAGAGAAACCTGAGTCTAGCCATGAGGGCTTATGCTCCCACTCAGATTGTCCTCG AGACCGCAGG[C]TTCGCCACAGCTCAGGTTGCTGAGCTGTACATGACTGCCTGCCTGCCAGG GCTGCAAGCAAGGCTTGTCTTCTATCTGGGGACGCTGCTCGAGAGGCCGAGAGGCCGAGAAC ATGCCAGGTGTCC
U37690	54 A G ---	---	GACCAGCTGAACCCACCCACCCGCTGTGCTGACCATGGGCCCTGAGGTCCT[AG]CCCCGAATTC ACGAGGCTGAGGCATCCGGGAGCTGGCGTAATGCCTGGCCGAGTGTGTATCCCATACCCCACT CTGGAAGGAACCATCCAGTAAAGGCTTT
V00540	39 T C ---	---	TGAACCGTTTCAACATGGAAATGATCTGATTGACTAAT[C]ACACCAGTCCACACTTCTATGACT TCTGCCATTTCAAAGACTATTTCTCCTATAACCACCGCATGAGTTGAATCAAAATTTTCAGATCTTT TCAGGAGTGTAAAGGAACATCATGTTTACCTGTGCAGGCACCTAGTCTTTACAGATGACCATGCTGAT A
X15943	106 A T ---	---	TCAAGAAGGTGACTGCCCTTGTATGATGGGATGGAGATGAATGACTGGTTTTACTGGGTGTAA AACCACCTCTGAGCCTCTCTGAGACCATGTGGTTTTAAAJATATCCATAAGGGAAGGTACCCACAC CAGTATCTGAGTTCAGTAGCTAAGACCCTAGAAATTTGGATTCTCTGTTTTTTCATGCTCTCCTT GTAAACCTTGAGATCATCAG
X52011b	148 C T ---	---	AGGAAGATCCCACCGACCTTCTCGCCTAATCCTTTAGATTAGGTGCACATTACATTAAACATTTAGGA ACCCAGACCGAAAGTTGCTGAAGGGAAGGAGACACATTACAAAGAAAGTTGCGAAAAATTCGG AAATCTGTTGTGCA[C]TGTCTCAATGAAAACGCCCTTCGGCTTTTATTTTTTTTGGAACTG CGAGTGGCTTAGGCTAGCCT
X52011a	118 A C ---	---	AGGAAGATCCCACCGACCTTCTCGCCTAATCCTTTAGATTAGGTGCACATTACATTAAACATTTAGGA ACCCAGACCGAAAGTTGCTGAAGGGAAGGAGACACATTACAAAGAAAJ[C]GTTGCGAAAAAT GCGAAATCTGTTGTGCACGCTCAATGAAAACGCCCTTTCGGCTTTTATTTTTTTTGGAACTG CGAGTGGCTTAGGCTAGCCT



X54741	24 A G ---	---	CAGGCCACCTGCTCTCTCCAC[AG]TGACAGCTTCTGAGTCAACCCCTCTGTCCAGCCAGCTCCT GCACAAATGGAACCTCCAGGCCCTCCAGGCTGCGGCTTGCCAGGCTTGCAAAATAGGAAGGCCAG GGCAGAGCTGGAGACGATCTTGCTGGCAGGCCCTGGGCTTGTCGCCAGCCCACTGGGCCCTTCTCC AGCAAGCAGTGC
X54869	99 A G ---	---	AAGCATTGCGTTACAGTGCATCAGATACATTTTATATTTCTTAAATAGAAATATTATGATTGCAT AAATCTGAAATGAATATGTTATTTGCTCT[AG]ATACAAAAATCTAAATCAATATTGAAATAG GATGCACACAATTACTAAGTACAGACATCTAGCATTTGTGCGGCTCATTTTGTCAACATGGTA
X66924	147 G A ---	---	GCGGTGCTGACACCTCCAGAACGAGTGTGCGGCCCTGCTGGACCCCGGGAACTCTC CTGCCGGAAGCCGACGGGATGGGCCCACTTGCCTGCCACTTGACTTCAACCAATCCCT TCTGGAGACTTG[A]AACCTGGTGTGCTCAGGAGCGAAGACTGTGAACCTTGTGGCCTGAAGAGCCAGA
X78932	62 T G ---	---	GAAATGTGAAGAAATGTGACAAAGCCTTTAAGCGGTTGTCACACTTGATTGTATATAAGATAA[T/G]T CATACTGGAGAAACTCCAGAAAGTGTGACAAATGTGACAAACATTTAATTAATTCTCATACCTTA TTGCACAGGAAAGCATTTATACTTGAGAAAAATTTGATAAAGAAATGGAAGATCATTAAATATCTGCT CATATCTTAACATCAGCGAGTT
X80026	25 T C ---	---	CTCAACCCATAACCTCAACACATCT[CT]ATCTCCACCCACATCCCACACATCCACCTCCATCC CCAAACCCATCTCATCCCACTACAGCCCCAAACCCAGCCCCAGACTAATCCACAGCCATCCCCAA CTCATCTCATCCCACTGCAGCCCCAAACCCAGCCAGGCCATCCCCAAACCCATCCCCCAAGCC AACTCAACACCATCC
X80197b	99 G C ---	---	ACCCAACTCAAGTCCAGGCCACAGGCATCTTCTGCCCTGCCCTTGTGGCCCATCCAGTCCAGG CGCCTGGAGCAAGTGTCAAGTACTTCTCCTTG[CT]GACATTTGAAAGACCCCTCCACTCCTGGCCTCA CATTTCTGTGTGATCCCCCCTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCTAGAAAG
X80197a	28 A G ---	---	ACCCAACTCAAGTCCAGGCCACAGGC[AG]TCTTCTGCCCTGCCCTTGTGGCCCATCCAGTCC AGGCGCCTGGAGCAAGTGTCAAGTACTTCTCCTGCACTTTGAAAGACCCCTCCACTCCTGGCCTCA CATTTCTGTGTGATCCCCCCTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCCTAGAAAG
X85106	150 G A ---	---	GGCACCCAGAGTGACACAAAGTCCAGCAGGAGGCGCGCCCTCGCGGTGTCGGTGTCTTTT CAGCCCGGAGAGGTCTGACCTGGGGCTTCTCAAGCCTCACTGGGCAAGCTCCCGGCCGCTCT CTTTTCTCCCAAGC[G/A]AAACCAATGCGCCCTTCACTCGCGTGGCGGAGGCGGGGGCTT CTTTCAGAGC
X87160	128 T G ---	---	ACCACAGCCATGGTCTAAGGACATGGATCGGGTGGCCCGACAGCTGTGCACAGGGGACCCCTCTGCCC CACTCTGGGCTTTTCAGATACTCTGACCAAAAAGCCTGCTTTAAACCGCAAGATGGGGCT[G]GGGC ATGGCAGGAGGAGCCATCGGGTACTACGCGAGCAACACTCACTGTCAGGCTGAGATAAATCCC GGGA

[illegible]

1282	130 C T ---	---	GTGCGATCACCACACAGTCTAATTTTCAGATGTTTTCATTACCCCTAAAGAAATCTTGACCCATTAGCAATATTCCCTCATTCTGCCCTCACCCCCAGGCCCTACTCTTTATCGCTATAGATTGCC[C/TA]CTTGACATATCATACACATGGAGCCATACATATGTGTGCCCTTCATGATTGGCTCTTTCACTGAGAATAATGTTTTCAGGGT
6810	68 C T ---	---	AGTATCACACATACCTTAATATATTAGATATACACAATAATAAATCACTCCCTACCTTGAAACATTTA/C/TJAGAAAGCATTTTAAATTTACAACACAAGCTCAACGAACCTACAATAAGTCTAGTAGTCTGTTACGTGCCAAGGATAAGGCTGAACAATAAATTAACCCCTTTAAAAATGCTATGAACAAGTACAAATTTCTTTTGAGTCTGCAGAGCAATGACCACCTAAGAAATATTTTAAAGGC
6817	118 A C ---	---	CCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTATTTGCTTTTGTATCCAGTTAAGACCAACAGCATATACAACATCATCACTAACTCAACAATGTAGCTGACGGTAAC/A/CJTGTTGGATACCCCTGTGCTCTACTGGCCCTCCAAAGGCATTGAGGGATCATCAAGATGTTGGACACCTTGTTCAAATCTTGGTTCAGGTGGCCCTGTCAGATCGGCTTTTGGTTGGTTGCTTAG
6819b	212 C ---	---	CCATTTATTTTCTCTAAATTTTAAATAGAAGACTTTAATGGAAACATTTAGTACCATCATGTCAACCTGAATGCCAGCAATACCTCGACTTTTACACACGACGAGGAGCCTAGTAAAGCCCGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTTTCATATACAAAATTTTCTGCTATTTTGTCTTAGCAAAACAGCAATAACTTTTGTTTCTCTATATGACACCTAATATCCA
6819a	166 G T ---	---	CCATTTATTTTCTCTAAATTTTAAATAGAAGACTTTAATGGAAACATTTAGTACCATCATGTCAACCTGAATGCCAGCAATACCTCGACTTTTACACACGACGAGGAGCCTAGTAAAGCCCGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTT[G/T]CATATACAAAATTTTCTGCTATTTTGTCTTAGCAAAAGCAATAACTTTTGTTTCTCTATATGACACCTAATATCCA
681xx	39 A G ---	---	CTGGTATGTCATAAGCAATCCATAATTTGTTATAGCTATTJAGTJTTACTATGACACCAATTTGGGACAACAGTTATATATGTCAGACACCAACCAATGTCCCTTAAGATATGCAGCAAGCACAAATCTGTCTATGGTTAACAAAAGAAATGAACGTCTAGG
6972b	149 G T ---	---	AGGATTCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCTCCTCTGTACCTCTGGTAGAATTCGGCTGTGAATCCATCTGGTCTGGACTCTTTTGGTTGGTAAACTATTGATTATTGCCACAAATTCAGAG[G/T]CCTGTTATTGGTCTATTCAGAGATTCACACTCTCCTGGTTAGTCTTGGGAAGTGTATGTCTGAGGAAT
6972a	122 A G ---	---	AGGATTCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCTCCTCTGTACCTCTGGTAGAATTCGGCTGTGAATCCATCTGGTCTGGACTCTTTTGGTTGGTGTAAJAGJCTATTGATTAATGCCACAAATTCAGAGCCTGTTATTGGTCTATTCAGAGATTCACACTCTCCTGGTTAGTCTTGGGAAGTGTATGTCTGAGGAAT

7598k	210 A C ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTGGAGAAATGAAATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTCCCGTATTTCCCT CAATGCAG[A/C]
7598j	208 A T ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTGGAGAAATGAAATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTCCCGTATTTCCCT CAATGC[A/T]GA
7598i	192 G T ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTGGAGAAATGAAATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTCCCGTATTTCCCT CCTCAATGCAGA
7598h	144 C T ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTGGAGAAATGAAATTTCTTGAGGATGCCCTTTTA ATATTTGATCC[C/T]ATATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTCCCGTATTTT CCTCAATGCAGA
7598g	142 C T ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTGGAGAAATGAAATTTCTTGAGGATGCCCTTTTA ATATTTGAT[C/T]CCATTATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTCCCGTATTTT CCTCAATGCAGA
7598f	120 A G ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTGGAGAAATGAAATTTCTTG[A/G]GATGCCCTT TTAATATTTGATCCCATATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTCCCGTATTTT CCTCAATGCAGA
7598e	83 C T ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAA[C/T]CAGATTTACCTGGAGAAATGAAATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTCCCGTATTTT CCTCAATGCAGA
7598d	77 C T ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGC[C/T]GCTAACCGATTTACCTGGAGAAATGAAATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTCCCGTATTTT CCTCAATGCAGA

7598c	56 A G ---	---	AAAGGTAAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCA[A/G]AGGAAC TCAATGAAATAAGCCGCTAACCCAGATTTACCTTGGAGAAATGAAATATTTCTTGAGGATGCCCTT TTAATATTTGATCCCAATTATGTGAGAGATTTCTGATATGTTATCTTATTTATTTTCCCGTATTTT CCTCAATGCAGA
7598b	47 C G ---	---	AAAGGTAAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACA[C/G]CCAAGCCAAAGGAAC TCAATGAAATAAGCCGCTAACCCAGATTTACCTTGGAGAAATGAAATATTTCTTGAGGATGCCCTT TTAATATTTGATCCCAATTATGTGAGAGATTTCTGATATGTTATCTTATTTATTTTCCCGTATTTT CCTCAATGCAGA
7598a	30 A G ---	---	AAAGGTAAATCAAAGTCCCTCTATAAATT[A/G]GATTTACAAAAGACACCCCAAGCCAAAGGAAC TCAATGAAATAAGCCGCTAACCCAGATTTACCTTGGAGAAATGAAATATTTCTTGAGGATGCCCTT TTAATATTTGATCCCAATTATGTGAGAGATTTCTGATATGTTATCTTATTTATTTTCCCGTATTTT CCTCAATGCAGA
7998c	116 A T ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTTATTCAGACATCTTGCCAGCTCTCCTGTA ATACITTTAATGAATGGGTGAGTCTATCTTCTCAAGGTCCCAATA[A/T]CCTTGAGGTTCTCT
7998b	94 A C ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTTATTCAGACATCTTGCCAGCTCTCCTGTA ATACITTTAATGAATGGGTGAGTCT[A/G]TCTCTCAAGGTCCCAATAAACCTTGAGGTTCTCT
7998a	75 A T ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTTATTCAGACATCTTGCCAGCTCTCCTGTA ATACITTTAATGAATGGGTGAGTCTATCTTCTCAAGGTCCCAATAAACCTTGAGGTTCTCT
8071	119 A G ---	---	AAATACAGAAATTTATTTAGAACTGTTTAAAGTAGAAAAAACCCCTGTCAAGAAAGACCCAGGTGG AAAATGGGTCCCAATAAAATGGAATTTTAGGGCAACAAAGTCTAAAAGGCC[A/G]CAAAAAGAGA AATAGCACCACTGTCAATTTGAACAATGGCTAGTTACTTGCAATTTTGGCATTGTTAATCACTGAATC TGGGTTTCTCTGAATTCACACAGAGCATGCACACACATTTTATCAT
8467b	93 C T ---	---	AAGGCTTTCCTCTAAACATCAGTCTACGGAGAAACTGGGAAATCCTGGATATTTGGCTTATCACTT TGACGCAAAATCCACTTTGCTGTAA[C/T]GGTCACTCCGAACCTCCCTTCAGAGAGCAAGCAAAA TTAAGTGTGATACTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAAAGGAAAAATTAAGT
8467a	70 A G ---	---	AAGGCTTTCCTCTAAACATCAGTCTACGGAGAAACTGGGAAATCCTGGATATTTGGCTTATCACTT TG[A/G]CGCAAAATCCACTTTGCTGTAAACGGTCACTCCGAACCTCCCTTCAGAGAGCAAGCAAAA TTAAGTGTGATACTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAAAGGAAAAATTAAGT
8498	84 C T ---	---	AGGGTTCAGGGTTGGTTTAAATCAGGCTGCACACCTTTCAAATCAATCTGACATCTCTATGTCA AACTGGCTTCAGCTAG[C/T]AATACCTTCAATTAATCGAAAGAAAAAATGCTTTAAGGAAAAAA AATCCAGTTTAAAGAACAAATTAACATTAGTCTTTAAATATAAAGGAGGGCTAATGTTTCATGTTGCT TTATACATCTCTCTCAATACAGAACCCAGGAATGTAATTTTCTTAACCTCAG

WI-18562	29	G A	---			CTAAGGAAAAATTTAATGATGGAAATATC[G/A]ACAAATATTCAACATCATTTAAAAACAAGTAG CTTCTCTATTTCACATAGCTAGTTGGGATAGAAATAGAACTAATGTTTACAATGATTCCTACATT TAGCATTAAATCAGAAACGA
WI-18618	51	A C	---			ATAGCAGACTTTTAAATCAATGCCAGAGACAAAGTGAGGCCGAGCTAAGAAC[A/C]CGCTCAGCTTCG TTACAATGAAGAAATGGTTTCCCTTCGATGCAAGTATAATTGTAAACCACAGTGCTCGCACAGTTC AC
WI-18683	22	C T	---			TAAGCTGTTCAGGACTGGACT[C/T]GGTCCCTTTATTGAGACTGACAGGCCAGTGGGTCCACCCAAA CAAAAATAAATTTCTCTCCCAAGCCTGCCTGCAGT
						GACTTTGGTGATTTAATTGCTTTTCCCTTAAATATAGAAATAGGTGTAATTTCTCTTTTGTCTTTT ACTACA[G/A]CCGGAGTGGTAAATACTACTACTGCCAACAAACACGGGCATCCACTCTGCTCTCAA TGCCTCTCCGTGAGAC
WI-18520	75	G A	---			AAATAAAGTTTTATTGGCACACAGCCAAAGCCACTGGATGACACATTTGCCACGGCTCATCTTGCAA TACAATAGCAGGGTTCACTAATGTGACI[G/G]ACATGGTGGCTCACAAGCCAAAGATATT
WI-18563	94	A G	---			GTCCTATTTCAATTTAGCTAGACCCATTTCACTTCTGTTTAAATGGCTACATTTGTTTTCATTGTGAGAC IT[A/GTCCATAATTTAATTAATCAGTGCCATATTGAAAGACATTTGGATCGTTTCCCAG
WI-18582b	69	T A	---			AACITTTATTTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGCTGTAGATTTTGAAG TGGTAACAGGTACATAGGTAAACCAA[G/A]TATATAGCTTATTGGTGAATCTTCATCCT
WI-18723f	94	G A	---			AACITTTATTTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGCTGTAGATTTTGAAG TGGT[C/A]ACAGGTACATAGGTAAACCAAAGTATATAGCTTATTGGTGAATCTTCATCCT
WI-18723e	71	T C	---			AACITTTATTTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGCTGTAGATTTTGAAG TGGTAACAGGTACATAGGTAAACCAAAGT[A/G]TATAGCTTATTGGTGAATCTTCATCCT
WI-18723c	96	A G	---			TTTATTACAATAATTTAGGTGGCACAATAACTAACAGCTTCTGA[G/A]ACAGGAGGTAAACATTTCTCA TAGACTTTGCAACTCAGCCAGAAAGTAAAACTCGAAATA
WI-18619	44	G A	---			TTATTCACAAAAGTGATATTGCAGAGGGTCTGGGGGCTGTACATGGCAGGGCTTGGTGAGCTTTG TACATGGG[G/A]CTGGGAGACAAGGGAGCCCTCCAGGTGAAGGTAATTTTAAATAAAAAATAA TGGAGCTACAACACACCCCG
WI-18715	76	G A	---			GTAATAAGTTTTATTGGCACAGCCAGCTGTTTATTCATATGCCATTGACATCTGCTGTGTCCT ACACAGCAGGGTGGGACCTGCTCTTCACGGGAGAGCTA[G/A]TTGTTTAAAGCAGTGGTCCCAAC CTTCTGTGTCCTCCCGTG
WI-18535	107	G A	---			AGAGTGGTCAGAACACAGCCGAATCCAGGCTCTATCACTACTAGTTTTTTCAGTTCTGGCAGGTGAC TTCATCTCTTCGAACTTCAGTTTCTTCATAAGATGGAA[G/C]TGCTATACCTTACCTACCTCGTAAAA GTCTGATGAGGAAAGATTAACTAATAGATGCATAGCAGCTTAAACAGAGTGCATAGCATACACTGTTT TCAATAAATGCACCTTAGCAGAAGGTGATGTGTCTACCAGGCAGACGAAG
D17525	107	C T	---			

DWU-133c	313	A G ---	---		TAATTGGCCACTGCCCTATTATTACAAAACAGAAATGCTCATGACCTTTTATGTTACCATCCT TTAATAGATCTCATACACAGAAATTCAGATCATGAATGACTGACAGAAATTTTGTGGCAGTCCT GATTTAAACTAAGACTGGCTTGTTAAATGAATATGTCAGTTTGAATTTAATAGTAACCTCC AATTCAGTAAATGGTATCACTCGTTACCCCTTTTAAAGATATGATTAGACT
DWU-133b	236	T C ---	---		TAATTGGCCACTGCCCTATTATTACAAAACAGAAATGCTCATGACCTTTTATGTTACCATCCT TTAATAGATCTCATACACAGAAATTCAGATCATGAATGACTGACAGAAATTTTGTGGCAGTCCT GATTTAAACTAAGACTGGCTTGTTAAATGAATATGTCAGTTTGAATTTAATAGTAACCTCC AATTCAGTAAATGGTATCACTCGTTACCCCTTTTAAAGATATGATTAGACT
DWU-133a	199	C T ---	---		TAATTGGCCACTGCCCTATTATTACAAAACAGAAATGCTCATGACCTTTTATGTTACCATCCT TTAATAGATCTCATACACAGAAATTCAGATCATGAATGACTGACAGAAATTTTGTGGCAGTCCT GATTTAAACTAAGACTGGCTTGTTAAATGAATATGTCAGTTTGAATTTAATAGTAACCTCC ITCCAATTCAGTAAATGGTATCACTCGTTACCCCTTTTAAAGATATGATTAGACT
DWU-36	102	C T ---	---		ATGAGATCCTTTAAATCCTCCATGAACGTTTGTGGTGGCACCTCCTACGTCAAAACATGAAGTG TGTTTCCTCAGTGCACTGGGAAGATTCTACCTGACCAACAGTTCCTCAGCTCCCATTCGCC CCTCATTATCCCTCAACCCCGCCACAGGTGTTTATACAGCTCAGCTTTTGTCTTTCTGAGGAG AAACAAATAAGACCATAAAGGAAAGGATTTCATGTGGAATATAAAGAT
DWU-387	169	G T ---	---		GTGTATAAATGCAACTGTTGATTTCCTCAACATGGCTCACAATTTCTATCCCAATCTTTCTGAA GATGAAGAGTTTAGTTTAAACTGCACCTGCCAACAAAGTTTCATATATATAAAGCATTTATTTTA CTCTTTTGAGGTGAATATAATTTATATTACAAATG[G/T]AAAAGCTTCTTTAATACTAAGTATTTTCA GGTCTTCACCAAGTATCAAGTAATAACACAAATGAAGTGTCATTATTCAA
DWU-447b	172	--- --- ---	---		ATTTTAGTGCTTTGCGTTAAAAAATCATTGCAAAAGTATTCTGAAGCTGCCAGTCAGAT GGGCTGTGCCATTTAAATCAGTAAATTAATTAGTTTATTAGAGCACAAGCTTAGCTAATCAA CCATTATTTTCATTTGTTGTTCTAAGAGGATTGANAATCAGTTAGTTTAAATGCTTTCTGTTAG GCCTTTCTTTCTTACAATGAAGAGATGATTCTCTAGTTTATGGTTA
DWU-447	85	A G ---	---		ATTTTAGTGCTTTGCGTTAAAAAATCATTGCAAAAGTATTCTGAAGCTGCCAGTCAGAT GGGCTGTGCCATTTAAAGTACACTGTAATTAATTAGTTTATTAGAGCACAAGCTTAGCTAAT CAACCATTTATTTTCATTTTGTGTTCTAAGAGGATTGANAATCAGTTAGTTTAAATGCTTTCTG TTAGGCCCTTTCTTTCTTACAATGAAGAGATGATTCTCTAGTTTATGGTTA
DWU-476	63	C G ---	---		GTAAAATTCAGTTTTTTCCAGTTCCCTCTTTTGTGCTGCTCTCAATTAGCGTTTAAAGGTGAG[C/G]AT AAATCAACTGTCCATCAGGTGAGGTGCTGCTCCATACCCAGCGGTTCTTCATGAGTAGTGGGCTATGCA GGAGCTCTCGGGAGATTTTTTT

DWU-505	67	A T	---			TCATAAGGGCAGTATCTCCTCTAGCTAGTGGCCCATACAGAAAATCTATCACCATACAAAATTTA  A/TJTGCAATTTATGTTTAAAGCACAGGTGTACCGAAAACGTGAAAAGTCTGAATTTATGGGTT CTATGCATGCATTTTGCCTAACCTAGAGAAAAGAGTTTGATAAATTTTACCAGCTTTGAAGATGGAT TAACITTTGACITTTGAGCTTTAAACTTTTAA
DWU-512	131	A G	---			AAATCCAGGGCATTCGAATCTGTTTTTCATGATTTATAGAGGGTTACACAAAAGTGCCACTTATTAA AGAGCTTCCACAGTGAAGATGGAGAAGGTGAACCTGCTTTGAATATCCAGATGTTTGGTC A/G  TGCATGGCAGTGAGCAGGTATGTTTTGCTTTGCTTGCACTGAAAATTAATTTGCTATCAAGAGC AACTATGAACGGTTTTTATCAAGATGCTCCAGAGTGAAGATGCCGAG
DWU-525	97	A C	---			AACTGCATATAGATAATTATCCAGGATGTGGCTCATTTTTCAGCTTGTTCTATACTGTTTGT ATATACAGTTTTTGTAAACCATATGATTGA C AAGAAGAAAAGTCTATGCTTAGGCCAGTCAGTACA CCCAATTTTAAAAAATAACATATCTTGTCTTTCACAAATATAGTTGAACAAGATTTCCCTAAAAAT CCACCAGGATTAACTCTCTAAAATCTAGTCTCTGATTGC
DWU-59	94	C T	---			CATTCTTTGTGAAGGTAAATGGACTCACAGGGGAAGAAACATGCTGAGAAATGGAAGTCTACCGG CCCTTTCTTTGTGAAGTCAATGGC C TJGAGCCGTTTTCAGTCCCAGGTGGCAGACTCGTTTTTG GTAGTTTGTTTTAACTTCAAGGTGTTTTACTCTGATAGCCGGTGAATTTCCCTCCTAGCAGACATG CCACACCGGTGAAGAGCTCTGAGTCTTAGTGGTTAAGC
EST11	68	C	---			CTTGATCATGGGGTGAATTTTGTGTATCTGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAG CAGCAGGTGCCAGGGTCTGGATCAGAAAAAAGGCA
WI-19856b	63	C T	---			CACACTGGCATCTAGGCTTCGCCCTGCATTGCAGAAGGAGAGCCAGGTCCCTCCTCGAGAA C TJG CTGGTTCCCGCAGCCACACCCGGCTTGCACCACACAGGCTGTGAGGCAGGAGGTGGTGAAGACGT AGCTGTAGACCCAAAGCAACCACCGCCCTGGGACCCCTCGGGAGAGGAGCAGCTTTAGAACATGGAA AAGTGTGGTCATCCCATCATTAGACAAGACACATCCTACATAATAAAAAAGT
WI-18014	40	A G	---			TCCATTTACATTTGGTGGCATTTGTTGAATAGCTACAGAA A G GAATGAAAGTGCACCATCAGAGT GTAATTAGGTCTGTGTGACCCAGGAAGTGTCTGTTAAACAGAGATTTCTCAAGGGCAAAGTGGCTTCT A
WI-18036b	97	T A	---			TTCCAATGTAAGAGTCAAGTACCAAGTTAAACCTCTAGAAATACAAAGAGAACATGATAAAATCTG ATCACAGTGGAAAAATTTTAAATCTTTCATAA T A J CTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18036a	27	T C	---			TTCCAATGTAAGAGTCAAGTACCAAGTT C JAAACTTCTAGAAATACAAAGAGAACATGATAAAAT CTGATCACAGTGGAAAAATTTTAAATCTTTTCATAATCTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18046	72	C T	---			TGTAAGGTGACTTCTATAAGCTTCTCTAAACTGTCAAACCTTTCATTTACTGAGATTTATTCAGGGCCAAT GTGTC J T GTTGGTCTGAGATTTGATTATCAGCTGGGTGAAGTTAACCTGTTCTCTGTTTCA



WI-18063	105	G A	---			AGGCTTTAACTGATAACAAATTTGCCCTTTAATCACAACAAAACCTCTGCACCTTTTCATTCCTTCCTTC
						CCATGTTTTCTGATTTTGATGTAAACTTTAAAAATTTGGT[G/A]TCCCTTTAAACAAATATACTGTAGCTGCA
WI-18078	86	A T	---			AGTTGAAAGATCAGAGAGGTTATGGTTGGTGAGTAGCTGAACCTCAGATTCAAACCTGGTCCAGTGTG
						TTGTTTTTTCAGCATCAGTATGTCCACTAGCCAAAGTTGATCTCTGCAGTATCTACATGTGGT
WI-18091	90	T C	---			CCAAAGCTCACTCAGTATTTAATCATCTGCTAAATTTTCATCCTTTTGTAAATCCATCAGACACTGTGGT
						TTTCATCTCTAGAAGTTTGACTTTTGGGGCTTTTATACCTTCCATATCTCAACTTGTAAAGC
WI-18119	38	T C	---			GCAATCTGTAACAGTTTTGGTAGTGGTATTACAGAGGATTCJTTGTAAATGGATTGGAGTACTTAC
						CACATTTTCATCTGCTCTGAAATAGTTTCACTAACCAACTACTGACAAACAGTTTAATTTTGGTCTT
WI-18142	66	T G	---			TTCAAGATAATTACAATTGGAAGGGGACCAATAATCCACTTTTAAATCGAAAATAATCTATATACT
						T/GJCCCAATAAATCAGTAAATAAGCTTCAAAAAGCCTTAAGACACCAAAAAGAGGAAAA
WI-18178	68	T C	---			GCATAGGTTGAGGGGTGTACAAGAGGAGAACCCAGATTCAGTCCATGCCTGGAGTTAGTCTGGGGG
						GT/CJCGGGCGGATGGACACACAGACACATAGATCTGGCATCTGATAGCAGGGCATACAG
WI-18244	35	G T	---			TCAATCTGAAAACCTTGCTGAAGCCAGCATGGGGTGTGGGGAGGTGATTATGGCTGGGGAGAGATG
						GGCACTCACCCGACAGCAGCATCTAGCACACAGTGACAGGGACGTTGAGGTGGCAGAGGGCTTT
WI-18245	115	G A	---			ACAGATGTCAGTTGTTGAAATGGCCCATTAAGATATGGGCCTTTCTTGTAAAAAGTCAATCCAAA
						AGGCTTGGCAAGAGTTTGCTATACAACGGAGGGACAGAGAAACATGA[G/A]CTGGGAGTAGGCTCT
						GACAGAAGGTGGGCTGTC
WI-18261	26	G A	---			GATTGAAGGGATGCTTTATTTAAC[G/A]TGAAAAGCGTGATAGAGGAACTGTTTAAAGATAAACAA
						CTTATAAATCTCCCAATGTAGAAGTGAAAGATTG
WI-18268	88	C T	---			TAGAGGGAAAGGAGGTGGCTGGCTGGGCCCTCAAGACATGAGAAACGGGTGGTGGCTTCCAAGC
						TTCTTACTTCCCCATAGATC/TCCGTGACAATGTCTGCAGAAAGCCCTCCAACTGGAAAC
WI-18299f	107	C A	---			TCACAAGTCAATCTCCCATCCAAATGACAGTTTGCTAAGATCATTAACCTGGTTGCCAAATTTTTT
						ATCTATTTGGGTCTGAGAAATCCACAATTTTGA[G/A]GAAATCTTTTGCCAAATTAATGACATATTCTG
						CAG
WI-18299e	101	A G	---			TCACAAGTCAATCTCCCATCCAAATGACAGTTTGCTAAGATCATTAACCTGGTTGCCAAATTTTTT
						ATCTATTTGGGTCTGAGAAATCCACAATTTTGAAGAAATCTTTTGCCAAATTAATGACATATTCTG
						CAG
WI-18299d	77	G A	---			TCACAAGTCAATCTCCCATCCAAATGACAGTTTGCTAAGATCATTAACCTGGTTGCCAAATTTTTT
						T/GJATCTATTTGGGTCTGAGAAATCCACAATTTTGAAGAAATCTTTTGCCAAATTAATGACATATTCTG
						CAG
WI-18299c	67	T G	---			TCACAAGTCAATCTCCCATCCAAATGACAGTTTGCTAAGATCATTAACCTGGTTGCCAAATTTTTT
						T/GJATCTATTTGGGTCTGAGAAATCCACAATTTTGAAGAAATCTTTTGCCAAATTAATGACATATTCTG
						CAG

WI-18299b	52	G A ---				TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACCTTG[G/A]TTTGCCAAATTTT TTTATCTATTTGGGCTGAGAAATCCACAAATTTGAAGAAATCTTTTGCCAAATATTGACATATTCTG CAG
WI-18299a	48	C T ---				TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACCTTG[G/A]TTTGCCAAATTTT TTTATCTATTTGGGCTGAGAAATCCACAAATTTGAAGAAATCTTTTGCCAAATATTGACATATTCTG CAG
WI-18307	76	G A ---				TCAACTTGTAACCAAGTTTAGCAAGCAAGAGTACTCTCTTAGAGACTTTCAGTGGACTTAAACTCAG TTTCCGCTG[G/A]TGCTATGTAAAGCATCCAGATGGTTTATTGTACTCTGCAATCTGCTTGGTCAC
WI-18324	72	C T ---				TTTGGTATGAAATCTTTCTCTGACATTTACCAATCATCACTTAAACTCCGGGGGTGGGTACTGATT TATC[C/T]TAGATCCAAATAAAGCATGCAGAAAGTG
WI-18350	48	T C ---				ATGAAAGTCACCTTCAATCATAGGGTCAAGAGAAAGAAATGTTTTCAGA[T/C]TAAATCTATGAAAA GGTGTATCTGCTTGCATTTAAGAAACACACAAGTCA
WI-18395	77	G C ---				TCITGACATGATCTGTGAATTAACGTGATTGTGGTTGAATTTCCCTGGAAAAATTTGAAGAATAAATTG ATTATTCAAG[G/C]JGTGCAATGGTTTATACATATCTCTCTCTTCTTAATGCAAGCTATG
WI-18398	62	G T ---				TGCAGTGGCAAGACACTCTCTCGAGGAAAAAAGAAAAAGAAAAACAACACTCAAGGGTT[G/T] GATAACATTGCCAGTATAACCATTAATTCAAAACAGCAGCAGAAATTTGGAGGATAATTTGTT
						CTCGTTGGTATTCTCTCATCC[C/A]JTCCCTTTTCGCTCTTCTTAAATTTAAAGAAAAAGCAATGGAATT TTAAAAGATCATCTAAGAAAATAAGAACTTACATATGTAACTTAACTTATCAACTTGTACAAAAGTC AATGAAAA
WI-18396	21	C A ---				AAGATGGGAAAGAGGAAATC[C/A]JTCTTTCTTACTAGAGATTTTCTCCCTTTAATCCTTTTCAAAT TCAAAGGATCATCAAAGGAGCAGGTGCAGAAAGCTCTGGGGCCAGAGGCCCAAGTGCTA
WI-18409a	20	C A ---				AAAAAGGAAAAAGGATGGAGTAAGAGAGAGAGACAGAGAGGAAACAAAATAAGTTTCTGG[C/T] JTTGGCTGATCTGGGTGATCAGGTGGACACTATTATCCAGAGGGGAAACACAGAGAAAAAAAGG TTTATAGGTGGGAGAGAGGA
WI-18442	62	C T ---				TTGATGTTAATACTGTCTCTGGAGATCGGCTAAAAT[G/A]AAAGCATAGTTATTATTAGCTTTGG TATACTCTGCGACAGATTTAAACAAGTAAGACATATATCAACCTCATATTTCCAAACCA
WI-18452	38	G A ---				ATATAAGCTGGAGACTGTGGAGGTGAGAGGCAGTGGGACTAGCTGTTGAAAGAGAGAAATGTAGC AGTAGTAAAGATGAAAGACTGCAAGGATTCAAACA[C/A]CJGGTTATGGCAATAGAGGTGAAAAAGAAA AGGCCATATAAA
WI-18489	102	A C ---				CTGGTGGGAGGAAACAAATTGTGGTATTTCATACAATGGAAAACTCTTCAGAAATAAGAAAGGAA CAAAACCACCTGAATCACACAACATGGACAAATCTCAAATCATATTGCTGATGGAAAGAAACCATTC TAAGAATACACAGTACAT
EST5b	93	A ---				

EST5	93 A ---			CTGTGGGAGGAAACAAATTGTGGTATATTCATAATGGAAACTCTTCAGAAATAAGAAAGGAA CAACCACCTGAATCACACACATGGACAAATCTCAAATCATTATGCTGATGAAAGAAACCAATTCA TAAGAATACACAGTACAT
EST6	48 C ---			TTAGCTACTTTTCAGAATTGAAGGAGAAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGCTCT GAACAAAGCTTTCTTTCCCTTTGCAACAAGACAAAGCAAGCCACATTTGCATTAGACAGAT
EST8	158 A ---			GGACAGGACCTCTATTCGCCCTGGTCAGCAGCGGCTGATGGACTAGGCCCCAGGGATACTGGGC CTCTTCTAGGGGGCTCTCCAGGACCCAGAGCTGTTCTGCTTTGAGTTTCCCTAGAGCTGTGCGGCCA GATAGCTGTTCTGAGTTGCAAGCAGCATGGAGATTGGACACTGTGTGCTTTTGGTGGGT
WI- 18740c				TCCTCATTTGTTGGGATGATGAGAAGAAATGATTTGGGAAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAATCTCATTTACCATCATGTATC/G/G/AGTAGGGATAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI- 18740b	96 C G ---			TCCTCATTTGTTGGGATGATGAGAAGAAATGATTTGGGAAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAATCTCATTTACCATCATGTATC/G/G/AGTAGGGATAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI- 18985a	105 C T ---			CCAAAGTCTCCTGTTGCTCATAAAGAAGTTTTTGGGATGGGAGAGAAATCCAGACCATCTTGGGGCA GCCAGGCCCTTGCCTTCATTTTACAGAGGTAGCACAA/C/TJGATTCCAACACAAACCCCTTCCCC TTTTTAAATGATTTCTGTTCTAATGCCATAGATCAAAAGGCTCAGAAACCATTTGTGTGTTTCTCTT TGAAGCAATGACAAGCACTTACTTTACGGTGTGTTTGTGTTTCTTAT
WI-18746	114 G A ---			GCCAGCAGCTGAAGTCTCTTTCTCTCTCGGCTGGAAGAACATACAGTACCTTTGCGTGGATCA AGCTTGTAAGTCTGACCGTTTTTATATTACTTTTGTAATAATCTT[G/A]JCCACATTCCTACTCAGCT TTGGATGTGGTTACCG
WI-19112j	212 G A ---			CCGTGTTACACACACACAATGGCAAGCATAGTCGCTGTTACGGCCAGGGGGAATATGCCAAGG GACCCCTTAATGGAACACACAGATCAGTAGTGCTATCTCATGACAAACCAAGAAACCGACGACAAA TCCTTTGCGAGATTTCTCTAGTGGCTTAGAAACATGGCTTTAAGAAACACGGTGATATCTTTGAG GGTGACAAGGC[G/A]JCTCTTCAACACAGTTCCATACCAACTGCTTTGCTCTAG
WI-19092	232 A C ---			TGGTGGCTGGCTAGTGTCTACAGAACATAATTTGCCCTCTATAGAAGGCTATCTTAGATCATGT CTCAATGGAACACACTCTCTTTAGCCCTTACTTGAATCTTGCTATAATAAGTAGAGCAACACAC ATTGAAAGCTTCTGATCAACGGTCTGAAATTTTCATCTTGAATGCTTTGTTATTAAGTGAATTTTC TTTTAAGCTAACAAAGATCATAATTTT[C/A]JATGATTAGCCGGTAACT
WI-19057i	175 G A ---			CCCATTATTATAGGCCAGTGTCTCAAGAGTAGAGGAGCGTCTACTGGTCTTTCAACTCCTTCA GTCTCTGACGGCGGACTTTACCGTGACAGGGAGGTGATTTGTACGTCCAGGCAACCGCAGCCACTG TCTTCATGCAGGAACCAAGTGCCAGATCCCAAGCTC[G/A]JCTCTTCTATCTTGGTTTGGCCACA

WI-20103	168 C T ---			TGGGACTTCCAACCTAGAGGATGTGGGAATCCAGCTCAATGATACAGGATAAAGTGGGATGGGCT AGGATGGACAGGCTGTGGATATGGGAGTGCATGGTCAAAGTCTATATCCAGATGGTCCAGGTACAG TGGGCTTCCTGGGCTGGAGCTGGGTCCTCCCA/C/TTTCATTCTGCTCAAAGCTTCTTGAAGGAGC TGGTTTGACTTCAACTTGCTAGAGCCTAGCCTCATCTTTCAGTCAACTGGGA
WI-20441	111 G A ---			GCCTACCCATTTTGCACATATACATATGCACCACCTTTCAGTGGCAACATATATATCCACACTA TAAACATACCACATTTATAAATCTTGTAGGACAAGAAATGGA/G/ATTTGAATAAGTACCCCCCAA CATATACAAGAAAGTTAGCATACTTACCCCGTTTTCTACATACATCAGAGGCAAAATAAGAAATCTTT TAAGAAATCTCAAGACTGGCTCATGGCAAAATGAATATGCTAAATTTGGGGG
WI-19911b	116 A G ---			TGGTTACAAAACCTAAGCCCATATACAAAATTAGGAACACATTTAGATGCCTCTTTTGAAGAACGT TTTAGTCTTTTAAACTGAGTTTAAAAAAAATAACAATGCAATTTTAA/GJACACTGTTTTGAAA ACTTAAAGTGCAGCAATA
WI-20613c	165 A G ---			GTCTCAAGGGGGAGAAAACCTGGTCTTTTATGTACAAAGCACAGATGATAGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAAATGGCATGGGAGGAGGAGTTAGAAAAAACATCTTAAAC AGTCTCTTAGAAGGCCAATAATAAAGTTGGA/G/AAAGGGAGTTTCCACGCAGCAGTGGTGAGC TGC
WI-20613b	156 A C ---			GTCTCAAGGGGGAGAAAACCTGGTCTTTTATGTACAAAGCACAGATGATAGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAAATGGCATGGGAGGAGGAGTTAGAAAAAACATCTTAAAC AGTCTCTTAGAAGGCCAATAATAA/CJAGTTGGAAAAAAGGGAGTTTCCACGCAGCAGTGGTGAGC TGC
WI-19984	47 A G ---			CAGTAAAGAGGTGATTCAAGTTGCAGTAATACACTGACAGGTAATAA/GJATAACATTAGAAAA GCAAAATTCCTTTAACTTAAGGACAGACTGAACCATCAGGTATGGTCTGAGATCAAGTAATACAGG TAGGCAAGAGTTTTCACACTGGAAAATGAAGGCAGTTTCCAAATACTGTGAATTTACAAACAT TGGGGGAAGG
WI-20122	135 T C ---			GCCAGTTGGAATATGGCCTATACGAACCAAGAGTGTATACAAAATGGAAAGTGGTCATCAGGCAATA ATTGTTCTCTTGGAACTGCAACCGACTGCCATGCTCTGTGGGACTTACACATTCAGTTTGACAGI T/CJTGAANAACCAACTGGAGCTGCTTTTCCAGAATGTTCTGTCTTCAAATAGGAATTCATG TTATTTCTTCTTGGCTTAAGCTCTTATATCTTCAAATGACCTAAGCTGA
WI-18846a	49 G A ---			GAGTGCCATACCTTCTCCCAGGCTCTGCCCAAGAGCAGGAGTGCCTG/GJAAAGCTGGGAGCGT GGGCTCAGCAGGCTGGTCACTCCCATCCCGTGAAGACCTCTTCCCTCTCAGCAGGCCAAACATG GCCAGACTCCTT
WI-18959	123 G A ---			AGCAGTGGCCTTATTCATCCCAACCAACCGCTCTTGACCAGGCTGCCTCCCTTGTGGCAGCAACGGC ACAGCTAATCTACTACAGTCTTTTAAAGTAAATGGTCGAGAAAGAGGCCACCTG/GJGGAAGCCG TCCTGGGCTGGCAGTCCGTGGGACGGGATGTTCTGGCTGTTTGAATCTCAAGGAGCGGAGCAT GTCGTGGACACACAGACTATTTTAGATTTTCTTTGGCTTTTGCAACC

WI-20146	31	T C ---				TGAGCTCTGTGAATTCATTGAGCAGTTAGCT/C/CATTTGAGATAAAGTCAAAATGCCAAACACTAG CTCTGTATTAAATCCCCCATCACTACTGTTAAAGCCTCATTTTGAATGTGTGAATTCATATACAGGC
WI-18922	74	G A ---			---	TAGGAATTGGTTTACGCCCTGAGGCAATTAGACACTTTTGAAGATGGCATAAACCTGTCTCACCTGGAC TTAAGC/GA/TTCTGGCTCTAATTCACAGTGCCTCTTTCTCCTCACTGTATCCAGGTTCCCTCCAGAG GAGCCACCAAGTTCTC
WI-18763b	53	A G ---			---	TTTCTGTGTGTGGGGTCAACCGTACAATGGTGTGGGAATGACGATGATGTGA/GA/GTATTTAGAATG TACCATAATTTTTGTAAATTTATTTATGTTTTCTAAACAAATTTATCGTATAGTTGATGAACCGTCA TGTTTTTGCCAA
WI-18763a	38	A G ---			---	TTTCTGTGTGTGGGGTCAACCGTACAATGGTGTGGGA/GA/GTACGATGATGTGAATTTAGAATG TACCATAATTTTTGTAAATTTATTTATGTTTTCTAAACAAATTTATCGTATAGTTGATGAACCGTCA TGTTTTTGCCAA
WI-18771b	75	G A ---			---	CTCATTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCTAGAGATGTTGGG AACAGAA/G/A/AAATAAACTGAGTTTAAAGGGGACTTAACTGCTGAATTCACCTGTGGA
WI-18771a	57	A G ---			---	CTCATTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCTAG/GA/GATGTT GGGAACAGAGAAATAAACTGAGTTTAAAGGGGACTTAACTGCTGAATTCACCTGTGGA
WI-18820	70	T C ---			---	GGGAAAAATTTGAGACGCAATACCAATACCTTAGGATTTGGCTTTGGTGTATGAAATTTCTGAG GCC/C/CTGATTTAAATCTTTCATTGTATTGTGATTTCCCTTTAGGTATATTGCGCTAAGTGAAACTT GTCA
WI-18742b	51	C T ---			---	ACAAAGTCCTGTAGCCCCCTCACCTTTCTGTCTTTCACCTTTTGCCAATGTAC/ATATCGGGTTTGTTT TCTTGATTTATTTAAACGGTTGTGTTTCTCTTTTCCACGGAGTTCAAGTAAAGCCGCTGCAGGAGA GTTTTACC
WI-18882	94	C T ---			---	GTGTGTCAAAAATGGGGTCTGCTCCTGCTAOCCTGACCCCTTCCCTTTCCCTGCTTCTCTCCCTCATCA TCATTTCCCAACAACATCCTCTGCCA/C/TTACACAAACAAACGTAAGTTTCAITTTGGGCAAAAAATTGA GC
WI-19970b	167	G A ---			---	TATAAGCCGAGTCACAGGACGGCCTGTCTGGCCACAGACAGGGGCTGCTGTGGAGCCTGCCAACCC GGCCCCGGCAGTCAGTCACGCGGGGAGGAGGCTGCCCGTTCTGCCAGTTCTCACTGCGGGGACC AGCAAGGCCCTTCTCACTGGGTTGGTCAAAAG/GA/ATAGTCAACCTTGGCCTGGTGCATCCACAGAGGA TGTTGTTCAAAACCAGAAATCTTTTAAACGACTGACCTTCCTTAAAAACAGA
WI-19970a	126	T C ---			---	TATAAGCCGAGTCACAGGACGGCCTGTCTGGCCACAGACAGGGGCTGCTGTGGAGCCTGCCAACCC GGCCCCGGCAGTCAGTCACGCGGGGAGGAGGCTGCCCGTTCTGCCAGTTCTCACTGCGGGGG ACCAGCAAGGCCCTTCTCACTGGGTTGGTCAAAAGTAGTCAACCTTGGCCTGGTGCATCCACAGAGGAT GTTGTTCAAAACCAGAAATCTTTTAAACGACTGACCTTCCTTAAAAACAGA

WI-19067d	202 T G ---	---	TATTGCTGCTTGTCACTGCCTGACATTACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCCTCCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTCTC TTGGGCTCTAGTCTGGAGAAATGTTGTAGGGGTTATTTTTTAAAGTTCATAAAGAAAT/ GACATAGTATTCTTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19067c	153 G C ---	---	TATTGCTGCTTGTCACTGCCTGACATTACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCCTCCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTCTC TTGGGCTCTAGTCTGGTGTGAGAAATGTTGTAGGGGTTATTTTTTAAAGTTCATAAAGAA ATACATAGTATTCTTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19067b	151 T C ---	---	TATTGCTGCTTGTCACTGCCTGACATTACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCCTCCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTCTC TTGGGCTCTAGTCTGGTGTGAGAAATGTTGTAGGGGTTATTTTTTAAAGTTCATAAAGAA ATACATAGTATTCTTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19067a	57 C G ---	---	TATTGCTGCTTGTCACTGCCTGACATTACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC TGCACATTCCCTCCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGGT CTCTTGGGCTCTAGTCTGGAGAAATGTTGTAGGGGTTATTTTTTAAAGTTCATAAAGAA ATACATAGTATTCTTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19106	247 T C ---	---	TTAATCCAGCCCTACCTTGTAGTATTTTAAAGGACAGTCTCAAGCACTAAAGTGGCTAAATTC AATTTATGGGTATAGTGGCAATAGCACATCTCCCAAGCTTAAAGACAGTGGATCATGAAAGT GCTGTTTTGTCTTTGAGAAAGAAATATGTTTGAGCGCAGAGTAAATAGGCTCCTTCATGTGGC GTAATGGGCCATAGCCTATAATTGGTTAGAACCTCCTATTTTAA/TCTGGG
WI-18944	147 A G ---	---	CAAGGCAAAATATCAGGAGCTTTTACACACCTACTAAAAGTATTATGTAGCTGAAACAAA AATGCCAGAGGATAATATTGATTCCTCACATCTTAACCTAGTATTTACCTAGCAATTCAAAACCC AAATGGCTAGAACI/AGTGTAAATTAATTTCAAAATATAAGTCTACAGTTAATTATGTGCATA TAAACCAATGGCCTGGTTCAATTTCTTTCTTCTTAATAAATTAAGTTTT
WI-18952	232 G A ---	---	CCCATCCCTGTGAAGGAGTAGGCCACTCTTTAAGTGAAGGATTGGATGTTTCATAATACATAAA GTTCTCTGTAATACAATAATATTATGCCCTCTCTCACAGTCAAGGAACTGGGTGGTTTGGT TTTTGTGCTTTTTAGATTTATTGCTCCATGTGGGATGAGTTTTAAATGCCACAAGACATAATTA AAATAAATAAACTTTGGGAAAGGTAAI/GI/ACAGTAGCCCCATCACAT
WI-18932d	177 C T ---	---	CACACCTCATGCTAGCCTCACGAACTGGAATAAGCCTCGAAAGAAATGCTTGAAGCTTGTA TCTGATATCAGCACTGGATTGTAGAACTGTTGCTGATTTTGAACCTGTATTCAGTTAACTGTTCCC CTTGGTATTTGTTTAAATACCCTGTACATATCTTTGAGTTCAA/C/TCTTTAGTACGTGTGGCTTGGTCA CTTCGTGGCTGAGGTAAAGACGTGCTTTGTGGAAGACAAAGTCTGTGGCTTG

WI-19042	193 A C ---	---	TTTGTCAGTGTGCTCTCGCAATGCCCTCAGTAGCATCTCAGTGGTGTGTAAGTTTGGAGATAGATG GATAAGGGAATAATAGCCACAGAGGTGAATTTGTGCTTCAAGGACATTTGGTGAAGTCCCAACAG ACACAATTTATCTGCGACAGAACTTCAGCATTTGAATTTATGTAATAACTTAACCA[AC]GGCTG TGTTAGATTGTTAACTATCTCTTTGGACTTCTGAAGAGACCCTCAAT
WI-18984	208 A C ---	---	ATTGGCCCTGTACAGTTTGTCTATTATAAATTCATTAACCACTACAGGTGTTGAATGTTTAAAA TGTAAGCCCTCCAGTTTCTAGTTATTTCTGAGTGTGACAGAGCTATTTCGCAGTGTATTAAAT GTAACCTATTAAATGAATCAGAAGCAGTAGACAGATGTTGGTGCATAACAATATTGTGATGCATT TATCTT[AC]ATAAATGCTAAATGTCATTTATCACTGCGCATGTTTGACT
WI-18851	90 T A ---	---	GCCTCAATTGGCGATTGATTCAGTGGCCACAATGTAAACAGGTTGGTAGTTGTTACTATTGTAAT ATACCTTTTCCCTATTGTTATCT[AT]A[GT]AATATAGGATCCTGGAATGAGACCTGGTGGAA
WI-18821b	76 T C ---	---	TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC ACAGAGGC[TC]GGGGTAGCCATTGTGCAGTCATGGCCGGGGGAACTTGCCAACTTCGTGTCAG GTGCTGTGT
WI-18821a	69 C T ---	---	TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC A[CT]JAGAGGCTGGGGTAGCCATTGTGCAGTCATGGCCGGGGGAACTTGCCAACTTCGTGTCAG GTGCTGTGT
WI-19021a	20 C G ---	---	ACTCCTGTGCTGTGCTCCAT[CG]ACTGTCTCTTTGAACCCAGGAAAGTCACAGAGTTTAAAGAGAA GCAATTAACATCTGAATCGGGAACAAGGGTTTATCTAATAAGTGTCTCTCCATCAGTTG CTACCTTACCACACTTCCCTGTGATTTGCGTGAGGAGCGTGGCATCTACTTACGTACGTGGCATAAC ACATCGTGTAGCCCATGTATGCTGGGGTAGAGCAAGTAGCCCTCCCTGTC
WI-18908	70 G C ---	---	TGGAAATTCCTTCATCTGGAACCATCAGAAACACCCCTCACACTGGGACTTGCAAAAAGGGTCAGTA TGG[GC]TTAGGGAAACATTCCATCCTTGAGTCAAAAAATCTCAATCTCCCTATCTTTGCCACCC TCATGCTGTGTGACT
WI-19037b	155 A G ---	---	CACGGTCTCTGCATCGTTACCAGAGCCCTCTGCTCCTAGCCACGCCCTGTATACCCGCGCAATA TCCCCAAAGCTTTGGTCTCAAGTCATGCCGAATTTAGATGCTGGTCAATTTCTGGAGAGGGTC CCCTCCCTTACGAACACA[AG]AAACCCAGCCACATGACTAGCACGCTGTGACGGGACCA GTGCAGGCACCTGGGGGTGGAAGTGTGTTGACACAGTGAATGGGAGGTGG
WI-19037a	47 C A ---	---	CACGGTCTCTGCATCGTTACCAGAGCCCTCTGCTCCTAGCCACGC[AC]CCTGTATGACCCGCAAA ATATCCCCAAAGCTTTGGTCTCAAGTCATGCCGAATTTAGATGCTGGTCAATTTCTGGAGAGGG GTCCCCCTCCCTTACGAACACAAAAACCCAGCCACATGACTAGCACGCTGAGCTCTGCAGGGACCA GTGCAGGCACCTGGGGGTGGAAGTGTGTTGACACAGTGAATGGGAGGTGG
WI-19064	66 T C ---	---	TTGAGGAGGTGGGTGAATGCTCTTGGCAGGGATTTGTGACACTGCAATTCCTGGGCTGTGTTCTT/ C[CGGGCTCT]CTGGACCTTGACCCGTGGATACAGGCCATGTGCCATGTTATTTGGGCTCTGGAGGG TGGTGAATAAAGGC

WI-18972a	112 A G ---	---	---	AGGCTGTGGCTTATGTACCCCAACAGAGGGGTCTGAGAAAGTCTGGCTGCTGGGATGCCCCCTGCC CCCTCTGGAAGGCTCTGCAGAGATGACTGGGCTGGGGAAGCAG/GJTGCTTGTCTGGCCATGGAGCC TCATTGCAAGTTGTTCTTGAACACCTGAGGCCCTTCTGTGGCCACCAAGGCACTACGGCTTCTCTCTCC AGATGTGCTTTGCTGAGCAGACAGAGTCAGCATGGAATGCTCTTTGGCCA
WI-19016b	184 C A ---	---	---	GTTTGCAACCAACATGTGCTCTTTTCAGTCATTCAGTCTTTAATATGACATGGTAGAGAAGATAAG GTTATGGCAGGTAATTTTGTAAATGTGATTAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAACCTTAGATACATAGCCGACTGTACAGAGGTTCACTCAAC/CJCTCAACACTATTGAC TTTTGGGCTGGATAGTCTCTGTGTGGGGTTTGCTTGTCACCTGAG
WI-19016a	161 C T ---	---	---	GTTTGCAACCAACATGTGCTCTTTTCAGTCATTCAGTCTTTAATATGACATGGTAGAGAAGATAAG GTTATGGCAGGTAATTTTGTAAATGTGATTAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAACCTTAGATACATAGCCG/CJTTGTATACAGAGGTTCACTCAACCTCAACACTATTGAC TTTTGGGCTGGATAGTCTCTGTGTGGGGTTTGCTTGTCACCTGAG
WI-20096	21 T C ---	---	---	GGTTTGGGGCATTTATTTCT/CJGATAGAGACTGGCACAAGCTTTGGGCTAAGGACACCCGGCCCCC ACCTCATCTAGAAACAATCTCTCGCCAGACTTG
WI-19591b	156 C A ---	---	---	TGGGGCAATTTTAAACCAACAGGCAAAATATACATATACCTGAATATAAGGTAACCTCAAGCCCATG AGTATAAGATTAAAGCAGTTACTTTATTTGAACAAGGAAGTGGCATAAGCAACTCAGTGTGCCCC CTTAGGGTGGGAGCTTCCC/CJACTACCACTCCCCACCCCAAGGCATCATTTTGGGAGAAAAA GTGCTCTATCTGGCTAGCTGTGTTATCTAGGGATTGCACCTTCTTACACGG
WI-19591a	45 T A ---	---	---	TGGGGCAATTTTAAACCAACAGGCAAAATATACATATACCTGAATATAAGGTAACCTCAAGC CATGAGTATAAGATTAAAGCAGTTACTTTATTTGAACAAGGAAGTGGCATAAGCAACTCAGTGTGT GCCCTTAGGGTGGGAGCTTCCCCCTACCACCTCCCAAGGCATCATTTTGGGAGAAAAA GTGCTCTATCTGGCTAGCTGTGTTATCTAGGGATTGCACCTTCTTACACGG
WI-20310	125 G A ---	---	---	TCCTCCAGCTCTGTATCCTTGTCTTGGGGTCTGTGTTACGGCCCCCTCCAGGCAATGTTCTTCAT TTAGGTAGGAACAAAGGCCAAAGAACATACAAGCCCCAGCTCTAGAGGCTCCA/GJTCAGAA CTGGACCTTTAACTACAAAGGAATCTTGGATGAATATTTTACGGGGCTTCAGGAGCAGGTAGC AGAGCCAAAGTGCACACTCAGGCCATCTTCTCCCAATGTCTCCCCGGGGG
WI-20860	224 G A ---	---	---	CTCTCCCCTAAGGAGCCTTGGCCTTGCAGCCCCATTCAAGAGGGATGGAAGTCACAAGACAATGAGT GGAGCCTCATGCCCTCCCATGAGGAAGCCCTTAGTATTGCTGACATCTGCCCTTATCCTGTCTCTCCT CCCCAGTGTCTCACACTTGGGCAAGCAGAGTGGTGGCAGACCCAGCCTTGAGAGCTCTTGAGACC GGAAGGAAGGGGGCTCATTG/AJGGTATGGCTTCTGGCTCTCTGGCTT
WI-19359a	39 T C ---	---	---	GACGTGGACAAAGGAGGTTAAATGAATACCTTGTGTTTGT/CJCATGTTCAAAAAAGAGTATTAAT ATTTGTGACTGCATCTGTGAATGAAGACACTCAAAAAGCCATGTTTCCAACTTAGGTTAATAATAA GGCTATTGTCCACCACTCTCGGGCATTGTGCAATATCTGGGCTCAAGTGGGAGGCCACGCTG GGAACAAGGCCCTCAGAAACAAGGACATGCAGCTCCCTGAGCCAGTTCTCT



WI-19766b	93 A G ---	---	TGGCCTCAATGACTGGTACATTGGAGAAGCTGTGCAGCAGCATCCTTTCTGTGGTGGCAGGCGAGGAGATGAACCATAGGAGCCAAAGTCA/GJGACAAACAGAGAAGGACACCAAGCCTGAAACCCCTCGGACAAACAGCAGAGTTACAGCTGAGGGATGCCCTGGAGGTTTCTGACCCCATGAGAGGCCCCCTCACCTCTTACCCTCTCTACCAACCAAGCTCTCGGCGAGTCATGGACTTAT
WI-19766a	31 G A ---	---	TGGCCTCAATGACTGGTACATTGGAGAAGCTTGAAGCAGCATCCTTTCTGTGGTGGCAGGGCAGGAGATGAACCATAGGAGCCAAAGTCAGACAACAGAGAAGGACACCAAGCCTGAAACCCCTCGGACAAACAGCAGAGTTACAGCTGAGGGATGCCCTGGAGGTTTCTGACCCCATGAGAGGCCCCCTCACCTCTTACCCTCTCTACCAACCAAGCTCTCGGCGAGTCATGGACTTAT
WI-20512d	126 C G ---	---	CTTCCTCTGTTGGCTTTGCATTTGTGCGATTGGAAAAACCACTTGGAAAGGGACTTTCTCTGCAAACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCTTGACTGA/GJAAAGCTTAGAAAGGAAGTAAATTGCTCTTTGAATATGATTTAGGGCGGGGCGTGGGTGGGCTCACGCCTTATTAATCCCAGGCACGTGGGAGGGGCAACGCGGGTGGGATCACTGA
WI-20512c	59 T G ---	---	CTTCCTGTTGGCTTTGCATTTGTGCGATTGGAAAAACCACTTGGAAAGGGACTT/GJTCCTGCAAAACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCTTGACTGACAAAGCTTAGAAAGGAAGTAAATTGCTCTTTGAATATGATTTAGGGCGGGGCGTGGGTGGGCTCACGCCTTATTAATCCCAGGCACGTGGGAGGGGCAACGCGGGTGGGATCACTGA
WI-19599	230 C G ---	---	GGGCTTAAATTTCCCTCTGTTGGGACTGGTCTCTCCAGTTACAGAAAGGATCGACCCCTTTTCCATAACCCCTTCTACATTGGAAAGAGCACACCTTGTATACAGATGGCTCGGTGAAGTCTTTTAAACGGACAAAGGTAAATCACAGCTAACAAACGTGATGTTGGCTCACAGTAACCAACACCTCTTTTCAGAACAGAGAGCGTTAAAGTAAAGGCA/C/GJTTCCAAAGAGTAACACTGCTA
WI-20679	82 T C ---	---	TGTTTGAATAAAAAATTTCCATGGTCTTAATTGAAGTGTATGTTACTTTCTTTTAGAATATCCTTTTTCATTAAAAATAAT/CJCTAAACCACTCTATGTTTCAACCTTCTGTTTAAACACTAAGATATGGGTTTTGGAAAGGCCACAGTCACCACTCCATGAAGTGGGCGAATGGTCTTTTGGAAAGCTCTCAGGGTGTCTCCAGAAA
WI-19909a	29 T C ---	---	CCAGAAATAAGCCTGAATATCTCTTTCT/CJTTAAAAATAATTTTCTCTTTTGTCTCTCCAAATAATCTTAAATGAACCTGTCTAGTCTATTTTAACTAGGCAATTATAACACTACCTAGGCGGGTTTTTCTTTTATACCTGTCTGTACTGTGGAAATCAACTAA
WI-20341	221 G C ---	---	TTGAGAGGCTGAGAGAAGGCTGTTGAGACATTGTAATAAGTGTCTAGGGCATGAGACATTAGGAAGGCCACAATTATGAGTAATGAATGTGGAGGCTGATGAGAAGTACTGCTCCCATTTGTTTAGCAGGAGGAGGAAAGTATCTGGGGTCTCTGGCAGCAAAAGCGTGTGTAATAATTGGGTGACGTATGCATCCCCCAATGCAATTGGTTT/CJAGTCTCCAGTGAGCTGTGGGCAAGTCT

WI-20113	60 T C ---	---	---	TTCTGGTACATGGTAACTGCTCAGTATTACTGAGTGAATGAGCAAGAACCTGAAATACTGTCGGA AACAGTAAAGCAAAATTACCACAAATTAGGAGGAATTTTTCAGACATAGGATATTTAAACAT CACTCAATACTGGAGCATGATTAGCAATAAATCTATTCCATAAACCCAGGTAGATAAATGTCACA GCTTTAAATATAGTTAAGTACAGTTGATCCTCGTTATTCATGGATTCCGTATT
WI-20895	107 G C ---	---	---	TGATGGCAAAGTACAAAGGCTCTGAAAGAACAGAGTAACAAGAGCAGCGCAGTGCAGCGTGTGGC CACTCCACCAGGAGAACACTTGACTTCATTAAAGGCAA[G/C]CTTTACTCTGTACTTTTCTCTC CCACATAGTTTAAACCAATAGAAAGGCATTCTATTCTCACACTACTGCTCTCTAAGGTCCTAGGAA TATACTGGTACTATAGCAAAACAGATGCA
WI-20721	72 T C ---	---	---	CCTGCAATCACAAAGTGGAACCTAGTTGATATTTTGAAATCATACTTGATTTAACCCCTTCAGAAA TTCTATT/CJAAACACTAGCAACTTCCTTTTATCAGA
WI-19415c	161 A G ---	---	---	CTGGATTTAATATTTCTGGCCTAATAACCAATGTAAATCAATAAAATTTGGTCAATATCTCCACCTC ATTTCTGCTAACATGTTTTCAGGATTCCTTAAGTAAGTATTGACGACTGAGACTAGTCCGGCAAA GTCATGAGACCCCTTAGCTGATCTCATJA/GJAACTCCACCTCATGAAGGAGATGATTCACATCTCAA GCTAAGGTATAAAGTGTGGACATACAAAGGCTTACAAGTTTACACTTCCTG
WI-19348c	103 C T ---	---	---	GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCATGCACCTTCG GCGGTGCGATGAAGAGACTGTTGGTCATGGCGGTGA/CJGTGCTCTTCCAGGCTCATATGGATGTCCT CGAGGTTGCACAGGGAAGTCTGCTGTGTAGAAAGCTCTCTC
WI-19348b	98 G A ---	---	---	GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCATGCACCTTCG GCGGTGCGATGAAGAGACTGTTGGTCATGGC[GJA/GT]GACGTCTCTCCAGGCTCATATGGATGTCCT CGAGGTTGCACAGGGAAGTCTGCTGTGTAGAAAGCTCTCTC
WI-19635	98 A T ---	---	---	ATTAGTTCGTGTTGGGCCACATTCAAAGCCATCCACACAAGCTCTTGTAAGCCATTGTAACACAATG TTAAAGGTACAGTAAATAACAGTATTATJA/TATCTTATTGTAGCACGGCTGTGAGGCTCAT GTTGAATGAAGCATCCTTAGGCAGCACGTGACTGCATGCAGATATGTGTGCTGAAAGAACTTTGCCTT T
WI-19641a	46 A G ---	---	---	TCCAATTTTCAGAAACATGTTCCATGTTTATTGTGATAAGCACTAGJA/GJTATTATAGTCTCATGTTT TTAATTTATGAATAACGCTGATTCATTTGATTTTGATTTACAGAAGATGTCAGGGCTATCTCATTC AGTTATTAAATGAATGGATCAGAGTAGTAAGTCAAGATAAGTGCATAATGTGGTTTAAATTTTAAAA AATACTCAGAAATGAGGTAGTATTTAATTTTAAATTCACCCACCTTG
WI-19642b	52 C A ---	---	---	ATATAGAGTACCATCCATGGTTTCAAGCATGGCTGGACACATTTATCCCCCT[CJA/GGGTAAACCAG GACTATTGCATGAGCATCTTTAATACGTATTTTGATGGACACAAAGTTTTCATGTCATTA
WI-19673b	180 C T ---	---	---	TC TGCCATGATCACATTGTGATGAAGAACATGATGGTCACTAGTAGGTAACCTTTCTGTGTCATTGCCT TACTCTCAGTGAGGTGCTAGTGGATTACCTACCCCTGCTTTTGATCACCACCTGTAAATCTAATAGT GAAAGGGCAAATGATGCTCAGTATCACTGTGAAACATTTTC[CJ]CTTGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTTCCACAGCTCAAAAAAACACAGCCC

WI-19673a	35	G A ---	---	---	TCGCGATGATCATTGTGATGAAGAACAATGATG[G]ATCAGTAGTAGGTAACCTTTCTGTGTCATTG CCTTACTCTCAGTGAGGTGCTAGTGGATTACCTACCCCTGCTTTTGATCACCACCTGTAATCTAAT AGTGAAGGCAATGATGCTCAGTATCAGTGTGAAACAATTTTCCCTTGGACCAGCTGAAAGAA TCTTGAGGAGCTGAAGGCTTCAAGGTCCACACGTCAAAAAACACAGGCG
WI-19724	35	A G ---	---	---	TTTATTTGGGAACAAAGGATTGTAATTTGGTAA[G]CTGAGTCACGGTGGCCCTGAGTAGTGTC CTAGAAAGCAACACGAGAGTTTGGTTTTCTCTT
WI-19307	196	T C ---	---	---	TCCTCTCCCCAACTAGATGGTATTGATCACTCTGCCCAAAATGGTACCCCTTCAGCAAGAAGCTG CAAGCCCTCTTGGATTGCTTCATGAGAAATGGTGGCTTGGATGGAGGTGACATTCCTTGCTGT GGTAACTGCAAGAAAGGAACACAGCAATGATTCATAGAGGCCCTTTAAAGAGACCCG[7]CTGG AAATGGGCCATGGTCTAATTTGGTGTGAAATAAATAACCTCTTTGGCTG
WI-19269	85	A T ---	---	---	CTTCCCTCATCCCTCTCCACCACCATCCCGGAACAAGTCTCCAGGATCCCTGCCCACTGGC CATTTGGAGTGTCC[A]TTTGGGTAGCAATGTGGAACCAACCCAGGCCCTTTGGGAGAAAAATGG AGGGGTTGAGGAGTCCAGAGGGGCTTATTGAGGCCCTTTGCCACTTGCTCATAGCGGAGCTCG ATCTCTCATCATCTGGACAGGTGGAAGCGAATCTTCCCGGGCGTAGGCA
WI-19946	122	C T ---	---	---	CAATGGACTGAATGAGTGGTGGTGGGGGACACACACACTTCAATACACGTCAGGTCG CTTCCAGTTTTAGAAACAGAAATCTGCATCTCAGCTCAGACGACAGAGAGGT[C]TCTTCTCTG ACCCAGACGCACTCAGAGCGAGGCTGGTTTCAAAACTGCATTTAACCTGGCCAGAGAGTTCAAC CGTAGGCATCTTTAATAAATACTCACTCCAGCAAAATGTGGTACGGTTACTAA
WI-19956	141	G A ---	---	---	CACAGCATGGTGAATAGCATCAGATTGAATGAAAGTTTGTAAATGCAACCATAAATAATTATA ATAATATACATCAAGTAACCTTACAGCACACATTTTAGGCCAAGTTTGGATCTGTGGACCT CAATG[G]A]CTCTCGGAGAACGACCCACGTTAGCAGCAGATACCTTACAGCTTGTATCTACTCAA GTGATGGCCAACAGAGCTTCTGAACCTCTCTCTGGGAGGTAGCTGACAAG
WI-19076	40	G A ---	---	---	TTGGTTGGATACCTTGCTGAAAAAAGCAGTTTTAT[G]ATTCAAAATACCTTTTAAAAA GTATTCAGCACAAAGATTTCTGTAACTAGATTATGTTGTAACCTTTTCTAAATCTGTAGGAG TGTCGGTTGTTAAGAACTAGAGCTTATTCCTATTCCAAATCTATCTGCGCTCCTGAAAAACTGCAGA AAGGCACCTGAAAGCTGTTCTTTAAGATATGGGATTTCTTTTATCTT
WI-20218	26	T C ---	---	---	CCACACACTCTGTTTTATAAGCTA[T]CJAGGACAGAGCAGAGATGGAACCTGAAAAACAGGCTAG AAAATAACATAAATTGGAGGGGAACAGTGGGATGCAGAAAGATGACACAGCCACATGTGCCCA GTCAAATACTTTTAGTCCCTGCAGCAGAAAGATGCCAACCAAGTCTCTATCTGCTGGGATCCTGCC ATGGATGCAGGAGAAAAA
WI-20295g	154	T G ---	---	---	CAACCTTTTGGACAAGGGGACGTGAATTTCTGATGAAAGTTATCTACCAAGTTTAAATTCATAATTG GGAATTCCTCTTTTAAATATCTCCAGGCTTGAATGGGAGGGCTGGCTCTACCCCTTTCTTTCCCA TCCAGTCTATTGCCAGAT/GJCCAGAGAAAGCGCGGGAAGCCAGCTCTCCAGATAGCCACTGTGG GTCCGCTTCACCTTCTGTCGACTCTCATGCTGGGACTTGTCTTTCCGGG

WI-20361a	192 G A ---	---	CTGGAGTGTGACCTAAGTGACATTTTTTTTAAATGCCAAATACAGTAATCTCCAAGCTTTTAAATGG CTTATGCAAGATGACAGAAATATGTGAAATCTGATTGTCCAGAGTTACACTCTGCACCTCCAAAGCTA CAACAGTCCACAGCTGAGAGGTTCCCTATCTCTACTACTGTGACAAATTTAGC[G/A]ATCCTTC AAATGGGAAAATTCCTAACTACAGAGACAATGGGTCTACAGTAGGCCCG
WI-20572	75 A G ---	---	GAGCCAAACCCAAACAAATAAAACAGAACTCTTTTGTAACTAAGTCATACCTACTTTCTTCT TCAGAAAT[G/G]TCATAAAACATCATCTTTTACAACATGGAGAGCGAGTAGGCCATAATTTGTTCA AATTCATCTTTCTCAAAATTTTAAATGTTTAAATCCAAAGGTGCCTATTGAATCTTCCAAAATA AACTGCCTATCAGGTATCATACCTGCAAAATGCTTCTAATATCTCTTGATTAT
WI-20588	133 G A ---	---	CATGACAAAGACAAAGATCAAGGAGTAACATAAATTAAGTTGAATAAATAGTATACAGCAATC TTCACITTTTAAAGAAATGTGAGATCCTTTGTTGGTTTTTATTTCCCTAAGTACAAAATGCTAAAC[ G/A]GGAGCCGAGCTCTCCGCAATCAGG
WI-20593	79 A G ---	---	TGACCTCATACTGGGTTCTGGTTAGAACACAGCCACTAGAACAACTCCAGTCTTTTTCAGTCTGTG CTGTACTTCAG[G/G]TTTAAATCTGGGAATGAGCATGCAGCAATGCTCCACCAGATGAGGAAGAAA AGCTGTTAAAGGAACTCAGGATGTTGTAGGAAGGGGAGTGGATGCCAGGCTTCACCAGACTAT CCAGAAGCCATTCATGGGTAATTTGGTCTGCACTACTGTGAGACACTGAGCT
WI-19765	57 T C ---	---	TTCTTTGCCAAGCCTGTTCTCAAGTTATTCAGAACTGGGTGTATACCTTTGTCTCAT/C]ATGTATCT TGTCCCTGCTGCTTTTAGGTAGCAAGGTGTATGAATCTTTAAGTTTGTGTTCTTTTCCCTCGT GGTATCAGTGAATACTGATCTATCTCTGGCTAGGGTCAATTTACAAAATGGCCATGGAAGTGAAGC AAAAGGCCACGTTGGGATAAAATCACTCACCATCGACGCCACCAAGTAT
WI-19066i	239 A G ---	---	TGACAAAGGAGAGAGAGGAAATCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTAGCCAGTCCAATCTCTACGAGGAAGTGG CATATGTTCTTGGTTGGTCAACCCTGTAGCTGAATTAATCTTCCATATCCGGATGCTCAATTACAGT ACCATTCAGGCAAACTTTTCTTAAACGCCCTTCAC[T/G]GTTCTTTTA
WI-19066g	184 C T ---	---	TGACAAAGGAGAGAGAGGAAATCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTAGCCAGTCCAATCTCTACGAGGAAGTGG CATATGTTCTTGGTTGGTCAACCCTGTAGCTGAATTAATCTTCCATATTC[C/T]GGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCAC[T/G]GTTCTTTTA
WI-19066f	148 T C ---	---	TGACAAAGGAGAGAGAGGAAATCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTAGCCAGTCCAATCTCTACGAGGAAGTGG CATATGTTCTTGGTTGGTCAACCCTGTAGCTGAATTAATCTTCCATATTC[C/T]GGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCAC[T/G]GTTCTTTTA

WI-19066e	147	GC	---			TGACAGGGAGAGAGAGGAAATCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAGTGG CATATGTTCTTGCG/CJTGGTCAACCTGTAGCTGAATTAATCTTCCATATTCGGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAACGCCCTTCACCTAGTTCTTTTAA
WI-19066c	100	GA	---			TGACAGGGAGAGAGAGGAAATCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATAATGTTCTTGCGTTGGTCAACCTGTAGCTGAATTAATCTTCCATATTCGGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAACGCCCTTCACCTAGTTCTTTTAA
WI-19066b	87	CT	---			TGACAGGGAGAGAGAGGAAATCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCA/CJTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATAATGTTCTTGCGTTGGTCAACCTGTAGCTGAATTAATCTTCCATATTCGGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAACGCCCTTCACCTAGTTCTTTTAA
WI-19066a	72	CT	---			TGACAGGGAGAGAGAGGAAATCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCA/CJTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATAATGTTCTTGCGTTGGTCAACCTGTAGCTGAATTAATCTTCCATATTCGGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAACGCCCTTCACCTAGTTCTTTTAA
WI-20660	105	GC	---			TTTACAGCGAGTTTTCCCGTCTCAATAAGTATGAATCTAAATAGATTAGGGTGAAGAAAAATGTG TGCTAAATAAATCTCCCTTTTGAATGTATATTG/GJTAAAGGGAAGCATTAAATATTA CAGACATAATTTACAAGGTTCTGAACATGAGTGATTCCATCTGTTTCTGTACAAGATAGAACAAA AAGCTATCCACCCCGCCCCCAAAAATACTGTTTAAACACACTATGTTTAAAGA CTGCTGCCAGCTTCTCTTTGGCCCTGCTCCAGATGGCGGTCTCTGGCAGCCCTCCCTCAGTCTTCC TCCACCCGCTCTTCTTCCAGCCCTGCTGCATGCATGTGCACCCCTGGTTC/TJTTGGCTCCATCGCC TTGAAAGCTCTGAA
WI-18768	120	CT	---			TTCCCCAGGGTTCTGTATTGCAGCTAAGCTCAAAATGTJ/GJTATTTAACTTCTAGTTGCTCTTGTG GTCTTCTTCCAAATGATGCTTACTACAGAAAGCAAAATCAGACACAATTAGAAGCCCTTTTCCATAAA GTGTAATTTTAAATGGCTGCAAAACCGGCAACCTGTAACTGCCCTTTTAAATGGCATGACAAGGTGTC AGTGGCCCCATCCAGCATGTGTGTCTATCTTGCATCTACCTGCTCC
WI-19087	37	AG	---			GAAAGCCAGAGATTAGCCCGCATTCGGCATCTGTCAACCAGGACAGAAJATJGTCATGGACAAGGGA TGAGCTTTACAAAGATGATGCACCTTTGGAGATCAGAAAAATTCATATTTAAGCAAAGTGATACAAACA CAGTGATTTGGGAATGCC
WI-18790	49	AT	---			AGGAGGCTGTTCCAGGAGTCTGCCAGCAGCCCTC/GJGTGGCCAAAGCCAGACACTCACCCACCTT CCCCAGTGGCCCGGTGGATCTGCTGCTAGGCTGGAGTCAAGGATTCAGAAAGACACAGGCTGCACA GAAAGAGCCAGATGGACCTGAGTGTGGTTCACAGCCCCCTACACTCAAGGCTGAGAGGCTCAGGAA AGTCA
WI-18987	35	GA	---			

WI-18919	26 C	---	---	TGGATGAAACCACAGGGATTCCGGA[C/T]GCCAGACCCCAATTTTATACTCACTTTTCTCTACAGTG TTGTTTTGTGTGTTGGTTTTATTTTTTATACITTTGGCCATACCACAGAGCTAGATTGCCAGGTCT GGGCTGAATAAA
WI-18741c	64 G	---	---	CTTCTGGTCAAGGCTTTGGACATCTCTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTC[G/A] CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAATTTTACAAGCCTGGATGAGGCTACTGA
WI-18741b	38 G	---	---	CTTCTGGTCAAGGCTTTGGACATCTCTCAGTCATCA[G/C]ACAGAGTATCTCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAATTTTACAAGCCTGGATGAGGCTACTGA
WI-18741a	23 T	---	---	CTTCTGGTCAAGGCTTTGGACAT/GJCTCTTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAATTTTACAAGCCTGGATGAGGCTACTGA
WI-19179a	170 G	---	---	TCAGAAAGCAGACATGGCATCTGTTCCCTGCTTGTGTTGTTGTGTACCTTTACGAGACCTGAATT TTAGAAATTGCCAGTGCTGCCAGAGTGAGTGAGTGAATTTCTCCTTTCAAGTAAAGATAGGCTATCTC AACACTGCTGAGTGATTATATAAACATATCAACCA[G/A]TAGCATTAAACCCATTTATTTCTGTCTCCTT AGTGTCTGAAGATGCTCACCAGTTTCTGTGTACAGTAAGGCAGCATGT
WI-19212	46 T	---	---	CCAAAGTGCATCCATGTTTGAATTTCTGATGAGACTAGAGTGACAGT[A/G]TTTCAGAACCCAAATGT CCTCAGGTAGTTTGGAGCATCTCTATGAGATGGGATTATGCAGATGGCTATGCAAAATGCAGCTGC ATAATTACACATTATCAAAGTCCTCTTACAAATTTATTTCCGCAGCATGTCAAGTAAAGTAGACCCA ATGGGGAGAGAAAATGCCTGCTTCTTCCCTCTTTTCTGCACTGCCATAT
WI-19183	210 G	---	---	CTGTTGAAGGCTTCTCAGGCAAACTCCAGCTTAAAGCCCTAGACAGGTAAGAGCACACATTGGATG GCAGCATGGGTTCTCCCATTTTATGGCATGAAATATGTGGTTTAGAATAAGGAACAAGCATATT CCTTTGCCAACAGCCTCACTAAGAGGCTTTTGTCTGAGTCAAGCAACACTTGCCTGCTCTGCC CTTGGAG[G/C]TGCAATTTGACCTGCTCTCACTGGTAAGTGACTTGGTGGC
WI-20014b	214 T	---	---	TTGAAATCCAGTCTCCTGGCCCCCAGGCAGGCTGTCAACCATAGAAATGCTTCTCTACTGGGGTC GTTCTGGCTTTTGTTAGAAACTTGGTCTGAGATGTTCTCCCTGTCCATTACCATTCGATGTTCTTT TGTTCAGAGCAATGTTTCTGTTATCTGAAACTGGAACCTGAACCAAGTTGCCTTCTCTAGTCACC AAGCATACTT[C/T]CTGGCTCCCCAAGTACTTAAATGTTCTCATCTGT
WI-19041	198 T	---	---	GTCTCCCCAGAGTCTTCTGCACCCCCAGCCCCCTGCTCCTGTAAAGGGGATACAGAGAAGCTCCCCG TCTCTGCATCCCTTCCCAGGGGGTGGCTTAGTTTGGACATGCTGGTAGAGACTCCAGGGCGTG CACGGTAGCAGATGAGGCCCAAGCTCATCACACAGGGGGCATCCTTCTCAATACAGCC[T/C]G CCCTTGCAGTCCCTATTTCAAAAATAAAATTAGTGTGCTCTGCTGCTGT
WI-19135	20 G	---	---	CAGTTACCCCTGCTTGGCTC[G/A]AAAGTGTCAATCAATTTGTAAATTTTAGTATTAACTCTGTAAAAGT GTCTGAGGTACGTTTTATATATAAGGACAGACCAAAATCAACCTATCAAGCTTCAAAAACCT TTGGAAAGGGTGGATTAAGTACAAGCACATTTGGCTTACAGTAAATGAAGTATTTTATTAACT GCTTTTGGCCATATAAATGCTGATATTTACTGGAAACCTAGCCAGCTTAC

WI-19236	54	G A ---	---	TACACAGAGGTGCGCACTTGACTCTGAGGTTGGGTGTGGAAGGGGAAAGG[G/A]GATGGAGAC CTGCTCCCAGCTCTCTGTGACCGGTTTACATGGGAACAGGTTAACATCTGTGTAGGGGAGGT CACCTTACCCCTTTTCATAGGGGAAGAGTGTACACTCTCGGTATCTCAGGGGAATGGGAAAG AATCTTTCAAGGGCAAGAACTCGTGGGAGGATGTCTGTTGTATGTAACTACT
WI-19144	222	G C ---	---	GTGCCAGTCTTCCAGAAAGCAAGGACTGCCCTTCATTACGCCCTTGTGACCTCCAGCCCTTCTTAAGG CTCAGCCCCACGGGACTCTGGTGGCTGCCAGCTTGTGAGCTATCTATCTATATTCATTTCATAGCCAA ACAGGAGACCCCTTTCAGGACTTGCACACAGGGAGGCTGTAGCCAGGAACCCCTCTTCCCTGGT CTGGCTCTGCTGGAGCG[G/C]TGGGAACCAACACCTTCAGTGGCTGGTG
WI-19139b	110	C A ---	---	CCCGTCTAAGGGAGAAAGCTAATGTTTCCACAGACTGAACAACGTTATTTACAGAGGGTAGAC GGCAGATGCCTGACAGAGAGTGGTTGGCAGACAAACACTAG[C/A]ATTTACGGGTGTGGGCAC ATGGGTGTGGCACTGGACGTGTGCAGCATGTGGCGGTCTCTGTGTGAAGCCACCGTCTCTCTTTGG GGGGCCGGAGATCTAGCATCTCTGAAATCCTGGCTGTGAGGCTTTGAAG
WI-19139a	66	C T ---	---	CCCGTCTAAGGGAGAAAGCTAATGTTTCCACAGACTGAACAACGTTATTTACAGAGGGTAGA[ C/T]GGCAGATGCGCTGACAGAGAGTGGTTGGCAGACAAACACTAGCATTTTACGGGTGTGGGCAC ATGGGTGTGGCACTGGACGTGTGCAGCATGTGGCGGTCTCTGTGTGAAGCCACCGTCTCTCTTTGG GGGGCCGGAGATCTAGCATCTCTGAAATCCTGGCTGTGAGGCTTTGAAG
WI-18910	112	T C ---	---	GGCTGGGACCTTTAGGAAAGTGAATGCAGGTGAGAAGAACCTAAACATGAAGGAAAGGGTGCCT CATCCAGCAACCTGTCCCTTGTGGGTGATGATCAGTGTGCTGTG[C/G]GCTCATGGCAGAGCATT CAGTGCCACGGTTTAGG
WI-19235	173	A G ---	---	TTCAGGAGGTGGAGTTGCTGTCAGCTCTCCTGCTGTGATGTGGAAGCTTCTGATATTTGAAGAAACA CGAATGTCTCTGTAGCTTCTCTTCTACTGCCCCAGTATGCTCTGTATTTATCAGCGATGCCCTCTGT CACTCATGCCCTTGCCTAATTGTTCACAATGGTGGAA[G/G]GCTTCATGTAAATATGATCAGGACCCACC TCCAGTTCTTCTGAAAGTGTACAGTGTCCAGCCGGTTCTGCAGCCTA
WI-19222	179	C T ---	---	CGTTTTCCTAACTCACCCAGTTTAGTTTGGGATGATTTGATTTCTGTTGTTGATCCCATTTCTAA CTTGGAATTGTGAGCCTCTATGTTTCTGTTAGGTGAGTGTGTTGGTTTTTCCCCCACCAGGAAGT GGCAGCATCCCTCCTTCTCCTCCTAAAGGGACTCTCGGGAAC[C/T]TTTCACACCTCTTCTCAGGGAC GGGGCAGGTGTGTGTGTGTACACTGACGTGTCCAGAAGCAGCATT
WI-19117	134	A G ---	---	AAATAATGCAACGCGAGGAGGAGAAAGAAATGCCTAAGACAAGAACATTTCTCATAGAACAATTG ATCTGTTTACAGGAACAACCTTGCCCTGAAATTTACACAGTGAGACTGTACATAATTGCATGAA A[A/G]TAGCTATTTTTTCCTAAGACATTTTTCATTCATGAATATTTTCAAGTTTTTTCATACTGTACA CATTTCTTAAACACATGATACCAGCAGCAACTGAAATGAATGCCGAATTTG

WI-19134c	263	C T ---	---	---	CTCCTGTTGTCGACCTGACAGGGTGACACAGCCCCCTTTACACACTCTGTCTCTCTATCTTCTCTGGGTAGA TGCCCTGGGTAGGGCTGAGTACTGAATGGTCTTCCATCCCAAGAGGGGTGCAGCCAGGGTCAG GCCCTTCAGAGCCAGGGCTAGAGGATGCACGGTGGCTAGAGCCAGCTGCACATATCTTTTCAGAGCAC TTCATCCACTTGTCTCTCCCTACCTCGGCACCCCTGGGTGGGAAGGG
WI-19134a	162	T C ---	---	---	CTCCTGTTGTCGACCTGACAGGGTGACACAGCCCCCTTTACACACTCTGTCTCTCTATCTTCTCTGGGTAGA TGCCCTGGGTAGGGCTGAGTACTGAATGGTCTTCCATCCCAAGAGGGGTGCAGCCAGGGTCAG GCCCTTCAGAGCCAGGGCTAGAGGATGCACGGTGGCTAGAGCCAGCTGCACATATCTTTTCAGAG CACTTCATCCACTTGTCTCTCCCTACCTCGGCACCCCTGGGTGGGA
WI-19224	112	C T ---	---	---	GGTTTACCAGTCTTCCAGGGAACTCCGATGAAGTGTCCACAAAAATGAGCGAGTGAACCAAGA AGAGGATGACATTAGATCCAGGAGATACACAGAGGAGATAATCTCTCAGGATGCTGTGAAGA AAGATCCCTGGATCCAGGATGATTATAGGACAAAGTTGTTCAATCCAGCAGGCCAGAAAGACTTCC AGGGAACTCATTCAAGGAGGTGAAAAATGATGGATGACTCTCCAAAGATGAAAA
WI-19201	179	T C ---	---	---	GCAGCTCTAAGGACCACTGGCCATTAGCTCTGCTTTGATGGCATCTCTTCCACCTTGTCTCTC CTTTGCTCTCTGTGTAGTGGCAGGTATGACAACTCATCCAGTGGAAACACAGCCTCACACTGCC CTTCGCCCCCACTTTGCCAGGTGCACCGAAAGGAC/TCTGGGGGATAAAAAATTCAAAAA GTGTGATGTGCTCAGAAGGTGACAGACTCCATGCTGCTTGGCCTCAA
WI-19034	45	T C ---	---	---	GAAATGGCTCCACTCAGAGCTACCCGGTGTGATGAGGATAGGGAA/TCTACTTCTATTACATTAAG GCAACAGCAGTTAGTAAAAAGGTTTACAGTGTCTGTCTGTTGAAAGTGAATATAAATTTTTTG CTAGCCCATGATCAATCGACTTCTATTGTTGATATAGACTCAGCATTTAAGTTCTGTCGAATTGAC ATTTGCTACTATATAAACTTAGTCCCTAAGTCTTCTTATGCTGTCTATATA
WI-19102	25	C G ---	---	---	TGTTCTGAGTCACGCTGAGGAGAG/C/GTCTCACTCAGGAGTTGATGCTGAGATGATCATGAGTTCA TGCAGCGTATATTTCTTTGGAAACAGAAATGAAGCAGAGGAAACTCTTAATACTTAAATCGTTCT TGATTAGTATCGTGAGTTGAAAAGTCTAGAACTCCTGTAGTTTGAACCTCAAGGGGAGAAGGTAT AGTGAATGAGTGTGAGCATCGGGCTTTGCAGTCCCATAGAACAGAAATGGG
WI-18548b	65	A G ---	---	---	AAAGGAGGGAGAACTCTTTTACATAAATGCCTTGATCATCTCCAGTCCCTCACTGGGGAA/W GJAAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18548a	62	G A ---	---	---	AAAGGAGGGAGAACTCTTTTACATAAATGCCTTGATCATCTCCAGTCCCTCACTGGGG[G/A/A AAAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18700	97	T C ---	---	---	GGCAGCAGCTTTTTTAATTGAACACTTCTCTTGAGGACACACCTTCTAGTACAGTTAACAAATGGT TACACCTGAAATCTGCTGAGAGCAGAGCTT/CJAGATCCACAATTGCAAGGCCACTGCTGGCTCA CTTCTCTACA
WI-18501	121	C T ---	---	---	CAGAGGAAAAAGTTTATTGATCAGCCACAGAGGAACAGAGAAACAGACACAAGGAGTTCTGTGT GCATGGAGGAAATCAGGGCGCCGNACAGCTGAACCTGGCAGGACAGAGGGGGC[G/T]GGACAGCA GCGCATGCCACAAACATTCA



WI-18017	87	C A	---			ACAAAGAAATGGAATAGGTTGCGAAACCTTATCTGCATGTACAAAGTAATCCCCGTAGATAA GGAGAGGCAACCCNCGAACA[C/A]ACTGCTGGATAAATCGTTCAATAAATTATATCTCTTTGCAT CAGAGCTGGTGGAAATCAT
WI-18148b	101	A G	---			TTATTGCGTTCCTTCGATAACCTCTCTTTGGGACTATGAGATCATCACCAGATGTGAAACGAAAGCA GTGATTTTCAGAAACNTCGATTCTGAATATCC[C/A]JTGCGGCATATGCAAGGAAGATGA
WI-18254	64	T C	---			TATACGGATCATGTATTTGTGTGACCACCACCTACACAGTCAATTTGTAGAGCAGTTAAATCAC[T/C JGCCAAATCCCTCTGCTTCCTTTGTAGTCAGTCCTCTCCCAACCCAGGNACTTGGCAACCTGTTT TCCGTTCCCTAGACATTT
WI-18265b	117	C A	---			CAATGGGTGGACTGAGTGATAAAACGCATATTGAGAACAGCGCCTTCTGGCCNCTCTGCGTCC AAGGCTGTAAAGTCTCAGGATTGCTGCTAAGTGAGCCATGAACGGCTG[C/A]JGTTTTCAACCTTTTC CTTGGGTGGTTCTTCAG
WI-18295	40	C T	---			ACCACACATTTGTTGAGAGCCTATTGTGGAGAACAAACAG[C/J]TTGGGAAGTAAAGTTGATTACT TCCTCTCCAAGGATGATATGTTAATGAATCCCTTNCCTTAGCTTCATTCTTCATAATGCCAAA
WI-18459b	64	T C	---			GGGCAAGAGACAGAGATTTAATTGAATAAAACTCCAGGCTGTGACACGGGTGGGAGACACAAAT/ CJAGTAAATTAACAACATAATATTTANATGACAGTGCAATTAATTAACGTCCTGGTAAAGCCAGAG GGGAGGAGGGGCTCTTCA
WI-22585	56	A G	---			TTTATTTAAATTTGCATCCTGAGATAATAAAATTTTATCTGACAAGTGAACAATG[A/G]CAGAAGC AGCAGTGAAAGTTTCGGAGAGGCAGGTATCCTTCAATTTGGCACAGCTGTATAGATTGA
WI-21155	36	A G	---			GGGCTGTGGAGTAACAGAACTTGATGGAAATTTGGC[A/G]JCTGTGTAGAAATGATCTAAAGCTTTC AGACAAATGGCAGA
STS-F02766b	88	G A	---			GCCTTTGCTCTTTGCTGCTCAGAGGCCTCAGATGGATACGCAGCACTTCTTTTGAACCTTTTAT TTTCCTGGCAGGAAGAAGA[G/A]JGGATCCAGCAGTGAGATCAGGCAGGTTCTGTGTTGCACAGACAG GGAAACAGGC
WI-19888a	98	C T	---			GGCAGATTCAACCCATAACAGAGAAATAACTCCTTATTGGAAACAAGGTTTTATTTTGATATGATG AAATATTTTGGAACTAGAAAGTAGCAGTG[A/C]JTTGGACAACGTTGTAAGATATTAAATGCCACT GAACGTTCATTTAAATGGTAATTTTCATGTTATGTGTAATTCACCTCAATTAAGAATGGAACATGT CTTATAATTGTAATACATGAGANCATATTTATGTTGGAAGTGAACACAAG
WI-21485	82	C T	---			TGAGACCATCCTCTCAACAAGAATCAGTCAGTTCAGCACTAATTTCCACACTGAAGTCTACG CAATTTTCATGCAG[A/C]JTTGTGCACACAGTACAGTGCACAAATCCAGAGGGCAACACATTGTAATT CATATCATCCGTTTCCAAA
WI-20601a	125	T C	---			TCAGAAATGCTTTCCACTGCCCCAAACCAAGAAATTTAATGAATGNCNCTTACAATTGAGATGACTT GAAGTTAAAGAAAGGTACCTTCCCTGGAGGTGTCATGACAGGATTAGTCTCTCTGT[T/C]CTTTGGT GCAAGTTTGAACCAAGTATATGTAACATTCATCAGAGCACTGTCTTCCCTGTGAGATCCCCACTAG

WI- 20561b	94 T C ---			CGTTGCTATTAAAGATGGCTGTTTATAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCAATTATG TACTTCAGATGAAAAATCCTTACATGTCGCGGAATCAATGTCTTTTAAAAATTCAGATAAAGAAATTT NCATTTGAGGAGACATACAATTGTAA
WI- 20561a	25 A G ---			CGTTGCTATTAAAGATGGCTGTTTAAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCAATT TTGACTTCAGATGAAAAATCCTTACATGTGGAATCAATGTCTTTTAAAAATTCAGATAAAGAAATTT NCATTTGAGGAGACATACAATTGTAA
WI- 20116e	69 T A ---			GCTTTCATTTCTGTCAACCCACCCCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAACAT A/T/AJATAAATCTATATCATATATTTATACACACAAACACACTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCCTCTCCCATGCCACTTAAAAATGNGCACAGGTTTGCTCTATGCAA GAAITTCACACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGGAGATAA
WI- 20116c	59 T A ---			GCTTTCATTTCTGTCAACCCACCCCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGA CATATATAATCTATATCATATATTTATACACACAAACACACTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCCTCTCCCATGCCACTTAAAAATGNGCACAGGTTTGCTCTATGCAA GAAITTCACACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGGAGATAA
WI- 20116a	22 C G ---			GCTTTCATTTCTGTCAACCCACCCCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGA CATATATAATCTATATCATATATTTATACACACAAACACACTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCCTCTCCCATGCCACTTAAAAATGNGCACAGGTTTGCTCTATGCAA GAAITTCACACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGGAGATAA
WI- 20466b	133 G A ---			AAAGATTTCAGTCTGGGACACAGTTTGGAAACACTATTTATAAGTTGCACATATACAAACAG NTCCCAATGGTGAAACTGGTATTCTAAGATGAAAGCTTAAAGTGAACATAATGAAGTGAATAAACGC G/ATGTGAACATAATGTTTAAAGTTAGAGCTTGTCTCAAGTCAGTACAGCTCTTAAGATAATAAAT ACAGTAACACTACTTTTTATTCTTTGCTCTTTATCCCTTTGAGGTTGGATT
WI-21444	39 A G ---			CTGGCAGCAAGTAACCATTTTAAAGAACTACTCTCAAC/GAGTCTTTTTTATGGGGTATTTCA GTTGTTAACAAAGTTAAATACCTTATTGGAACATACTCTTTGTTATTCGAGGAAGAAGAATCT ATAAGATTGACTTACTCATTGTTGACTGGTTTTTGAAGCCTTACTGGGG
WI- 21034b	148 T C ---			AGAATGGACAATGATGCAGATGATTGTGAGCATTTTGTAGAGCAATTTGTAGAGAAAGTGGTATTAGAAGTACAG CATAAATTTAAATGTAACATGCTTATCTAGCTAACCTAATCTGTTCTGTAGAAATTAAGTGGTATGG GAGATTGGATAGATTCGCGCTAACCTATCTCAATTTTAAAGTAATGTAGCAA
WI- 22091c	205 G A ---			GGCGTATTGTATGCAATGTCCACACAGTCAAGCTATCATTTGAAATCCAAATATTTCCAGTAGAG ACATGCAGAGCAATGTCAATGTAAACATACAGCATATACCTCCCCCTTAAGTGACTCATAATTC ATTACTGTGTGTAGCTTTTAAAGGTTTAAAGTTTAAAGTTAGTATTAAGTGGTATTACTTGAGGGCA ACA/G/AJAATTACGGCTTAACAACACACTAAATCATGAGGCTCAGGGATTG

WI-21805a	45 A T ---	---	CAATGCTCTGAGTCTTCACTAGCTGATTTAATCCTATATTATJAAAAAAAAATCTATAGTCTG CAGTCTTTGACATACCTCAAGGGTGGATATGTTGGATGCAGACTCCATCAATATGTGTGGTT TTGTTGCTTTTGTAGCTTAACTGCTGTTAGNAAATCCAGAGGAATATGATTGAGGCCAGAGTTA CATTGGTTCATAAAATTCGAACAGTTGAAGGCTGTTTTGTTAATTGCTG
WI-21778b	155 T C ---	---	AAAAATCCATAAATTATGAAACCCCAAGTTACAGAGAAAAGTTCGTAACTTTTTATTGAATTTATTGAC TCTGCCCGGTGTCGTTGCTGCTTTCAACTCCAGTCTGCAATGCCCTGTGTAGTGGGTGCCAG GTCTGGGCTTCTGAGGTCTTCJGGTAGAAGGAGGGCAGGTGGT
WI-20907	241 A C ---	---	TGAGTCAGTGGTCAGATGGGGCAGTTGCGCTCAGCTGCAGTCCCTGACTCCGGAAACACTGTGCCCTCT CAAATGATCTAGAGCTCATCCTTGGCGGTACATGAGGGGCAGTTGTTCTAGTACCCATTTAGCCG ATGGCTCTCAAGCCAAATTCACACTGGGAAAAACACACCCCTCACAAGATGCCTATCCATTTGAGTTC ATACAGGTTTTAGTAGCTAGAACTAAAAACATTTTTTAJAJAATTATCTA
WI-21449b	222 C T ---	---	AACAGCAGCAGTCACCTCCAAAATGCAAAAAAATTAACAATTTTTAGAATAAAATTAATGTTTA TAATGCGGGTCAGAAGANTTGAAGGTACAACAGAATCAATCACGCAGCAGTGGAGGGCTGGAG AAGCCAAAGCCCACTGGTCAGGGGTCCAAGCTGACAAGAGTCCCAACTGAGAGGTCTCCACACCC AAATCATACCCCTCAGCTTCCCAJCTTGACAGAGCCAGTGTCTCTGGGTTAG
WI-21558a	157 G A ---	---	GCTTACAAGGAAGCCTGTGGACAGGGCAGNTGGGTGGAACCGACTCCAGCCTGGAAAACTGCCCTC CCATCCCTTACGCCCTTCTGGCTTCCGGCTGATTTCTCGACAGCAGTCTTGCCAGGGCAAGG AGCTGTGGTGGGGGCGATG/AJAGCCAGGGACTCCCTTCCACAGATGAGGCCCTAGGGCTGCAA AAGGGCCCCGTGAAGAGAGATGTGGTCAAGGCTTTATGGGTCTCTCCACG
WI-22187b	178 G A ---	---	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGGCCGTGGCTAGCAGAGCTCATGGNGACCA GTCCTGGGCTGACCAATGGGTGATTACATTTAAACCAACCAACCAACCAACCAATACCAAGA ACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTG/AJAAATTTTCATGAAAAATTTCC CCTAAACCATAACAAAACTGTCTCTTACCCCAAAAGTGTGGAGGAAAG
WI-22187a	110 C A ---	---	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGGCCGTGGCTAGCAGAGCTCATGGNGACCA GTCCTGGGCTGACCAATGGGTGATTACATTTAAAAACCAAAJCAJCAAAACAAAAATAACCA AGAACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTGAAATTTTCATGAAAAATTTCC CCTAAACCATAACAAAACTGTCTCTTACCCCAAAAGTGTGGAGGAAAG
WI-21609b	146 G A ---	---	TCATGAATATGCAGCTCCATAATCTTCTCCCTTGTAAACAGTGCAGTCCGTTTCAACAGCTGTAAA AACAAGCCCCAAACCAAGACATCAAGAGGCAAGAGCGAGTGCGCAGTGAGAGGGAGCCCTGTAAAG GATGTTTCAAAGJG/AJAGGGTCCCGGCTATGTGGCCACTGTGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG

WI- 21609a	42 C T ---			TCATGAATATGCAGCCTCCATAATCTTCTCCCTGTAAACAAAC/C/TJTGCGAGTCCGTTTCAACAGCTGT AAAAACAAGCCCAACCCAAAGACATCACAAGAGGAGGAGAGGAGTGGCAGTGAGAGGAGGAGCCTGTGTA AAGGATGTTTCAAAGGAGGTCGGCTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG
WI- 22512a	104 T G ---			ACATTCCGAGCCAGTTTTTTCATATTGCTCCACTGCCTAAATCCCTTGGTGCCCTCCCTAGGGCTTCA GGGTAAGCCCTGACATCATGGTCTTTGTGATCTGT/GJACCTCACCCATGCTCTCCACCTNAGTTCC CACATTTCCCCACGCTAAAGGGCAGGCAGCTACACTTGACTGCA
WI- 21028b	139 A G ---			ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAAATTTCTGCCCTTTAAGGGCTCA CAACACTAAAGATTCACATGAAAGGGTCGTGATTGATTGAGCAATCTAGGGG/A/CJTATGTGACAG TTTC/GJTGCACTGGTACAGAACACACAGGGAGTTTCACAAATTTTTTATACAATGCTTGGGAAT CTACGG
WI- 21028a	121 A C ---			ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAAATTTCTGCCCTTTAAGGGCTCA CAACACTAAAGATTCACATGAAAGGGTCGTGATTGATTGAGCAATCTAGGGG/A/CJTATGTGACAG GGGTTTCATGCACTGGTACAGAACACACAGGGAGTTTCACAAATTTTTTATACAATGCTTGGGAATC TACGG
WI- 18829d	58 A G ---			ACAACATGCCTGTTACAGGGGGGAAAAATCCTAGGNAATAACTTATGTGACTCTTG[A/G]TTTCA TCATACAAGACAAAGCACAAAGCACCACCCATGCCTCTGAGGAACATTGGACCATGCACCCTTGAAA AA
WI- 18829b	35 T A ---			ACAACATGCCTGTTACAGGGGGGAAAAATCCTAGG/AJAATAACTTATGTGACTCTTGATTTC TCATACAAGACAAAGCACAAAGCACCACCCATGCCTCTGAGGAACATTGGACCATGCACCCTTGAAA AA
WI-20964	87 G A ---			AGCCAACCTAAGGCCCAAAAAATTTCTTAATATAGTTATTATCGAGGGGAGGGGAAGCAAAAGGA GCACAGGTAGTCCACAGAATA[G/A]GACACAAAGAAACCTCAAGCTGTGAGGTCAATTTGTAAATTA AAGAATACTAAGATTAGATGAACACACACTCAGAAATACTCTAGGAGAGCTGAAAAAGAAAGGAAC AGATGTTAAACAAAAACAAATTAAGGCTGCTGGGGAAACCTGAGTCCATGTTAAGCTTG
WI- 20059a	59 T A ---			CTCTGAACCTAAGGGCCGTGAAAGGCATGATTGGTTTTGGCACACAGAGTGGATAACCAAT/AJACAT TGGCTGGAATGAGGTGGTCAGGAAATAAANTGCACAAATCTAACACCATGTTGAAATCATGTCTGA GTTCTGGAGAAAGTTAAAGTGTAAATAATTACAAAGACTGACATGCAACTCTTTACCTTACATTATT CATCTACAGACTATTTTCTCCCTTAGGAGATGAGGAGTATGGCCCTTAGGT
WI- 22130b	165 C T ---			TGTTTTGAGGGCTGTAGCAGACTACATAATAGCGGTGAAAGCGGCTGCCCTTCCCTCTCTGACAC CAGCAAGGGGGAGGCACCATCACCGGCCCTGCCCATCATGCTCAATGATTACTAGCACTAGGAA GCCAACGGGAANAGACCCCGCGCTTGT[C/T]GTGTTTAAATCCAGGTTAAGCTATACACGTTTTAA ATACATGTCGGAGGTTACATGGTCTCATGCGTCCCTGTGATGGGAATGAC

WI-21661	117 GC ---				GCTTAGTCTCCACCCCTTTAAATGTACTCTAGGTACAAAATAACATTATACACATATAAGATCAGTCTTCCAACTTTAGAATGTATAAATAAGAAATGACATTTTAAATAAAATA[G/C]TTAGTCACAGTCACACAAACTACCTTCTAAGGAAACTGTCCAGTGAAGCCGTTAAATTTGTGCTTTCAGCTATGAAGGA
WI-21980a	25 TC ---				TCAGTTTAAACACATTTCATCAAGGA[G/C]AGATTAAATTAATGTCAAGTGAGCATAAAGGGAGATTATAAACAGAAAATGTGTTTCTGGGAACCAAGTTTCAAGTGACTCAGGATAAGTTTATTATTTTCATGGGTGAAGCCCTCGGATAAAG
WI-21636	71 AG ---				TGCTTGATTAATGTGGTGTACATTATCCTATTTTCACAGATGGAACAGAAAATACCAGCTTTTAAAGAGTAGCAATATCTATTATAATAATATTGAAATAACACCATAATAATATCACTAAGGAAGTAATCTAATTGTGTTGATTTGCAGAGGGAGAAAACATTACCTCTAGAGCTGAGGCTATTGTGCTCATGCAAACTCCAATCTGAAGGTGGTAGAACTAGGAAGGACAGGGATTTC
WI-22457a	112 GA ---				TTGCTATAATTTCCTTAAAAATGCAAAAGAGTACATCACAGCAGAGTATAGCCAATCACTCATTAGACAAACAGTAAACATACTGGACACGGTTTCAGGCATGAAGGATACAG[A/C]CAGTTAATTAACATAAGGAACAGAGTCCCTGCATTCTGAAGCATAGGATGGGGAACAGTAATGCAGATTAAATACCTGGGGCCAAAACCCACTGAACCTCACCCAGCTGAAAACACTGAAGGATACTGGGTAAGGA
WI-21524b	97 CT ---				GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAATAGCCTGATGACGACCTTCGCGTCATCTTATATGGTTAATAACAGCATTCCTGTCTACCC[C/T]GATGATGCTTCTCTGCAATGGACTATTTGCCCAGTTGCAACAGGGCTAAGATTGTCGCACTATGACAAATGAGTTGTTGTTGGAGTTGCGGTGTCCTGTCAGAAAAGATTCTTGACITTTCTCCAAGTTACTTCTCCAGGGGAIG
WI-21524a	35 AC ---				GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAAT[A/C]GCCTGATGTACGACCTTCGCGTCATCTTATAATGGTTAATAACAGCATTCCTGTCTACCCCGATGCTTCTCTGCAAAATGGACTATTTGCCCAGTTGCAACAGGGCTAAGATTGTCGCACTATGACAAATGAGTTGTTGATTTGGAGTTGCGGTGTCCTGTCAGAAAAGATTCTTGACITTTCTCCAAGTTACTTCTCCAGGGGATG
WI-22652a	32 GT ---				TTACCTTCCAAACCAGGCCACTTTGGAGAAAG[G/T]AAGAGAAATGCTATTAAATCAATAAGCCAAAGACAATAGGGACTACCTGGGTAGACCAAGATGGGCAGTCACCACATACCATCATCTCTGCCACAGAACCCTTGACATGCTGCOCTCCCTACTCCGCACTCACCTGTCTAATTGGGACCTGAAGCTTCAGCATCCCTTCCTTAGGG
WI-21703d	197 AG ---				CAACAGGCTCATGGAACAGAGCCCTAGGGATCCAGGAGCATAGGAGGTGGTGGTGGCAGGGCTCTGCATCCCTTTCTCAGCACAGCACCATCTTCACCCCTCTGGGAAAGCAGCATTTGGAGCCTACACCACTTGTCGCTTTCTCACCAGGGTAAGAAATGCAGGTATTTGCAGAGGGGAGTGAGTCTGGGAA[A/G]GTGGGCAGAGCACAGCTAGGGGCAAGGACTTAAGGGAACCTTGTTGGGGAAGAG

WI- 22703c	134	A G ---	---	CAACAGGCTCATGGAAACAGAGCCTAGGGATCAGAGGATAGAGGAGTGGTGGTGGCAGGGCTC TGCATCCCTTTCTCAGCACAGCACCATTCTACCTCTCTGGGAAGCAGCATGGAGCCTACACQ A/GCTTGTGCTTTCTCACCAGGTAAGAAATGCAGGTATTTGCAGAGGGAGTGAGTCTGGGAAAG TGGGCAGAGCACAGCTAGGGGCAAGGACTTAAGGGAACCTTGTGGGGGAAGAG
WI- 22663c	139	G A ---	---	CCCTTGTCAGTCTGTGCTCGCTTCTCACTGCAGTGGCAGGAGGAGCCGGCTCGCTAATCTTATTC CCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTGCACTGGTGCACTTACAG GC[G/A]GAAGAGCTTCTCATTTGCTGAGGGCTTTTCCTGAATCCGTGTTGAATGTGGGT
WI- 22663b	55	C T ---	---	CCCTTGTCAGTCTGTGCTCGCTTCTCACTGCAGTGGCAGGAGTGAAGCCGGCTC/TGCTAATCTTA TTCCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTGCACTGGTGCACTTAC AGCGGAAGAGCTTCTCATTTGCTGAGGGCTTTTCCTGAATCCGTGTTGAATGTGGGT
WI- 22663a	38	C T ---	---	CCCTTGTCAGTCTGTGCTCGCTTCTCACTGCAGTGGC/TGAGGTGAGCCGGCTCGCTAATCTTA TTCCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTGCACTGGTGCACTTAC AGCGGAAGAGCTTCTCATTTGCTGAGGGCTTTTCCTGAATCCGTGTTGAATGTGGGT
WI-22668	99	A G ---	---	TCCTTTATCTGCTGCTGCCTGAGTATTCTGGGAATCCTACAAGGATTTGAGGGAGCCCTTGGGATT CCAACTTAACAAATAGTTTCTGTAATATT[A/G]TTCTAGTCCATTTAGATTGTGTAATGATCTAA ATGNGTAACCATTTAATATCAAAAGTATAACAGCATTTAAGTCAGCTTTTCGAAGAACTTTTATT
WI- 22631a	52	T C ---	---	AAGATATAGTGGCAGGACAAGATTGGTCACGAAATCCTGGCTCAGTTCGAT/CJAGCACCATTT CAAGTTTTAGGCAAGGTATTTAACCTCTCAGGCTCATTTCTCTTTGTAAATTTGTGATAATGGACC TATGTACCATCATAGGGTACTTGGACAAATCAACTGAAATTTT
WI-20258	157	G T ---	---	AATCCACACTTTCACGGAGGGGAACAGCTGCCATGTCTCCAGGCTCACAGCAGCGGGCTAC TCTGCTGGTGGTTTGGTGGCAGGTGGAGATGGTGACGGCCATTGGAAACCGTAAGGCATGACAACG GGAGCCCGCGGGGTGTTTCAAG[G/T]CGCGTTGACGAGGTGATGGCTGGCAGGGGCTCTACAGA AGGAGGGAGCGCAATTCACAGCCTCTTGAACGTAGTTCCGGGGAAAGTACC
WI-22714	212	C A ---	---	ACTACACATATGCTGATTTCAACAGTAAATAACATTTTACATTTGTAGAGAAATCTAGGGTCT ACTAAATAATCTAGTACTTGTTCCTCTCTCTGCTAACTCTGACAGGAGTGTGGGGAACGAAGT CTGAAAGGATTCAAAGGGGCTAGGATTTGCCACAGATCCTGTAAAGGAAGGATGAGGTGAGCTT ACCAACCCCA[C/A]TGTAGTAGGGGCCAAACATCCTTAACAAGCTAGTTGCT
WI- 22734a	44	G A ---	---	TGGGGCTACTTTAGATGGGATGGGCTCAGGGTCTGGGAAGGCCT[G/A]TCTTAGAGACATTACCCA AATGATGAGAGGCGCAGTCGTCGAAGCCATAGTTGGATGGCAGACTTTTCCGGCAGAGGAAT AGCAAGTGCAAGGGCTGAGGGAGAAATGAACTTGGGCTTGTCTACAGGGTGAAGGCGGCCGGT NTGGCTGAGGTTTAGTGGATG

WI-22724	117 A G ---				TGATATGATGCTGAGATTGCTTCCAAATATGCCTAGGAAGGGAAGAGTGTAGAGATATAGGA CAATCAAGATTGTCAAAATGTATAGTAAGTGTAAAGCTTGTAAAGGGT[A/G]TATTCTATTTT TGGGATAIGTTGGGAAT
WI-22750	48 G A ---				TGTAACCTGTGTTTCTCTGAAAGTTGAGGGAAGCTGAGGCAGCTAAT[A/G]GGCTCATACAAAGGT TTGGAAGACCCATTCTGACTACCTAAGGAGAGTACGATTCTGACCATTTCTGACTGIGCT
WI-22775a	60 A G ---				TGCTGTTTCTTTAGTTTCATGACGTTTATCACAAATGTGCTACTGTTTCCATTGTTTACATC[A/G]TAGTA GGAAAGGGGAAATAAAGTCCCTAAGGGCAGCAATAATTTCTGCTTTGAATCCTTATTGAGGCAAA TATTTGTTGAGCACCAAGGGCCAGATGGGAAGTGGAGTATGTAGGTGTTGGGAGCCAGGAAAGGAAG GGT
WI-22808	143 C T ---				CTTAGCTAATGAAACTGGCTATGTGGACTATGATAGACCAAGAAAGCTACCCAAAGTCTGAGGGAG CCTAGTCTCTCTAAATGCAGACAATGTACCCATGACAAGGGCTACAGCTTGGCTTTAGCAACCCAGGA GGATGAAGA[A/C]TAGCAAACTGATTAAAGAGAGTAGGTATAAGAAACCAGGGAGAGTGGGTCCAAAT ATC
WI-21016	207 G A ---				TCTCTGTGTTGAGCCCTCATCCACCCCTCCAAAGCCCTCATGCCACACACCGTGTCCACATT CCCCATCCTCCCTGTCTGCTCCCATCTCAAGTCCAAATCCAAAGGCCAGAGCCCTGGCAGCTTTTCTG GGAGACAGCATGAAAAGGAGGGGAGTGGAGATGGCAGAGATGGGTGGAGCCAGTGGCTGTGGGTC CTG[A/T]TGGCGTGGTATGTTGGGGCCCAATCCTGAGGCCAGAGGTTCA
WI-21031	31 C T ---				TTGAACACCTGACCTGACCTCTGACATGTGG[C/T]CTCTGGTCCCATTTGTCTCAACGGTGGCACA TCTTCATCTTTGTTATATATCTGCAGGAACACTCAGTCTCTTCAGCAGCCGAGAAACACACACA
WI-21314	122 A T ---				CCATATCCAGTCTCTTTGAAGCTTCTATTGACTTTTAGGGTTCAGTTATTATATCCTTTATCACTAT GACTTTCATTTGATTTTTTATTGTTTCTTCCATTTCTCTGTCAAACTTTTC[A/T]TTTTGTTTATAA ACTGTTTCTAAACTCACCTAATCTCTAICTGTATTNCTGTAGTTCCTGAACTTCTTTAGAGG
WI-21186	95 G A ---				AGCGAGCATCAGAATCACCTAGAGGGTTGACTAAACAGACTTCTGGACCCCAACCCAGAGCTTCT GATTGAGTAGGCCTGAGGTGGGCTTAC[G/A]AATTAGTATTTCGAAGACCTTCTTAAGTGTGCAG ATGCTGCTTGTCCCGGGGAACACACTTTGAGAACTATTGTTCTAAATGTTCTCTCTCTTTCTTTAAA GGAGAGACAGGAATTCAGAGAAACTGCTAATTTAAGCATAATGTATTGAAT
WI-21187a	94 A G ---				CCACGATAACTATAAAGCAGAAAAATTAGCTTTGAAAAATCAATAACATATTTAGTAACACACATT CATTTTATAACACACATAAAGACACC[A/G]GGNCTCTCAGTAATGCTAGTCCAGGGGTTCTCAA AGTATGGCTTCAGACAAGCCCCATTTGCATCACCTAGGGGAATTGCTAAATGCAGATTCTCAGGCC CTACCTACTGATCTACTGAATCAGAAACTCTGAGGGTGAGACCAAGCAACCTGT

WI-21190	39 T C ---	---	---	TTTCCCCACATACCAATGCACCTGTTTGATATAAACTATT[C]GTGGGGTAAGCCCTTCITTTGGAGAC CAGTGACATAGACATGATCCCATTTATTAACAAATAATTAATAATCTGTACTATTACTGC TTTAGTTATCTAGTGTATTGAGAAAGGAGAGTCAGCATAGTTTATTTCCATGTAATAAAGCTT AACACA
WI-19937d	186 G A ---	---	---	ACCATGTGCATTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAACTTGGAAAGGAAA GAACATTTGCACAAACCAACATTTACATATCTGATTTAGACAAGCAAAAGCACTTCATGTTGCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTTGGTGTCTCAGCAAGT[C/GA]TCCAAACCTTC CAAAAGAAGCAGTCATTGAAAATGCTGACITATGCATTGCCTCAGGAAGAA
WI-19937c	185 C T ---	---	---	ACCATGTGCATTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAACTTGGAAAGGAAA GAACATTTGCACAAACCAACATTTACATATCTGATTTAGACAAGCAAAAGCACTTCATGTTGCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTTGGTGTCTCAGCAAGT[C/T]GTCCAAACCTTC CAAAAGAAGCAGTCATTGAAAATGCTGACITATGCATTGCCTCAGGAAGAA
WI-21117b	227 C T ---	---	---	GAAACGGGGTGCTAAACAAAGAAAGTCTCAGATCCCACCTGAAAATCTGTTCAAGTTTCACAGGCTC TCTCCAGAAAATGCATATGTACCAATTTGCATGTACATTTTCAGAGCCTTCAAATACATTTCTGGG TCCAATCACATACCTCAGGTTCCAGACTCTAGCTCCCAATATTCCTACAGTTCTGAAGANTTAGCAGT CCTCTCATTCTACAGTCTGATTT[C/T]TCTACTGAATCTTGGTGGGAG
WI-21122a	42 C T ---	---	---	TCACTTTGTATCATAAATCCCCTGTAAAAGCTAAAGTTATTCA[C/T]TTAACAGGAACTCTGTTTTCC TTATTCAAATGTCACAAGCCTGACGCGTTACTGTACATATTGCTAGCAGGAGACAACTGGAATACT AAACAAATACTGGAATTCACATTACAGACAGACGAAACCAACATGGGATGCCACACATAACTTCCT TTGTAGGTTTCACAGAGAGCCTATTGTGGGTGCT
WI-21254	53 A G ---	---	---	CAGTTTGTGTACAGGAAGGGCCCATGAATGTGGCGGGAACCTATTCACAGGAG[A/G]CAAGGAGAAAG CTGTTCTCTGG
WI-21054	23 G T ---	---	---	AAGGAACTGCATGGGTACAAAT[G/T]TCCAAATTCATACCTTAACAAGGTGGGAAACGGGTCAATTCT TGGCCTGCTCCAGAACAGGGCGAGTCTATGCACCTCTG
WI-21059b	181 T C ---	---	---	GGACACAGGTTAACACCATTAGCAATATCCGTTATCAGCCTTATCTTCCCACCTGAGCCTGGCTGAA CTACAGCTGCCAGCATTTCTGGGTTGCATTTCCCAGCTTCGTCACATCTTAATTTCAAGCTGAAA AATCCTGGGGAAGAGACATACTCAGTGAAGTCAATTTCTCTATT[C/T]CJATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCTAAT
WI-21059a	63 C T ---	---	---	GGGACCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATCTTCCCACCTGAGCCTGG[C/T]T GAACTACAGCTGCCAGCATTTCTGGGTTGCATTTCCCAGCTTCGTCACATCTTAATTTCAAGCTG AAAAATCCTGGGGAAGAGACATACTTCACTGAAGTCAATTTCTCTATTCTATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCTAAT



WI-20442	37 T C ---				TCCACGTGAAGGAAGAAAAAANGGGGGGGCTT/CJTAAGGTGGCACAATTTAAGAAAT ACCATCCATTTTCTCAGTCTAATCTGAATCCATACATTAAACAAAGTGCAAGTGATGAGACGAA CA
WI-21235	43 T C ---				GTGACAAGAGGTGAAGCAAGGGACAAAGGGGACAGGGCGAGTC/CJCTCGGGCCGATGTTCCAGGG CAAGCTACGTA
WI-22012a	57 T C ---				ATCAGAACTGCAATCTGCACATGAAAAGACCTGGGGGAATGCCTACATCTGGAATTT/CJCATTA ATCAACGTTAAATTTTGTCGACCAAGTTCTTCTGCTGATCATTGATAATGACAGATCCAAACAT GAAACTCCTGAAGCAAAATGAATATTACCTTGCTTTCATGCAAAATTAGGACCAAACTCAAAGG TTTCATCCATGCTGGGACACCAAGATCTAAGGAATTGTGACAGGGATCTCT
WI-21149a	167 G A ---				AGGACCTGCTCTCACACGTTCCCTCACCCCCACCAGCTTTGGCAAAGATAGTTGACTAAATACCACT AAATAGTGGCTTTTAAATGAAATGACCTTATTTATCTTTAACTTTAACTGAGTCTTATATA CAGACCTGCCAACTGGAAGCTTTTACACG/AJTGCTTCAGAAATGCGGCAGTATTGCACAATGGTT TGGGCAGGTTCTGTGTTAAACATGGGATGGAACCCAGGCTCTACCTG
WI-21376b	188 A G ---				GGTGCAACTTGAAATATGGTTTAAACAGGATAAGCATTAAAGGAAAAACACTTTCATATGTGTC TTCCATTTGATGAATTTGTTTCTCTCTTTATCCCCGCAAGTGGAGTTTCATGCTCGGTGAAACCA GACAGTGTGAATCTGTTCCAGCCCAATCTGCAGCATTAGGGATGAGTTCTC/N/GJGAAGTGATTCT GAACTGAGCACGCACTCATGTCTCATGTTGGGAACTCTGGGGAAGAGCCT
WI-21382d	125 C G ---				CCATTGCAGTCCAGAGATGAGAAACTGGACAGAGGCAATCATGAACAGACGGAGTCAAGAGA AGGGTTTCTAAGATGGAGAAAGTGGGGCGGGTTTGATCCAGTGGGATNNGGTTCCQ/CJGAGGTT GCAACCCCAAGGAAGTCTCTGGAAGCAGCACCACTGCTGATGGGGAGCAGAAGAGCTGCCATCCTC AGTCAGGGTCCGAGTCAGGGTCCGAGGAGAGCTGCTGCTCATAGTCTCGCAC
WI-21437a	201 G A ---				TCCCTGAGGTTGGAGTCTAGCATAGCTCCCTCCCTCAAAGAGGGCAAGGGGTCAGGGGCAGAGC AAAAATCCAGTCTGCTTCAACCAGGAGACTGCCCTTTGGGATGGAAGTTTCTGGAGCTCCCTCCATT CTATTCCTGTGGGGCAGGAACATGCCAGGGCTGCTGTTAAATGGCAGGGTCACTTTACCAGGGC/G /A/CAGGCATAGTGTGGCCCTGCTGCTGCTGGGGCCACCCTGGGGAACAGT
WI-21202b	156 A C ---				CAAAATAGAAATCTTTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATGTTGATCT GTTTTATGAACATGATTTTATAAAATGGTCACAATATATTTTAAAGTTAACTGATTATTGAGGG AGGAGGAGAGAGTTGACCA/A/CJGTCTACATGCATAGACAGTCTCTAAAGCGTATCTCAAAACATG A
WI-21202a	61 T C ---				CAAAATAGAAATCTTTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATGTTGTA TCTGTTTTATGAACATGATTTTATAAAATGGTCACAATATATTTTAAAGTTAACTGATTATTGA GGGAGGAGGAGAGATTGACCAAGTCTACATGCATAGACAGTCTCTAAAGCGTATCTCAAAACATG A

WI-21627b	153 A G ---	---	---	GCATGAAAGAACTCCAATCAGACCTTTATTCAATAAAGCAGCCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTCATTATGGATATTTATGCTAGGAATGACAA CAGTAAGGGCATTGCAA[A/G]TCCAAAGTCATCTAATATAAACCATATTTTACATAATTTGTAGG GACAGTATACTACTCTACAATAAATAAGGGTTTAAAAATGTTGCTTA
WI-21627a	106 A G ---	---	---	GCATGAAAGAACTCCAATCAGACCTTTATTCAATAAAGCAGCCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTC[A/G]TATGGATATTTATGCTAGGAATGA CAACAGTAAGGGCATTGCAAATCCAAAGTCATCTAATATAAACCATATTTTACATAATTTGTAGG GACAGTATACTACTCTACAATAAATAAGGGTTTAAAAATGTTGCTTA
WI-21399a	75 C T ---	---	---	GGATTTAGTCCCAACTTGATCTCAAAATTCACCTTCITGCATGTAAACAAGCTCAITCCCTCTAAAGTT TCAGTT[C/T]TCCACAGTAAGGAAAGGTTGGACCAGACATGTTGGACCGTAATTCCTTGGTAA CTGCCTCTGCATTTGTCTCTGAGGTTGTGTCTCTAGGACTAGGACTAGGATCTCTCTTCTTCTGCT TTACCTAGGCATAGTGCCTGATAGCAGGCTGAAGCCCAATTCATCTGT
WI-20329a	68 G A ---	---	---	CGATGCTGCTAAGATAGGAGTTAATCTTTACATGGTGAGTGGTCCAGAGACAAGACATCAAT C[G/A]TCTGTTAGCGAGAGAGACACTTTAAGTCCCAAGAGTACAATCCCATCTATGAGAC AGCAGTCTGGCTCTTAAAAACAGTAACCAATCAAAAAGAAAAGATTTAGAGGTTTCAGACATT AGGAACAANTGTGGCCAGAGATACCACAGAGCCCTTGAAGGAAAGGCCCTCACT
WI-21249	155 T C ---	---	---	TTCTGGCATTCAAATGTACATGTAAATCCAAATTAACAGATCAAAATTTGTACACTAAGTTTCAC TAGTATCTAAGTATCCAATCACAATGTATCTAAGTTTACATTTTAAAGAACATTATAAAGGTAAT AAAACCTAGGTGTACTTAT[C/A]TGGAAGTGTATTTATTCNATTTAACTACTGTTTCATTGCGTA AAGTATGTTGTCCCAATTTTCAGCTGTTTAAAGGAATTATAAAACATTGAGA
WI-21504	147 C T ---	---	---	TGACACAGCATCAATTTTCATGAATACCTTTGAAAGGGCCATTAGAAAAATAAGAGCCAATTTGGGTC ATTTGAGAAACATTTTCAGCACAATTACAGTGGGGCAGCGCGTTCGGCTCCAGCTGGGTTTCCOC AGATGCAACAAT[C/T]GCGGTTCTGGCTTCTCCACTGGTGGGATGGGATCGCGCTTCGGAGCTCT CAGGG
WI-21242	115 G A ---	---	---	CTGCACCGGAGGACAGCTGCTGGCAGGGACTAATAAACCTTCACCTGGCCATGGTGGTGGTGT CTCTATGACCGAGGCCCTGAACCGCGGCAGGGAGGGCAGAGAA[C/G/A]CACTAGCTTGGGGGTG GGCACAGCTTCAGACCCCTT
WI-21475c	181 A G ---	---	---	TAGCCCTCTTGCCAACATCTGSCAATNTGAGGCTGGGTGGACGTTGGCCTGATGTTGOCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGCTCCAAACCCAGGCTTCTCACTTGTCTACTAAGCACAG CAGTCTGAAGCTTGGGACCTGGGCAGTGCGTCTTTGGAGAAGGCA[A/G]AAAGGCCACAGCAGCAAC ACTTAGGAGCAAGACCCCTCCCGTTCCTCCACCCCTATTCTCCCTCCCTGAAG

WI-21475b	117 A T ---	---	TAGCCCTCTGCAACATCTGGCAATNTGAGGCTGGGTGGAGCGTTGGCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGCTCCAAACCCAGGCTCTCTCTCTGCTTACTAAGCA CAGCAGTCTGAAGCTTGGACCTGGGAGTGGCTCTTGGAGAGGCAAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCTTCCGTTCTCCACCTATTTCTCCCTGAAG
WI-20893d	207 A G ---	---	TGTTGTGTTCCAGCCACATCTTCTCCAAAGGAACCCCAAGCCCGTGTGCAGGCTTGTGCAGGG CTGTCTTCGGCGTTTAAAGTCTACTGAGGAATACAATCATTTGTACGTAAAGTTATCACCAGCACTCC AGGTCAGGCCAAACCTTTCGGTGGACCTGGGNAACCTGCCATTTCTCTCTTTTACAATGCAGT TTCJA/GJACATAACATTGGTAGAGTAACAACAACCAAGCCCTAAATG
WI-20893c	179 T C ---	---	TGTTGTGTTCCAGCCACATCTTCTCCAAAGGAACCCCAAGCCCGTGTGCAGGCTTGTGCAGGG CTGTCTTCGGCGTTTAAAGTCTACTGAGGAATACAATCATTTGTACGTAAAGTTATCACCAGCACTCC AGGTCAGGCCAAACCTTTCGGTGGACCTGGGNAACCTGCCATTTCTCTCTTTTACAATGC AGTTTCAACATAACATTGGTAGAGTAACAACAACCAAGCCCTAAATG
WI-19941c	71 C G ---	---	GAGCTCAAGGGAAGACCTTACCCAGATAGGGACTAACTGGAGGGTGGAGGAAACAAGGTGAAA GGTATC/GJGGTCTGGTGAGACAAAGCAGGGGGCCCTGAGAACACAGAGCAAGGTGGGTTTGAG GGACACAGCAGGTCAGGAAGGAGATGGGGACATTTCTTATCCAGTGCATGTCCCTTAAAT AACTGGGTACAGGAGCATTTGGAAGGAGAACCAAGGACAGAGCAAAAGCG
WI-21552b	166 C A ---	---	TGGGTACATGGACAGATGTATATGTTTATGGGTTATAGATATTTGATACAGATACACAATGTG TAATAATTACTTCAGAGTAAATGCGATCTCCTTCACTCAAGCATTTATCCATAGTTTACAAAGAA TCCAAGTATACCTTGTATTATTTAAAAATGTA/CJA/AAATTAATTTATTTAGTTACCCCC ATTGTGCTATCAATAATTCAATCTTATTCATTTCTTTGTAACCTATTTATTTGTA
WI-21552a	66 G A ---	---	TGGGTACATGGACAGATGTATATGTTTATGGGTTATAGATATTTGATACAGATACACAATGTG /AJTAATAATTACTTCAGAGTAAATGCGATCTCCTTCACTCAAGCATTTATCCATAGTTTACAAAG AATCCAAGTATACCTTGTATTATTTAAAAATGTACAATTAATTTATTTAGTTTACCCCA TTGTGCTATCAAAATTCATCTTATTCATTTCTTTGTAACCTATTTATTTGTA
WI-21512	54 C G ---	---	TCCTCGTACTTCATGCTCCCTCCCTGCCAGAACCTTACAAAATATTTCTGT/C/GJTAGAGAGGA AAGAGCTGGTGCCTGCTCTGGAGCAACGTCAGTCCGGGGAAGGCACCTCGTGTCTGTGATCTGTC TCAGTATGGGAGGTCCTCACTCGCCCAAGGAGCGCTCGGGCCAGAGATGAGAAATGCTGTAA TCAGTACAGGGGCTGCTGCTGGGGTCCCAACAGCTCTCTTTGGGGG
WI-21513b	192 G A ---	---	CACATAGTTTCTCAAGAAGAGGATGAACCTGAAACTCCTTAAGCGAGGACAAAGCAACTTCCATT ATTCTTAGTTTAGACCAGAACTTTTAAATTTATTTATTTCTCTTTTAACTGTCAAAATACACCAAATA CTTAGAGGAAATATTCACAGTATACCAAAACATTTTAAAGATAAAGAGGCGAGTGTAA[G/A]AGTAG TATTCTCTACATACCACAGTATACAATGATGCCTTCTCTGCAGGTTTAGGAAC

WI- 21514b	133	C T ---	---	TTGAACCTCTGAAGGTGGCTTATGTCGACTCCTCTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAGTATCTCAACATTACAAACCCCAATCTTCAAGGAAAGGAGCACATTACCATGGAGCJC /TACAGGACTCCAAGGACCTCAGAAAGCATTTAGCCAAATCTCCTTATGACGAGAAATAAATGAGG ANTTAAGGCTCAGATGGGGTTAAGGGTGATTGTCAAGGGTGCATAAGGAACT
WI- 21514a	100	A G ---	---	TTGAACCTCTGAAGGTGGCTTATGTCGACTCCTCTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAGTATCTCAACATTACAAACCCCAJAJGJTCTTCAAGGAAAGGAGCACATTACCATGGA GCCACAGGACTCCAAGGACCTCAGAAAGCATTTAGCCAAATCTCCTTATGACGAGAAATAAATGAGG ANTTAAGGCTCAGATGGGGTTAAGGGTGATTGTCAAGGGTGCATAAGGAACT
WI-22020	27	C G ---	---	ATGAAACATGTTGCAGTGGGATGAATTC/GJTATCATGATGCTAAGTGAATAAGCCAGACACAAA AATCCAAATGTATCATCTACCTGTATGAGGGTACTT
WI- 19576a	113	A G ---	---	TTATCGGTTCTTAATACAGTACAATCCTTTTGTGAACAAAAGTCACACTGGCAATGATTATTACA GATCCAAATAGACTCAGGCTTCAGACATAAAAATTTAACATTCJAJGJTCTAGTTCAGTGATTAGT CACAGAANTTAACATCTGCCCAGATGTACACAAATTTGGTAAAAACTACAGCTTCTCTCCACGGGGA G
WI- 21695a	141	A C ---	---	ATACACAGGCCACAAATTCAGGATGGAAGGCGAGTGGGCACTTGGAAAGTACTACACATGGCAATA AGCAGCCTATCTCTTTACCAACCAGAAAGTTTCTTGGGCACTGTGATGGCCAGACCCCTTTCCAA GGAAATAJAJCTACTACACTAAGCCTACACTGTACTGTGAGAGTCATGGTGGAAACAAGGCCACAGGC AGTGGGAGGAAATGTGATGACTTCACTGTGTTTCAAGNTTCAAGGCCACAGCAT
WI- 21574a	235	C T ---	---	AAOCCAGAAATTTAGGTACTTTTGTATTATGAGGAACCTCACTATAC TAGGAAGCAACTTATGAGTG TGTAATATTTGATCTAGCAGCAACTTTCACACTGATCTGGCAGGTGACAGCTCAGTGAACAGCGC TCATCACCTAAAGTGAGAGGCTGTCTATTCTCATTTGTGAATGTCCCTCAGAGTCACTAGGGAGCCATT GGCAGGCCAGGGAACCTTACTGCCTACTTCCJTCJTGCTGTGTCAGGTGGGA
WI- 21644c	151	T A ---	---	TGACTGCCAAGATTTAGGCCCAACTTAGGAGCAAGGGTCACCTCTAACCTTTCAGGAAGTCTTGGGT GTGACCCACTGCATAAATGGATTTTCAACCATANTATTTAACAGACTCAAAGTGTACATACAAGCTTG TTTCATAAATAAGGGAJAJTTCAATCAAGATCCATGGAATGATGCAGTTTAAATGTGTTCTCAGC TTGCCTACTGACCACTTTCCTTTTCTAAATATGGCAACAGCACAGCAAGTC
WI- 21614b	55	G A ---	---	TGCTTTAACCTCAAAAGTCCAAATAACATATAGACATTTTGANTATAGCTATCJAJJTTTTAACA AACCTCATTATGATCACTGTGCAATTTCACTCACCTAAAAACGGAACCATGACTATTATAAACA TTTACTGTGTGGGTTTGTGGGACTGAACATTAACCATACGTGATTCTTAAGGTACTAGGGAGTT GGAACAGCTACTACGGGTCAATGGTATTTTGGGCAGTTGGCTGTGTGGG
WI- 21615b	151	C T ---	---	GACCGAGAAAAAAGTCAAGGCATATGATGTTTGTGCAAGTATACATGACTATTTCAAGCTTATAGA GAAACTTGCAAAAAAGTACAAAGATGGCTATTTTAAATTTACATATTAAGATAAGGATGGACT CTTCACTGAGTATTATCTTAGGACACAATCGACGGATGTAATCTATTTGANTTATACCATAGGCC TATTCTATATTGGCCAAAGGGAAAGGTAGGTGGTACTGTGGAAACGGA

WI-21981	61 T A ---	---	TGTCATCTCATCTGGAGAATCATAGATGTGGCAGAAATACATATCTTGAAGAAAAAAATTAJGT CTCCCTTATGGGTACTGTGATTTCAATAGGGTGTGGGATAGTACATGACAACATGCATGGGATAGA CACTCTGTTCTCTACAGATCCGTGCTTTGGGAATTACAGGAACATAAAGGATATAATGGATGGGTT ATTACTTTTACATGTGGACAATCTAGTTGTAGGCGTTTAAAGTTAAATTTGG
WI-21660	120 C T ---	---	TCCAACTAGCCTCTCAGTATTTAGATGAGGATAGAACAGATACGGTGTAAACACGCCCTCTCCACTGCT TACTGTGTACCAAGAAAGGAGAAAGCAGCTACCCAAAGCCTAACCTGGCC[C/T]TGTCTTTTTCAG GCTTCTCAGGATGCCACAGCACATACCTGGGGAACCTGGGATGCAGGGAGAACCCAGGGTCTGTCTTC AGGAGGGTCACAGC
WI-19105c	211 C T ---	---	TGGAAGTAGCCCTTCTGGACAGAAAGAAATATTTGTGTCCATGTGGTTGAGTCTGTTAAGAAGGA CACTAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGGAACTCCTCCTT GTCTGTAGGTTTCCAGGGCTGGGCACAGAGGTGAGGGCAGAAATNTGGGGTCCAGTGGATCTCCCC ACAACTTC[C/T]TCCAGGGGCAGGATTTCCACCAGGGCCAGGGTGCCCCG
WI-19105a	33 T C ---	---	TGGAAGTAGCCCTTCTGGACAGAAAGAAATATTT[C/G]GTGTCATGTGGTTTGAAGTCTGTTAAGAA GGACACTAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGGAACTCCTC CTTGTCTAGGTTTCCAGGGCTGGGCACAGAGGTGAGGGCAGAAATNTGGGGTCCAGTGGATCTC CCACAACCTTCTCCAGGGGCAGGATTTCCACCAGGGCCAGGGTGCCCCG
WI-21760c	81 C A ---	---	CAACCTAGTCACTCTACTGATGCAATGATTTGGAGGTGTCTCTCTAGCTTTACAATAAGNGGAGG GACCTCTGACTGCA[C/A]CCTCTGCTCAGTTTCAGGGCA
WI-21760a	35 A G ---	---	CAAACTAGTCACTCTACTGATGCAATGATTTGGI/GJGGTGTCTCTCTAGCTTTACAATAAGNGG AGGGACCTCTGACTGCACCCCTCTGTCTCAGTTTCAGGGCA
WI-21569b	198 T C ---	---	TCTGCCATATTGTTCCAGCACCACTATTACTGTATTATTCTCTTTGAGGAAACCAGGNATTAAAG AAATCTGGTTTGAATTTCCATGATGCCCTAACTCTATGGTTAAATCCTTTTCTTACCAAAAGGA ACTTCTTAATCACCAGAGAAACAGAGGGAAGACTGAGATATGTTTGCAGAAATTTATCTCTACT[C/G] AGAGACAATTCATAGTTCATAATCTTTACGGGTTGTCTTTACTTGGGGGGC
WI-20934a	72 T G ---	---	CCAACATGCAACATAGTCTTCAATCTTAAAGTACATAGTAAAGGTATGAAAAACATTTGTATTCA GAGAA[T/G]TCTAAGACAAATGGTCAAAATTTCAATGGCTGGCAGTGTGGTAATTCAGCAGAC AAACAGCATGAGAAAGGCCGGGAGACAGTAATAATACGTGCCCATTTGCAATGAGTTACCCCAATC AAGCCCTTTTACCTCCTTAAGATGGCAGATTAGAAGACCCCTNTTCCCCAGGAGA
WI-21561	55 T G ---	---	TTTCCATTTTATTCAGCCGGCCATCAGAACATAGCATCTATACCTTCGAAACC[T/G]CCTCTTAAC CTCTCCAGGCAAGAAAGGAAAAAGTATGATCATATTTGAATTCCTCAGAAATGGTGGGATCTCAAGACTT TTTAGAAAGTGCCTTATTAGTATAAGAGGGCTTGAATATAATGATGATAAATGGTAGCCCTTCTGGA AATAATTTTGTAACTCIGTTTAAAAAGATTTTGGATGCATTGTCCCCA

WI-21981c	200 T G ---	---	AGCTTTGCTTGAAAATTTGGTACTTACTACCTTTGCAATTCTCTTTATTATTATTACTTTTATTTTCCGTAAGTTATTGGGTACAGGAGGTATTGGTTATATAAGTTCTTTAGTGGCGATTGTGTGATTGGTGACCCATTACCAAGGAGTATACACTGCACCATCTGGTCTTTTATCCCTCGCCCCIT/GJC
WI-21981b	73 G A ---	---	AGCTTTGCTTGAAAATTTGGTACTTACTACCTTTGCAATTCTCTTTATTATTATTACTTTTATTTTCCJG/AJTAAGTTATTGGGTACAGGAGGTATTGGTTATAAAGTTCTTTAGTGGCGATTGTGTGATTTGGTGACCCATTACCAAGGAGTATACACTGCACCATCTCGGTCTTTTATCCCTCGCCCCCTCTCCACTTTTCCCTCAAGTCCCAAAGTCCATTGTATCATCTTATGCG
WI-21956	26 T G ---	---	CCCACCTTGGGTCTCTTCAAGTGAATJ/GJTTCCCTTTCGTTCTCTTAAAGCCCTTTTAAATGAACCTCCATTCTGTTCTGAAACTTGCCTTAGTCTGTCTTCTGCTCATGCCCTCAGTCGAATCTTTCTTCTGAGCGCGCAAGGACTGAAGTTGCTGTGGACCTGTAGGGTTGACGCCGCTAACTCAGGGTAACTCCTATCTCTCCACCGGTAACAGAGGGGTACATTATGGGTCCAGGTT
WI-21966	148 G A ---	---	CAACATACATTATGGTGCCTTTTAAAGAAATGTTTACTGAGAACTGTACTGTAAACAACATATTTTTGTAGAACATGAGTGAGAGTGTGTGTGTGTGCGCGCGCGGCACGGCATGGCACTGAGGGGATTGCAATGGGJG/AJACAGGATAAAAAGGTATAAAAACCTTGGTCCGAAATCTTTGCTTATTAACTTGCGCCCTGCTCCTCACAATGTTTCTACACTTAATTCATAAGAGAGGTAGA
WI-21930c	146 G C ---	---	TATACTGGTTTTTGGTTACATGGATGAATGTCTAATGGTGAAGCTGAGATTTTAGTGACCCATCACTGAGTAGTGATACATTGTACCCAACTGTAGGCTTTTATCCCTTACCCTACCTTCCACCCCTCCCCATTTTGAGTCTTG/CJCATAGTCCATTATATCACTCTGTATGCCTTTGCATACCCATAGCTTAACTCCCC
WI-21139a	165 T C ---	---	GCTCTAGTGAAGAAATTCAGGACGCGGTCTTCAGAGCAGAGGGCTTGGTTCAAGTCCCTGTCTGCCACTTACTAACTGCATGACCTTGAGCAAGCCACTTAATTTCTCTGCTCTCTCTGTGAAATGGGTACAA
WI-20317b	217 G T ---	---	TGTGGGTCAGCAGTAAAGGAACTAATACATJ/CJGTACAGCACTTCAGCACAAAGCCCTGGGCACACAGCACTGCATGGAAATACACAGGTAACATTTTAAACAGTGGGGACAAAATTTAAGTACGTGGCCAGCGTGTGTGCTGTGTGTCATTAAAGACAATGTTAAGANTCAGGAGTACTTAAGTGTAGTGGTTACA
WI-22082e	179 G A ---	---	AATTTGTCTCTTCAGTTTTTCATTAAAGTAAATTCATAAGATGATATACATATTACTGCAGATAAAACCATCATCAGAAJG/JTJATTAAATTAATGCATATTTTGGGCTACTCTCAGGACTTGGTTTGTGCTGCCCCAACTGCACATAAATGTCCTTTTTTGTGAGTTATTGGTTGTGTGCGTTTTCTCTTTTGATAAGAAATATGTCCATTAGTCCAGAGGCTCTTGCTTTATCCGGATGACGGAGGTACACGGGGCGTCCGCTCAGTTCGCCGCGAAGGACGTATG/AJCTGAAGTGGGACGAGTCTACTCTCCCCCACAGGAGCCACGATTTCAAATCCTCTTTGCTGCAACCTCT

WI-22082b	67 C T ---	---	---	CAGGACTTGTTGCTGTCCTCCCAACTGCACATAAATGTCCTTTTGTGTTGAGTTATTGTTGTGTG[C /T]GTTTCCCTTTTGCATAAGAAATATGTCCATTAGTCCAGAGGCTCTTGCTTTATCCGGATGACGG AGGTACACGGGGCGCTCAGTTCGCCGGAAGGACGTATCGCTGAACCTGGACGAGTCTACTC CTCCCCACAGGAGCCACGATTTCAATCCTCTTTGCTGCAACCTCT
WI-20993	139 A G ---	---	---	AACACAACTCCATGCTTTCAAGATTTCCACACCCAGATACTAAGACATATTAAATTTACAGCAAT TAAACAGTGTAGTTTGGTACAATAACACATATAGCAATGATACAAATTAGGGGAAAAACCCCTGG GCTTCT[A/G]TAACAAGTGAGTATACATTAAAGACAGATTTCAGAAATGGCTTCAGGATTAAATTTGA TTAATTTAGAGAGAGCCTATTTCAGGTCTTCTAGCTCATCCACACATCACC
WI-21723b	125 A G ---	---	---	AAGCGATTTTATTAAATTGATTTGGACATACTGTAGGTCAAATAATATTTTCTGAAGATAACAATTA TGGACTTTAAAGCTCGACATAAAATTAGTACTTCAAAAGGTTAGTCATATTTCCCA[A/G]CAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-21723a	82 G A ---	---	---	AAGCGATTTTATTAAATTGATTTGGACATACTGTAGGTCAAATAATATTTTCTGAAGATAACAATTA TGGACTTTAAAGCTC[G/A]ACATAAAATTAGTAGCTTCAAAAGGTTAGTCATATTTCCCAACAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-22132	99 T G ---	---	---	CAACAGATGCTTGAGCCAAAAAGCAACATAGGCAGAAATACAATTGAGAATATCTTCATGTTTC AACCTTTAATCTGACTGCTTTTACTATCCTT[G/C]CCCCATTTCTTAATCTCTTTTGCTTACAA TATATTACCTTCTAGGTATCACCTCATCCTATAGGAATGCCCTTCTAGTTTAAATGTCTGCCCCAAACA ATACTAACCCATTGAAGGATACTATGGAACCTTTAAATGGGACAGTGGG
WI-21006a	106 A G ---	---	---	TGACAGATCACACCACATTTGTTTGTAACTTTTCTCTTCAAGAGTCACCTTAGCTTAAGCCAGAA GATTCCTTTAAAGAACACATACACACATGTGCACACACIAGAGAGGCAAGTACAAAAATGTAACC CCACCAAAGTGCATGTGAATGAAAGTGCAAAVAGGCTTCATTGCAAACTCTGAGGATCATCTCT CTGCTTCAGGAAAATAAACAGAAAGGTCCTAACTGCCCTAGGCCT
WI-21761b	138 C G ---	---	---	CTGAGGCCTGCTCTAACTTCATNTGACGGAGCGAGTTTCTGGCTTGGAAATAACTGAAAAGATTTCAT TTTCTCTTTGTGTACAAAGGATTCAAAATATTTTACATCTTCTCTGCCAGTTAAACGTGCCGTGG CTC[G/C]AATACACACCAAAAGCCAAAGCGTAACCTGGCTCAGGAAGGCTGGGAGGAGTGCCAG ATGGTA
WI-21079c	166 G A ---	---	---	AATGAAAATGCCACCCAGAGGTTAACAGCTTGCCATGCATGCAACTGTGTGCGCAAAATCAAGTTGT TTTAATACCAAGTGTGCAGCTTTGATTCCTCCATGAAATTAAGCTGTGTTGCTCACTTGTTTACATAA CTCAGGCCACCCCTGAAAATATCTGCTAGTGGG[G/A]AATTTACAACCCACTGACCCTCTCAGCTCAAA GCCAGATGACTATCACCTACACATCTGCCAGGTTATAGGATGGGCAAT

WI-21079a	50 G A ---	---	AATGAAAATGCCACCCAGAGGTTAACAGCTTGCCATGCATGCATGCTGTG[A]CGCAAAATCAAGT TGTTTTAATACCAGTGTGCAGCTTTGATTCCTCCATGAATTAAGCTGTGTTGCTCACTTGTTTACA TAACTCAGGCCACCCCTGAAATATCTGCTAGTGGGGAATTTACAACCCACTGACCATCTCAGCTCAAA GCCAGATGACTATCACCTACACATCTGCCAGGGTAATAGGCATGGGCAAT
WI-22129a	45 T G ---	---	TCTGTAGATTTAGCCATGCCATATATTTAACTTTTAAAGGAAAAGT[G]TTATATAACAGTCATTGCT TGGTAGAATCCAGTCTGTCAATAAGTTAGCTCTAACAGTTAACATTTGAAGTCTTATACCTTATATTTA AATGTTTAGCAATCTACTACATTTTCAAAATATAAATAATTTGGTTGCAAAATTCAGNAAGGGCA TTAACCAACATGGGACTGATCCTGGGGGCTTCACCTGACTAAGGTTTTTA
WI-21941	79 A G ---	---	TGGAGTTAAGTGGGCTCTGCTATTTCCCCAAAGAGGACTCGGAAGATGTTGATTCAGGGGCAGAGT GAGGGGCAGAC[A]G/GGATGAGGCTCTTCTGTAAAGTCCAAACAGAGCTCACAGATGCTGGGAGGCT GGGACTGCCAGTTGGGAGCTCAACCCAGAGAGGCTCACTGCATTGACCCACACCCCACTCACCC CAGCACACAGGCACACGAGGGGCACACGACACACGNTGCACTCAACACGC
WI-18916b	42 C T ---	---	AATGGCATCCCTGTGATACCAAAACATCTTCAGCAGCTCAGC[G]TGGCTTCCCACCTTCTTGGTACCC GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTCGCCCACTACTGCACTGGACACAGCCTCAOC AATGCCACCTTCATA
WI-18916a	35 G C ---	---	AATGGCATCCCTGTGATACCAAAACATCTTCAGCAG[G]CJCTCAGCCGGCTTCCCACCTTCTTGGTACCC GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTCGCCCACTACTGCACTGGACACAGCCTCAOC AATGCCACCTTCATA
WI-19828c	200 A G ---	---	TTCCCTTCTCCCCAAGAGTGGGCAGAAAAGCTTTGTTAACTCCTTTTACAGATGAAGAAAAACAA GATCAGAGGTGCTAAGTGTGTAGCCTAGTGCAGGNCCTCTGGCCCCAAATCTGGGTTCTCCCCAAG CCCATGCTTCTTCCACTTCTCACAATCTTTACTTCTCTGACCCCTCACCACCCCAAAAT[A]G JCTTTTAAITCTGGAAAAGAACCCAGCTGCACACTGGGCACACTTGACCT
WI-21863b	47 C T ---	---	CACAAGAGTCTGTACAACCTTAGGGACACCCAGCCCTGGCCCTG[C]TJAGCTGCATGCCACCCCTC ATATCCCACCCCATCCCAGCCTCCTGCCCCGACACCCCCAGGCTCCCTGCTGTGGTTGAAGTATTTT CTCCAAGGCAGGAATGAGTCCTTGATCCAAACCCACAGCATCT
WI-19860	51 C G ---	---	TTGACCTAAAGCCTAGCATAAATTAGCTAAGTAGAATGTTTCCAAAGATG[C]GJCTGCATCAGTAT CTCCCATCCCACATAATTTCTGTTTGAATTTGCCATTCAACCCATAAAATGGTGGGATCTACCTCCCT OCTTGCAAATTTGAGCTGGNCTCTGATCCTGCTCTAAGGATCTGAAGCC
WI-19889b	80 C T ---	---	ACCCAGCTCCTCTTACCCCTCTGGCTTTCAGTAGGCTTTGGCTAATGGCCANTGAACCTGCAGGGCAAG AGGAGTGAGGGG[C]TJACAGCATTTATTTCCCTCTTTCACTCCCTGTTAGCTTTGGTAGTGGCTGTAT TTCTCTACTGATAGTCTCTTGGCCACAGTGTAACTATTGC



WI-19891c	172 C G ---			TGTTGGTCTGAGAAATTCACAGCTTACTACAAGGAAGCTGAGAATTGCTTGGTGCCCTCCCCCCCCG ACTCCTCTGCTCGGGAACGTGGCTTTGNCCTCCAGACACAGTGTGAGATGCCAGCTCCTCAGCGG AGCTCCCGATCCCTCAATTTGCCATCTGTCTGACTC/C/G/CGTCTTCCGGGCGTGGGCGGTGCTTGT CAGGACGCGCGGGGAGGAAGGAAGGAGATCCAGGGTCTGTCTG
WI-20155a	81 C T ---			GCACGTAGGGGTAGCTTCCATGGTTCTCCAGACGGGTGTACATTACCCCTTAGGCTGACCAT TCCCTTGGGGGG[C/T]GCAAACTGCTTTGAGGAAATNCCCCAGGAGGAATAAACTAGAAAGACGC ACCTGCTATTTACCATACTATGGAGAATACAGCTAATGAAGTGGTGGCAGAGCTTGGCCGCTGTGA GTGCCCCAGGTAAAGTCTCTCTCTGTCCAGTCCAGAGCAGAGACTTCTC
WI-20270b	91 T G ---			AGCCATACAATGCATTGCAAAAGAAACAAGCAGCTGTACAGGAGTGGGACGCG[G/A]TCAGTGTACAT ACATTTCATGTCAGGATAAGGAGCA[T/G]ACACAGGATTATACACGGTGGCAGCGGTATAGGCA CGATGATACAAAATATAAAGTATATTTCCATCTATATAAATACACAGCTGGGTGGGAAAGGATGCT GGGTGATCTTGTTTCCCCCGCAGAGGGCTTGGGAGGCGGGGGTGGTGGAA
WI-20270a	53 G A ---			AGCCATACAATGCATTGCAAAAGAAACAAGCAGCTGTACAGGAGTGGGACGCG[G/A]TCAGTGTAC AATACATTTCATGTCAGGATAAGGAGCATAACACAGGATTATACACGGTGGCAGCGGTATAGGCA CGATGATACAAAATATAAAGTATATTTCCATCTATATAAATACACAGCTGGGTGGGAAAGGATGCT GGGTGATCTTGTTTCCCCCGCAGAGGGCTTGGGAGGCGGGGGTGGTGGAA
WI-20622	130 T C ---			CCACTTTCAATATTTAGAAAATGCTCAGCAGCAAAATATGAAAGCTTCAACACTTCCCTTTGTA ACTTGCTGCAATAAATGCAACTTTAACAACATACAAATTTCTCTGTATCTTAAAGTTGAA[T/C] TACTAATTTTATGATGTTACTCATATTTTATTTATTCATATACCTTTAATGACATCATTTGCCAATACATA CAATATTTCTNTAATTTATTTTACAAATAGCCAACATCTGTCATGCAG
WI-20768b	190 C T ---			TTCCACTCAAAACTCCACCCCAACCTTCTCGAAGGAGGGCTAACAGGACCTCTGCTGCCTGC TCAGGACTGATTACTTCAATCCAGCTGCAATGCAAACTGAAACTCAITCTGTATATCACCACTCTA CAGGAGGCTCTATTTCTGGGCACCCAGAGNTCAGCACACATACTGCTGGGA[C/T]CAGGGACTC GTAATTCGCTTGGTCCAACTCTTCTATGGGGTTTAGCTGCCCTCATTC
WI-20768a	71 C T ---			TTCCACTCAAAACTCCACCCCAACCTTCTCGAAGGAGGGCTAACAGGACCTCTGCTGCCTGC TCAIC/TGACTGATTACTTCAATCCAGCTGCAATGCAAACTGAAACTCAITCTGTATATCACCACT CTACAGGAGGCTATTTCTGGGCACCCAGAGNTCAGCACACATACTGCTGGGACCCAGGACTC GTAATTCGCTTGGTCCAACTCTTCTATGGGGTTTAGCTGCCCTCATTC
WI-21909	153 A T ---			TGTTTGGCTTTGGCCAGGTACTCTACTGCTTTACATAAAATATCTCATTTCTGTACATCTAACGGCAA CTAAGTATACGCTTACATCTGCTAGTGGCACCTAAAATAAGGATATTGTTGGTCATCTTTAAAGAAA TGCTTAACATACCAAAG[A/T]AGTGGGAATCAATAGATAAAATATTTAAGTCTTACAAAGCGTAC GACACTAAAGTAATATAGGATACCCTAAATTTATATTTCTATGTATGGAAG

WI-22202	128 A G ---			TGTTGCTTTGGTTGTTTCTGGAACATATTGGAACACTTGTTTTTCATAAGCTGTGCTGACAGT GGCACAATCCCATCCATCTTCAGGCCCTTTAATAAGGTCAATTATGAAATCTGAATTTCTA/GJTTAAT ACTCTGGTGCAATTCATCTGCAAAAGCAACTGGCACAACCACTCTTGGCCGGTGACGCTCTCGG AGAATCTAATATTGAGCTAGTTCTGTGCGGAACCTCTCCAGCTCAC
WI-22189	70 C T ---			CCAAGGATGAAATTTCCACATTTATTTNCTTTTATGTGAATAGAAATGGCAGTGAAGTGTCTATG AA/CJTGAGCGAGGAATGGGCATGGCGTGGCTGCGGTACAGCCTGGACGTTGTGCTTCCAAAGTACAC TATGTGGTGGAGACAAAGGGT
WI-22283	109 T C ---			GGGGAGGCATCATAGAAAAAACCCTCAGCCAGAAGTTAGGACATTTGTGATCTCAGCCACTAAGCA GCTGTATGACCTTGGTCACTAGGCCCTGCAGGCTCTGGTTG/CJTTCATTTGCAAAATAAACCCCA GACCGGTCATCTTTCAGTTCCCTCCAGCTCTATTATTTATGATTTGCTCTTAGTCTTTTATGAGCCA TGTATGATTTATCAGTCTCCCTGATGCACTCAACTCCAAATGATGCAAAAG
WI-22290a	136 C T ---			GACGTATCTCTGAGGGCTCTGCCAGGTGATTAGGTGAAGAGAGGTTTTATGGGCTCTAAGCACCG GCCAGTAGTGGGAATGCCACATGGAATGGGTAGTGGGATCTGGGGGGTCAAGACCTTGTCTTT [C/JT]TCCAAATCTCCTCTTACGCCAGAACCTTTCGAGAGCCCCCTTNNATTTCTCTCCCTCTATTCC CCTCCTTTCCCAATGTGCTAAGGTCCCAATCCAGACCCCTCCAG
WI-22292	53 A G ---			CCAGTGAAGGGTTTACAGCCATAGTAGGTTCCCCCATGCTCAGTACCAGA/A/GJTTTGAGTAC GGTGGTTTAAAAAATACTATCTGACCACAGTGGAA
WI-22387	186 C T ---			ACCTTGACACCTGCCATCCGGTGCCATCTCCTGGCTGGCACATCTATCCCACTCTGGCTCTGAAAG GCTTGCAACCAAAATGGGCAGCTGGGGCTAAGGCATATTTAAACAAAGGCTCCAAAGGACCCCTT TCACTGGGTCTAGCATCCAGCCTCTCTCAGCAAAGGCAGGATTGTGGT[C/J]CCTTGTGTTTTCTG AACAGGGCCAGGGCAGCAAGGCATGCCATCACTGCAGCACTCAACCT
WI-22395b	127 A G ---			GCCGTTCCAGTATTGATAATAATTTGTGTTAATTTCTATACAGAAATGGTTCTTCTGAAATATTT GTAGGGATGGATGAATGAAAGTGAATTAAGTCAAGATAAAGGGGGCAACTCTTTAAT/A/GJAAAG GAAATGTTACCAATCCATAGTGAAGAGTAGAATATGTTCTTTAGAGTAGTAAAGTCCCAAGG CTCCT
WI-22405	90 A C ---			TTTATGGCTCCTGAGTGCCTTACCCAGCTACACTTACCTGTATCTATAAAGTGAATTTAGAGT AAATACATTGGCTGTAAAGTCG/A/CJGATCAGGTGCTCTCCACCAAAAGCAAAACAAACTGCTGA AATGGCAAGGTTCTCAGTG
WI-22419b	67 T C ---			CCCTCTGGACAGTTTGTGTTTATGTTTCAGACAATCAAGGTCGCTTCCAGGCACAGCCAGTGC[T /CJ]TGGATGGCATCAGCAGGCTCCCTGCCCGGCCCTTGAAGCATGGCTGTGTGCAAGT
WI-21342d	59 T C ---			ATTTTCCCTTCTGTGTTTCGTATTTCCCTTTTTTGTGAGTAAATNAGCAATACACTGAAT/CJTGGA ATCTGCATGATTAAATAACATTAAACAAGTTCTATAAACACACCCCATATCAGAGTATAAGCAAGAG GTTGAAAAATATCCCTTAACCGAATGCAAAATTAGGTATCCCTCAAAATTGCACATTTCTCCTCTAGTT T

WI-21763b	154 A G ---	---	CATACCCCTTTAGGTGCCACATGATCTTAGTTAACAGTCTTGAGTCCCTCTTTAGGCTTCAAGA TAATTGTGATTTTCATCGCACCCAGATACTTCCAAGTGGAGCCAGGCTCAGACTGTCTCAGTCACT GCTCTCCACAGCTGATTG/CAGACATTTGCCTGTGCTTCTTACCCAGCAGCTGTCTAGTGCACCTT GA
WI-21763a	135 T C ---	---	CATACCCCTTTAGGTGCCACATGATCTTAGTTAACAGTCTTGAGTCCCTCTTTAGGCTTCAAGA TAATTGTGATTTTCATCGCACCCAGATACTTCCAAGTGGAGCCAGGCTCAGACTGTCTCAGTCACT T/CJGCTCTCCACAGCTGATTACAGACATTTGCCTGTGCTTCTTACCCAGCAGCTGTCTAGTGCACCTT GA
WI-22440	64 A C ---	---	CAGTCCATTGAGTCCCCAGTCGAGGGTGCAATCTTCTTATCTTGCTTAAGCCACTTGGGTAA/CJ TCCATTCCAGCTCTGCACCTTCTCCAGTTTCTCATGTGAGAAGTCCCTGGAGGGAGGCTTCTCTGG AAAT
WI-22449	74 T C ---	---	CAATGAATGTTGTGGCATATGATTNCCATTGTGTGACAAATTTATTAGCTGGCATCCGGAATACAGTAC TTCCTTTT/CJGAAAAAATACAAATGGGAACGTGACA
WI-21965a	112 A G ---	---	CAGGTTCCACCCAGAGGCTTTATTTCAGCCACTCAGGAOCTGGCTTCTGCTCCAGGCACTGAACA CAGTCAGGCTCTTCTAAACACTGGCAGGGACCTCCCCACAGCCJAG/CCCCACAGGTTCTCTGTT TCCAAAGTCTGTGATTCAGGCAAGACCTTCACACATTCACCCACTACTGCTGGAGAGGAGGTC ATGAGGCAGCCTGTGGTGCCAGCTCAGTGTGACACACTGCCAATGTGC
WI-21687c	115 C G ---	---	CACCTGGCAGTTGAGTCAGATTGTAGGAAAATTAACCCAGATGGGTCTACATTTTNTTCAAGTTCA AACCACATGTTTCCCTAGTCAGAAAGTCTCATGGACTTCTTCCCTAAG/CJGTGTTCTATGATCAGAC CACCTCCTAAATGTGGCTTTTACCCATTACAGGCTACAGTTGAATCAGGCAAGGAGCAGCTGCTGGAG AG
WI-22374a	149 T C ---	---	AGCTTTTACAACAAAGCGAGGGTTTAAGGAGCCTGAGAAGAAATTTCAACAATTTGACTATACAGAG TCTTCAATTTCCAAAAACAGTTAATAGTAACCTGGTGGCACATACAACTGCAATTTGAATACTCTGTAT TATTCAGTAACATAA/CJAGGNTCCTGCAATCTCTTCACA
WI-22250b	132 C T ---	---	ACTTGCTTTCAGGCAGGCAATTTCTGGGATCTAACTAGAAATCCTTGAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCACCTGATAGTGGGTATTATGGGGTCTCTGCTCTGCTGCTGTGTTATG/CJ GGANCCAGGAGTGGAGGAGAGCCGTGGAAATAGACAGGGGAG
WI-22250a	89 G A ---	---	ACTTGCTTTCAGGCAGGCAATTTCTGGGATCTAACTAGAAATCCTTGAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCACCTGATAGTGGGTATTATGGGGTCTCTGCTCTGCTGCTGTGTTATG/CJ GGANCCAGGAGTGGAGGAGAGCCGTGGAAATAGACAGGGGAG
UTR-04932-2b	192 G C ---	---	GCAGCCATCCTCTCTCCACACCTCCAGGCCACCTGGGGCCAGAGCACTCATGCCAGCAGCAC CTACGTGGCCCGAGTACGGACCCGCTGGCCCCAGGTTCTCGGCTCTCAGGACGTCCAGCAAGTGGA GCCACAGAGGTTTGTCTGGGACTCCAGCCAGGGGATGAGGCCAGCCCAAGACCTG/CJAGTGTCTC TTTGACGGGGCCCGCTGCTCAGCTGCTCTGCTGGGAGGTGAGGAAGGAGGT

UTR-04932-2a	149	C T ---			GCAGCCATCTCTCTCAACACCTCCAGGCCACCCCTGGGGCCAGAGCACCTCATGCCCCAGCAGCAC CTACGTGGCCCGAGTAGCGACCGCTGGCCCCAGGTTCTGGCTCTCAGGACGTCGCCAGCAAGTGA GCCAGAGGTTGTC/TGGGACTCCAGCGAGGGATGAGGCCAGCCCCAGAACCTGGAGTGCTTC TTTGACGGGGCCGCGTCTCAGCTCTCTGGAGGTGAGGAAGGAGT
stFIBBb	412	G C ---			GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGCGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTCCACAGGCCCTTGCCACTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACGCTCGAGTCCCATGTTGAGTACATCTCCAGATGACGCCAGGAGCCTCTCTGA AGGACCATCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
stFIBBa	341	T C ---			GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGCGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTCCACAGGCCCTTGCCACTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACACGCTCGAGTCCCATGTTGAGTACATCTCCAGATGACGCCAGGAGCCTCTCTGA AGGACCATCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
stGLV2	61	T C ---			GTCACAAGAGGCGAGCGCTCTGGGACGTCTCCACATGGCTGGCTCTGCTCTCACTCACTCTCTC CTCACTCAGGACACAGGTGACGCGCTCCAGGGAAGGGTCTTGGGACCTCTGGGCTGATCCCTGGTC TCCTGCTCTCAGGCTCACGGGGCCAGCACTGACTCACTGGCATGT
stSG1001	70	T C ---			GTTCAGGCTCATCTTGAACCTCTGGTGTCAAGCGATCTCCACCTCGACCTCCAGGGTGTGGGAT TA/T/CJAGGCATGAGCCCCCAGACCTGGACACAAAATACATTATATCTCTAAAGTATAGGATTACT TTAAGAGAAGGAACTAAAAGTATGATGGCTTACTTTCTAATCC
stSG1001	33	G A ---			GTTCAGGCTCATCTTGAACCTCTGGTGTCAAGC/G/ATCTCTCCACCTCGACCTCCAGGGTGTGG GATTATAGGCATGAGCCCCCAGACCTGGACACAAAATACATTATATCTCTAAAGTATAGGATTACT TTAAGAGAAGGAACTAAAAGTATGATGGCTTACTTTCTAATCC
stSG1002	63	A T ---			TAATGATAATTAGGGCATCTTCCACACGAGATGACACAATTGACCCCAATATCATTGAGGC[AT] AACAGTTTGGGCTGTTTCCAGTAGTATGACAGTGA
stSG1009	36	G C ---			GTGGAGAAAGATCGTCTTCTCTCCCTCCCATGACC[G/C]GGCTTCCCGGGCACTGTGCGTTTCC ACCCGAGACGGCTTGTAGGGACCCACTGCCACTCCGCTGTGCGTGGTTCCGCTCTCTAG GGCTCGAGTGTTTAAG
stSG1011	107	C A ---			TAGGCTTAAACCTGGAATCTACAAGCCAAAGTCCCTCCCTGCTGAGGGCAGTACCCTCCATTGGGC ACAGTCCAGACCCCAAGTCAAGATGCCCATCTCTTGGC[G/C]CTCAGCCCTCAGTTCTCTTCAATTCC ACCAGCGGTGCTGTTTGGTGTCTTCTCCAGTGAG
stSG1012	89	T C ---			TAGTAGGTAAGAAAAGCAAGGAGGATTGCTTATGCGATGACTGTTTACAGTGGTGCAGACTATGC CGTGTTCACGAACACTTTAATAT/CIGTGTGTAATCTGATTTTATCCCTGCTTACAAATG
stSG1017	42	C T ---			TTGAAGCAATATTGCTAGCACTCTGCTGGACATTAAGTCCG[C/T]GGGAGGAGAGTGAACAGGAA TCGATTCTTTGCTTTTAACTGCCCTTAGTAGGAGATGTTAAAATACITGGC

stSG1019 3	136 GA ---	---	GGAACAATACCTAAGGACAAAATACTATTATAAAAAAAGTCTCTAGTGTATATTGTGTAACACATTTCTGGAGCTGGTAGGAATAACCAATTTTATTTTCTGTAGTGCCATCTATACAAAATTTTAC TTG/AJTGGAAACTGAGATTTAAGTTGCAAACT
stSG1020 2c	143 GT ---	---	AAGCTAACTAGGTGAATGTGCCACTCAAAGTCTTTCCGAGGGAAGCTCAGTCCTGGCTTGGGAGAGTCAGCCTTGGTCACCTCATACGGGCTCCAAGCTAAGCGTCAAGGAAGCAGTCCCAGCTCTCTCGCTGTCA[G/J]CAAGACCACAAAGGCAGATGCCACTGCTGCCCTTTCTTCTGTCTACTTTCT
stSG1020 9b	75 AG ---	---	TCCTTTCTCTTTTCACTCTCAGTCACCATGATTCATAATAAACTAATTCCTCTAAGATCCCACCTTTATTTTTA[G/J]CTCCAATAAATGTAATTATCAGCTGCTGAAT
stSG1020 9a	34 CT ---	---	TCCTTTCTCTTTTCACTCTCAGTCACCATGATTC/TAATAAACTAATTCCTTAAGATCCCACCTTTATTTTTAACTCCAATAAATGTAATTATCAGCTGCTGAAT
stSG1021 8	29 TC ---	---	TACTAGACATGCAAAATGAGAAGATTACAT/CJGTGAATATTTAAGAAGTTATATTTGTTTGACATAATATGCATTGTACCCGGGCATAATAAAGTTAAAGCCAGTTATCTGA
stSG1025 2	108 AC ---	---	ATAGGTTTCAGGAACAAAATCATTAAATGGAATAATGAGAAGAAATCTTTATTTTGGACCAATTTTAGGCACCTAAGAGATTTCTTTCTCTCTTCCCTTGATCA/CJAGTGAAGATATGATAGGGAATTCAGAAATTTCTCTCTTG
EST10915 0	123 AC ---	---	CTGTATTAATTAAGAAGGCACATTAAATGAGGGACGGAAAAATCTACCTGTACACAAAATCTGTACTTAACAGCATCTTCAATAAACCTTTAAAGGATAATGGTTTACGATCATTTTAAAG/A/CJATTTTAAAGAACTGAGTTATTTGGAC
EST11023 1	166 TA ---	---	TTTTTTGTTAAACCAACCCCTGAAAGTTTCCACATGTGAATATAGATACAACAGTGAACAAAATATGTGGCCTCCCATGTACATTGGTTACCTATGTACAAGTATCCTATACACCAGTAAACAGCAGGGCAATTAGTCAATTAATAAAATAGTACATGTTAT/AJGTGTAATAAAATTTAAATTTACAAAGGCTTTTCCACTCGTGGATTTGATTCCTTTTGGAGGGAGTAACTCTGG
EST14096 8	71 GC ---	---	GGGATGTATATTACAGATAACACAACCTACAATAATACCATCAGACATTGAAAACCTAAGGCCATTCTGTGA[G/C]JTATTTTAAACCTGGTGTTTGACACATAATGATCTTAAAAAAAATGAATTTACCAAAACCAAGATTCTCTTCTAAATGAAAAATTTAATGCAGGTACAGGATAACTTTAGGGCTATATCTAATCTGAAG
EST22113 6c	125 CA ---	---	TGCAAAATGTGAGAAGGCAGAGGGGCCAACCCCTGGGACCTCATCTCTGTCTAGATGTGAGGTGCGCAGGGATGCTTAAGTCTTCTCTGGCAGAGACCCGAGGTGCAGAGATGATTCTTCTCA[C/A]CCCTTCCTCAGGGTGTGGAG
EST22555 7	60 GA ---	---	TCAAAGCATGTGTAAGGCACCTGCCCCGCCAGACCCCTTCTAATCTGACACACTGGAAGGT[G/A]AAACCTGGGAGAGAGAAGACACTCCCTCCCTAGCTTCTAOCCTGGGCCCTCCCAAGATGAGCATTCATCTTGGAGACCAAAATAAAAAAGGACAAAAGACCAGGGCTCAGAG

EST22917 6	74 C T ---	---	GTAAACCTTGCAACGCCATGCTAAATGGAAGCCTGACTGACCAGGGGCTCTTGGGCTCTCAATGCA ATAGAAA[C/TT]GACATGGGGCCAAAGACTTCCAGACAAAGCACGCGAAGGGTAGAGGATATAG GTTAGCATCATCTGGTTGTGA
EST36458 6	65 A G ---	---	CAAGTTAGAACCATGCATCAGCTTTTCATCCATGGTGAACCTTAACCCCTCAGGCTGCTCACTCA/A GTTGGTTTCTAGCCTCACTCGCACACAGGAAGCTTGAATTTGGAGGCTCCAAAGTCACTCTCCA GAGGGGAACCTTCAAAGAGGATTCCAACAGTGAAGCAGATCATGGGGCAAAAGTC/A/GJCTATGG GGCCAGACTGAGGTTGGACCACACAAAGCACTCCAAGCTGGGCCAATCCCAACCGCTGGTGAAGCCGC ACAGCACGGAGTAGCCAT
EST36745 3	56 A G ---	---	TGTGACCATAACCAACCTATGCAATAAAGAAAGAAAAAATCCTCAGTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGTCITTTTGAAGTGTGAATAAAAGTTTCATAGCATTTTGGGA ATTATGGTTTGAATAAATACAAATGTGTGATCTCCTGAGACACATTTATAAACATTCTGGTATG T/A/TJTTATGTGAGTGGTGCTCTAGTGGCCAAT
STS- R37410c	201 A T ---	---	TGTGACCATAACCAACCTATGCAATAAAGAAAGAAAAAATCCTCAGTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGTCITTTTGAAGTGTGAATAAAAGTTTCATAGCATTTTGGGA ATTATGGTTTGAATAAATACAAATGTGTGATCTCCTGAGACACATTTATAAACATTCTGGTATG ATGATATGTGAGTGGTGCTCTAGTGGCCAAT
STS- R37410b	139 G T ---	---	TGTGACCATAACCAACCTATGCAATAAAGAAAGAAAAAATCCTCAGTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGTCITTTTGAAGTGTGAATAAAAGTTTCATAGCATTTTGGGA ATTATGGTTTGAATAAATACAAATGTGTGATCTCCTGAGACACATTTATAAACATTCTGGTATG ATGATATGTGAGTGGTGCTCTAGTGGCCAAT
STS- R37410a	48 C T ---	---	TGTGACCATAACCAACCTATGCAATAAAGAAAGAAAAAATCCTCAGTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGTCITTTTGAAGTGTGAATAAAAGTTTCATAGCATTTTGGGA ATTATGGTTTGAATAAATACAAATGTGTGATCTCCTGAGACACATTTATAAACATTCTGGTATG ATGATATGTGAGTGGTGCTCTAGTGGCCAAT
STS- R42778	74 C T ---	---	CAATCTGAAGAGATGCATAGCGGATTGGTGGCTTTCAGCAGCTGTGGGAGGTGGGACTGAGGAGCG ACTGCTAATCAGTATGGGTTTCTCCCGGGATGGTGAATAATGTTCCGGACCTAGATA[C/G]TGACGA AGGTAGCACGACACTGTGAGTGCACTAA
UTR- 04350	125 C G ---	---	GAAATAAACTAAACTGCAAGCAAAATCACTGTTAATAAGAATTGTTCTTCTGTTT[C/G]GACAGTTG AAGTGGGTGTGAGATGGGCATAGCAATGAACAGTGGGAGCCAAATGAGGTCCTCAGAATCGGGGCAAA CTCCTCTGTGAAAATGTAT
stSG1026 6	55 T C ---	---	GTATAATTGAGCATAAGCCAAAGCCCTTTTAAATAACCAATCACTATCAATTTTATGAAATCTTTACA AGAT/GJAAGCACAGTAGTACAAATATTAAGCATCTCAAGTCTCCATTTAAGAGTTGACTATC
stSG1028 2	70 T G ---	---	CACCTTAGATATGAGGAAAATGGTTTAAATGGACACAAAGGAGTCAAGCCAGGTGGAAACCAACATAG TTTCATACCACGTTGAAACCATGTGTTTATGATATGCAATAACAGCAAAATAATTTTTCACCT[C/A]TTG TCAATGCCAATGCATTGAAAGGCCCCAGAAAATGAGAAAAGGATACAAAACCTTTTGTATAAAAAGGTA AGAATTCTGTGTG
stSG1031 0	128 C A ---	---	

stSG1033 1b	116 T C ---			TTTAAAGCTACATGTCTGAAAGAATGATGCTGCTGATTGAAATAAAGGAAGAAAGGATGCATTTCCGG GCTCAACCTGTCTAGGAAGGCTAGACCTCAACACCAACACCTCCATTCGCAATTCCTCTTTGG CTACTATGTCTTTTCCCTGACTTCTGCCTCTCCAGCTCTCTGGGCTGCTGCTTCCACCTGTTCACTGA CTTAGGACCTCC
stSG1033 1a	107 A T ---			TTTAAAGCTACATGTCTGAAAGAATGATGCTGCTGATTGAAATAAAGGAAGAAAGGATGCATTTCCGG GCTCAACCTGTCTAGGAAGGCTAGACCTCAACACCAACCAATTCACCTCCATGCATTTCCCTTTGG CTACTATGTCTTTTCCCTGACTTCTGCCTCTCCAGCTCTCTGGGCTGCTGCTTCCACCTGTTCACTGA CTTAGGACCTCC
stSG1243 b	225 G A ---			ATTGGCAATGGGAAATGACACCAATCATTTGATTACAGAAAATGGTTTATAATCCTCCTCTTG AAATTATGTTAGGCCAGCATGGTAGCTTATGCTGCAATCCAGCACCTCGGAGGCCAAGGAGA AGGATCGCTTGAGCCAGGAGTTCGACACCCAGCTGGGCAACATAGTAAGACCCCATCTCTGTTTTT TTTAAAAAAGAAATTCGTTC[G/A]AAAGTATTTTCAGACCAAAAAGGAGGT AACTGACGTATCACAGGGGCAAGTATCTCTGCATAAATTTGAACTAGTTTGCCTTCTTAC[G/A]CGCT TCACATTTTAGCATGGGCCAAAATTCAGGAGATGCCATGCAATGCCATAAATGGGGCAA AACTGACGTATCACAGGGGCAAGTATCTCTGCATAAATTTGAACTAGTTTGCCTTCTTAC[G/A]CGCT TCACATTTTAGCATGGGCCAAAATTCAGGAGATGCCATGCAATGCCATAAATGGGGCAA
stSG1345 b	60 G A ---			TTAATGTCATCCAGGGAGGGGCCAGGGATGGAGGGGAGGGTTGAGAGCGAGAGCGAGTTATTT TGCGTGGGATTCACCACTTTCCCATGAAGAGGGGAGACTTGTATTTT[G/G]TCAATCATTAAGAA GACAAAGGTTTGTGAACCTTGACCTCGGGGGGATAGACATGGGTATGGCTCTAAAAACATGGCC CCAGCAGCTTCAGTCCCTTCTCGTCG
stSG1385 b	117 T G ---			TCGTCTCCTTTCCAGTCTTCTGCCAGAAGCATCCCATGATGTTGTGACCCGACACACCTTTGTGTCT TT[G/G]CTTTGAGCACTTGCCACTCTGGCTGGTGTCTGCTGCCACTGAITGTACTGTCTTGTGCCCC GATCTGGTTCCAGACAAGGCTGATTTCAGAGACTCCACGTGGTCAAGGCTCTGTTGTTGTCATCCCT TGGCTCCTCCACTTCCAGTTTGGCTTCTGTCTCTCTCATTCAGTCTCTCCATGTGGCAACAAGATGGC TACTGGTGGTCCAGGTTTCAGCTCCTCTCAGCTTGGAAATCCAGCAGCAAGAAGATGCTCACTCCCA AAGTCCATAACTCAATCCTTTGGGAAG
stSG1427	103 T C ---			CCCTGGAGTTTCTGAACATAGGAAGAGAATGCAAGTCATGTTAGGTCC[G/G]CTCCCTTGCATGA AATGTGGGAGAGGGAAATAAAGTTAGGCAACATTTAGCAATCAACAGAACCCCTTCCCTATCCTACC GCA
stSG1471	50 A G ---			CAAAACCAAAATCCTTCCACGATATATTACTATTTAGTCTAAGTC/G]TTTAATCAAAGGTTGAGA ATGACGAATTCAGAAATTTCTTCATACATAAATGCTTCTTCTTAGTTCGAGATGGTA
stSG1483	44 T C ---			CACACCCACAAGTTTCATGCTAATGCCAAGTATCACTCTTGAGGACAAAGGCCAAACCCAGTGTGCA [C/G]AATGTGGAGGATGCTGTGTCAGCTGTAGTTACTAATGCAGGAAAAACCCCAATGCAAAAGAGGAA AATGCCTGA
stSG1696	67 C G ---			

stSG1847 b	95 G A ---	---	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAATGCTACCCCTAAAATGAAAGAATTT AGAGGTTAAATAAAACAAGTGAGAGACC[G/A]TTTACTTACATCAGTTCCGGTTTATAGACATTTGAA TCATATCTGAATGACTGACTTGTTCCTCAATGTGAAACCAAATTAATAAATACTTGATCACTGTGCT TCAACACACAACCTG
stSG1847 a	49 C A ---	---	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAATGCTAC[C/A]CTAAAATGAAAGA ATTTAGAGGTTAAATAAAACAAGTGAGAGACCCTTACTTACATCAGTTCCGGTTTATAGACATTTGA ATCATATCTGAATGACTGACTTGTTCCTCAATGTGAAACCAAATTAATAAATACTTGATCACTGTGC TTCAACACAACCTG
stSG1897 a	83 A G ---	---	CTTAATGCCCTTCTCTCTCTGCACAGGAGACACAGATGGGTAACATAGAGGCATGGGAAGTGG AGGAGGACACAGGACTT[G/G]GCCACCACTTCTCTCCGGTCTCCCAAGATGACT
stSG2022 a	86 T C ---	---	TGCTTGAGGTTTCAAACTCTGAGATATCTATGGCAAGTTTATAAAAAGTACATTTGATCAAGGTACAA TTTTAACATTAAATACAT[G/C]ATTCCTAATCTCATCTATTTAACATTAACACAGGCCCTTTGTTGT TGTTATTTTTCTCCCTACAATATTTCTGACTCTGTAGGACAGTGGGCCTCAGTTGGGGGTTGAC T
stSG2076	104 C G ---	---	AAACGTTGTCCCAAAATGTGTTTCAGTTTCAAAAGTATAAAATAAGACTTCTGAAAAAAGTTTACA ATTAGTTATAAACACATTAAAGATAATATTTGACATT[C/G]ACATCACAGTGGGGCATTTT
stSG2108 c	71 A G ---	---	TTGAGCAACAATGATTCGCGAATGGGCACTCCAACTCCAAACAAAATGATTGAGGGCTCCACAGAG GAG[C/G]TAAGGGGAAGACTTTTATAGGACAACCTGTAGAACTAAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGTCTTATTTGGTCTATCTTATTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
stSG2108 a	49 T C ---	---	TTGAGCAACAATGATTCGCGAATGGGCACTCCAACTCCAAACAAAATGATTGAGGGCTCCACAG AGAGAGCATAGGGGAAGACTTTTATAGGACAACCTGTAGAACTAAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGTCTTATTTGGTCTATCTTATTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
stSG2141 b	173 A G ---	---	TTATCCAGGGGACAAAGCTGCACAAAGGAATGTTCTCTCTATTTTAAACAAATGACTGCGTGTAC TGAATCTGACTGTGTGAAATAATCTCAGAAATGGCAGCACTGATGGGATGGGATGGTGCAGGTGGGT GCAGTTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAG[G/A]AGTTCCTATTATTATTTAAAGGC AGTTTCAGAGCACTGGCACTTCTGTTGCTCTG
stSG2141 a	113 C/T ---	---	TTATCCAGGGGACAAAGCTGCACAAAGGAATGTTCTCTCTATTTTAAACAAATGACTGCGTGTAC TGAATCTGACTGTGTGAAATAATCTCAGAAATGGCAGCACTGATGGGATGGGATGGTGCAGGTG GGTGCACTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAGTTCCTATTATTATTTAAAGGC AGTTTCAGAGCACTGGCACTTCTGTTGCTCTG



stSG2148	50 A G ---	---	TGGGAACAACCGGCTATAGTCTGAGTCATATTTTAGACCGTGATTTTC[A/G]AAAGAAACAATAA ATGTGGATTAGAAAGGAAACATCCATTACTGATTTTCGATACTTGTGATGTTCCACAGACGAGCTC ATCAC
stSG2175	68 C T ---	---	CTCAATGAGGACTCCATCAGCCAAAGCGGTTATATGGCAGATGAGCTGCTACAATCTGTTGTGTGCT [C/T]GCCGCGTGACTCAGCTAATGCTACCGGGTTGGAGCGCACACCGAGCCCGACACCTTTTCCAT ACCTGGGCAGAGGGAAGGGAGTGGAAGACCA
stSG2189	41 C T ---	---	CAAGTGGTGAAGCTGGGATTTGAGCCTGATATTCACACTA[C/T]CTACATTCCTCCAGTATAATA GGAAGCTCATCGCTAACTTTGAGCACTTAGTGTCTGAGTACTTCGTATAGGTTATCTCAATCCTACTC CAGCTTTGCGAAC
stSG2200	49 T C ---	---	TGTTGATGACCATAGAGGATGCAAAGCTCCGGGCTGGTTCTGTATGATG[T/C]TTTATATTTATGTAT AATGTCTTACCTGATGATACCAACATATTACTAGCCTTATAGATGAGGATGGATGGCAGCTTGGCTG GTCAAT
stSG2243	85 G T ---	---	CATTTTCTGCCTCTGCTTCCAGTACTACCCGCTCCAGCAACTGCCCTCTCGTATAAATAAGTATCAA GATGGTCAGTAGAAAAG[G/T]AGAGCATCTCTCAGCCCTGGAAGACAGTGTGGGAGCTTCAGCT
stSG2257	65 A C ---	---	TCAGTGATTGAGGAGCTGGCTAAGTCATGTCTAACTGTGTAGGCGAGGTATCAGAAGGGCAG[A/ C]CTGTCAGGAACTCTGCCAAGCACTGGGCTGCTCTCAGGCAGAAATTTCTTCCT
stSG2306	67 A G ---	---	GTCTCAGCGTAGAGGTCAGTGGTATAACAAACAGTAGCTATATGATATTTGGGAATATTTTACA [A/G]TATGCTCCCATTTGGGTTTCCAAACTGATACAACCATGAGGTGAACACTTTCACTGTTTCACAG TTCTCTCCAGAGA
stSG2334	70 T G ---	---	GAAACTACCCACAGCATCATGTTAAAGAAGAGAGATGAAAGAAAAAATCCCGCAAAAAACA AAAAAT/GTTCAGTGGAGGGGCTGTGGGAGGGGTGAATG
stSG2339	63 T C ---	---	AGAGCAGAATGGTGAATCAACAAGACCTCAAATTTGCTTGACTGCAGAAGTAAGTGTGTCAC[T/C] GTTCTCAGAGTCACCATTAACGGTGAAGTGTCTATTTCTGGCTGTCTTCTTATTCATCA
stSG2465	76 C T ---	---	CAAGACTAAGAAAGCCGACCCGAGTGGTCCACTCAAAAAAGAGATTTCTGATTCTACCTCAAAATG CAGAAACCA[C/T]TACAGATTAAAGAGAAACACACACACACTTTGAGAAACTCGCCCTTCCCTC ATCTTCAAAGTGTGGGGTATGCA
stSG2549	140 T C ---	---	TTGCAGGCTTGATTTCCACAATAACAAAGTCATGTATAGAGAAATGTGAAATGATACITGAAACCAA GATATATAAATATTGAAGTCATTTATGCCCTTTTGTAGTACTGGGTTAAATATGCAAAGCAGCTAAAG GAATA[T/C]TACACCCACCCCTTTTAACT
stSG2577	123 T G ---	---	AATTGCCAAATGAAAAATCCAGAGGATTTTAGACCAACTTTGCCCTGTTCATTTCCAGTTTGGT CCCAATATAGGCCCTTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAAGCA[T/G]GAACAATC CCGGCCACAGATTAATTAT
b			

stSG2577 a	121 C T ---	---	---	AATTGCCAAATGGAAATCCAGAGGATTTTAGACCAACTTTGCCCTGTGGCATTCACAGTTGGT CCCAATATAGGCTTCTGCAAGAAGAGATCAATGCCGAACCGAAGCTGTGAAAGCTGTATGAACAATC CCGGCCAGATTAAATTAAT
stSG2700	58 G A ---	---	---	ATCTCTCGACTGCTTTAGTGGGAAAGGAATCAATTAATTAATGAAGTCTCCGGCCCC[G/A]AGTCAC TCAGCGTTTGGGGAAATAAACCACTGGTCCAGAGCAGAGGAGGCTACTTGAGCCGGACACCA
stSG2724 b	101 T G ---	---	---	AAACAAGCTTTTGCAATTTCCACTACATTTTGTTGCTTTTATATTAATTAATTTGCAATGCTATAAT TTAATACTTAATCCAAATGCTTGCATAATCA[T/G]TTTTTTTAATCTGGGTGTTGAAAGAAC
stSG2776 a	65 G A ---	---	---	GTGGCCGATCTTTACTTTCCAGAAAGGGGTAAATAAAAACCTGTAGAAAGTCTCGAATAATG[G/ A]TATTGGCCCTTTGGAGTTAGGCCAGGAACCTCAACAAGGGACACTGCTGGCCAACCAAAAA ATATCCACTAATCCCGAATATAGTAACCTGCTTGTCGGAATG
stSG2791 b	109 G T ---	---	---	AAGGAAAGGTGGAGGGAAGGGAAGAAATTACAATGGTTAGAAAGAGCAACTAAAGATTATTC TATTATACTTCTGAACGGTAAACTAGCAATTTTAATAATATT[G/T]GGGTCCACTTAAATCTATTA AAGCAGAAAGTGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
stSG2791 a	100 A G ---	---	---	AAGGAAAGGTGGAGGGAAGGGAAGAAATTACAATGGTTAGAAAGAGCAACTAAAGATTATTC TATTATACTTCTGAACGGTAAACTAGCAATTTTA[A/G]TAAATATTGGGTCCACTTAAATCTATTA AAGCAGAAAGTGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
stSG2826	85 C T ---	---	---	CCGCAATTTTCAACACACATTCTATGAAAACCTAAGGGTGGATCATGTACAAACACAAAAACAAGC TCCCTCCCTCCAAAAACA[A/C/T]GAACAAAAATAAAGAAAAAACCCTATGAAATGCCAGGTTTA ATTTTTTTCC
stSG2850	88 G A ---	---	---	ATGGGTGCATTGTAAAGGCAAAATTAATACTTTTTCAGGCAGGGGTGGCAAAATTAATGAGCTGA TGTGTCCCAAGGGAGACGGCC[G/A]GGCTCACACATCCCATCAATACTCCTCCCAT
stSG3031	71 T C ---	---	---	ATACTCAGGGGGCTGAAGGGCAATGTGAAGAGTGACTGCAAGTCTGCAATTTCTGTGGTGCAGC AAAT[C/G]GCCCTTTATTTTAAATGATCCAGACATCTGGGCAGCATAGCT
stSG3058	81 G A ---	---	---	GTCCCAACTCCTCCTCTTAGAGAAAAAACTGTGATTACCTCAACTTGAATATGAACTGTGATTG AAAAAAGTCAAAAC[G/A]TGAAGAAGCATCAAGCCAAAAAGGCAAAACTGGCTGAGGC
stSG3092	94 T G ---	---	---	CAGCATCTCCAGAACATTCCTAGAACTGAACCATCTTGTACATATTGAAAAACAAAGCCAAAGTTC CAATCCAAAAATAATAATGAACGTGC[T/G]GATAAACATCTCTTATGGTTCCAGCCCCCTACTTT AGTT
stSG3230	95 A G ---	---	---	AAGAAGTACTTTGGTAGCTATTTAAATAAGAGGGGGTGGGAATGAATGTCGAGATACGAGCACCTG CATCTTTTAGTCAATTTGTCAGTGGAGTC[A/G]GTGGGTGCTAAGTGTCTGAACTGAAGTAG
stSG3245	160 G C ---	---	---	ACATCTCATACCCAGTAAGATGCAAGAAAGGAATATCTGAGAGCAAGCAGCCCTGCTCCAGGGGCC CAGGTATGTAGAGGCCAGTGGGGGTGGCCACTTGGTGTCTTACCAACCCCTGCCATCCAGTCTG GCCCAGTACCTACCTGGAGGTT[G/C]GTACTTGGCTTAAGTACTTCATGCTTTAT

stSG3265	42 T C ---			AGGTGAATGAGTTACTAAATGTAGCATTTATTTATAAGGAAT/CJGCATTGTGAATAGTTTCTCAG TTTTCAATATGGAAGATGATGATTTTCAGCCACATTCAGTGTATGTTCTTAAATACACAATCGAC AGGACTGTCTGTTTCAGTACAATGGAGGACAGCTTTTCAGGGCAAATGGGATTTCTTGATAATGCTAA ATCTGTCTTGTCAGCTGAATTTCTTGGGCTTTATGTGGCAGTGGTAAAAA
stSG3269 b	141 C T ---			TGTACTTACTGTGTCATCCTATCCATTCCCTCCCTGAGCCTGGAGTCTCTCCAGGGGAGACTAGG AGTGAAGGGAGGAGTCTCCCAAAGTTACCTTTAAGCTTGATAATTAGCTCCATAGCCATGCTAAA GCATGA/C/TJTGATGATCCCAAGTCCCTGACACATTTCTCTAAGAACT
stSG3269 a	24 A G ---			TGTACTTACTGTGTCATCCTATCC/CAGJTTCCCTTCCCTGAGCCTGGAGTCTCTTCCAGGGGAGACT AGGAGTGAAGGGAGGAGTCTCCCAAAGTTACCTTTAAGCTTGATAATTAGCTCCATAGCCATGCT AAAGCATGACTGTAGATCCCAAGTCCCTGACACATTTCTCTAAGAACT
stSG3284	130 C T ---			TTAACTCAAGAACTTTTCAGTTACAGGAAGATTTATCTAATATTAATGACTAAATACAAAAAGC ATAAAATGTTTGAAGCCATTTTAAAGTTGTTTGAATCCATATTAGCACTCAGACTTCCCCA/C/TJ TCCCTAACTTTTGTTAATTGCTGTAAATGGGACATTTGTGTTTGATCTACCC
stSG3292	99 A T ---			GTCTCAAGTGAATCTGTAATACATTTTAACTGCTGACITTCAAATCGGTACATGAGGCTTAGACATA CACATCATTGGACAAGTGACTTAAATATCTAA/JTTCAAAATCAAAATAGCATTTTCTTAACCTCAA TAAATGTATATCTTTAGCTCACT/C/AJCCAGTGTATCCATTTCCCAGCCGTAGAGCTTTCTG TTCTGTAGATTTGCCTGTCCCTGGACATTTGATATAAATGGAGTGTCTGTATCATGTTGCGACTTCTC ACCTAGCATGATGTTTCAAGACACATCCATGCTGTAGCATGCGTCAGTGTCTTATCCCTTTAA GATCCCCAGTATTATTTCTAAATTTGAACCTTGTTGTGGAAATAAAAAATCTGAGGACCACCTCAGAG GG/C/TJATAAGGGGAACCTCTTTGTCTTAGTTCATAAGGACTTTCT
stSG3369	69 C T ---			CAAGACTGTAAAGACGTAGGCCCTGTGAGAGTGAAGGAAGGATGCTCGAATTTGCCAGGACTCAGG CTTCAGCTTCACAAATCCCGAGGAAGGAATGACATTTCCAAAATGTCACTTTGTAGC/G/TJCTGGGT CAAAGTCTAAAGAGGACAAATAAATAGAGACT
stSG3398	125 G T ---			TCCTACTCTGTTAACTCAGTCTGGAGTAAAGGATGCAATCACG/JGJCTCACTGTAGCCTGGACCTCC TGGGTTCAAGTGATCCTTCCACCTCAGCCAACTGAGTAGCTGGCCTGGAGGACAAGTCAACCATGCCTA CCTAAGTTTTGTAGAGACAG
stSG3416 a	43 A G ---			GTAAGACAAAGTTTTGCTATGTTGACCAGGCTGGTCTTGAACCTCCTTGGCTTCAAGCGACCGTACCA CCTTGGCCTCCCAAGTTGCTGATATTACAGGTGTAGCCACTGCCCCCGCCGACTTTTAAACTGAAT GTTGAAATCATCTGCTCTTGTCTGGTAACTGA/JCAAAGTTGCTTAACCTTTGTGAAACCAC TTTCCCTTATCTGTACAAAATGGACAAACAGAACTTTTCCCTTCCCTC
stSG3424	173 T A ---			GTTTCATGTTAAAGATTAGGAAGCTGTGGATGTGAGGGGTGAGGTGATGTGAGGGCCTCACAGA ATGAGTGGCAGAGAGGGGCCCTT/AJGAAATAGCTTACTCTGTTTTCCTATC
stSG3436	88 T A ---			

stSG3463	103	C T ---	---	GATACAGAAGATAGTGGTATGGATGGATAGTGAAGGACAAATAATACAAATATATTTTATTG AAATAAACAAATAATGCATACACAGCTCAATGGGTAC[C]/TJTGGAACAAACTTGCTTGACTATATTA CTGA
stSG3491	71	G A ---	---	CAAGATACTTCATTGTCTCTAAGTAGTGCAGTCTGGGCAATATTTCTCAGCAACAAGGACGATTG AAGA[G/A]GTGGAATTACTGTGCAAGGAGTACTTTACCTCCAAATAGCCTGCAATTTAGCAGTCTGA ACAATCTTCTAATCTTTACTGGCACCTGTGGATTCTATTAACACTCATTTATACTATTTTCTGTGATG ACAGAAATAAGTTAAC
stSG3523	33	C T ---	---	TAGCCATCTTACTCTAGTTCTTTTGGGTTT[A]/C/TJGCATATATGTGTGTACAAACACACACACACC CCTAATTCCTCAATGCTCTTGGCATAAGTTTATCTCTTACTGGTCTC
stSG3536	213	A G ---	---	AGTACAAACACAGATTTAAAGAGCTCAGCAGTATTGACACGCTGGAAATTAATGGAGACATCCACTT ACTGGAAGTAAGGAGCTGGTAGCCTACCTACAGCTGCTACAAACCCAAATACAGAATGGCTTC TGTGATACTGGCCTTGCTGAAACGCACTCCTACTGTCATTCTATTGTTTATATTGTTAAATGAGCTTG TGCACCATTA[G/A]/GTTCTGCTGGGTGTTCTCAGTCTTGCCATGAAGTATG
stSG3583	112	G A ---	---	GAAAAAGCTTAACATACGATCCATGTGCAACCCCAACAGGATCTACGAACCTCTGGCATGATCCA CATCGTACACATACCATGCTGGAAGTGCACATCCACACAGGCAC[G/A]TAACATACACAGTACTGT CTAGTTATCAACACCTAC
stSG3586	60	G C ---	---	CCTAGTAACATAGTGAGACCTCGTCTCTACTAAAAATTTAAAAATCAGGTGGTGGTG[G/C]ACG CCTGTAGTCCCTACTTGGGAGGCTGAAGTAGGAGTGTGCTTGAACCCAGGAGATGGAGGCTACAGT GAGTTATGATGGGCCATTGCACTCCAGCTTGAGACTGTTTCAAAA
stSG3589	101	T C ---	---	ATATAGTGTGGTAGCATTATAAACTCCTTTAAAAAGCAATCTGGCCATATCAAAAGGCAAAAAAGT GTATATACCACCTGGCACAAAAACCCCAATGA[T/C]CCTATTTCCAAGAATGTATCCAGATGAAA GTATCCAACAACAAAAAGCTATATACAC
stSG3590	70	A T ---	---	GAGAGATGAGCTATTTATCTTTTACTTAAAGAAGTGAAGAAATGATCTTCTGTTCTAAAAAAA AAA[A/T]TCTCTGATGCTCTTGACCTGTAGGAACACATTCAGTTTCTACACT
stSG3619	78	A C ---	---	CAGTGAGACTTCTCATTTTATAGCAATACATTTTGCAGCTTAAATTTCTTGAATTCATACGCT TCTGTCAATTT[A/C]AACAACTCCAGAGAAAACTGGGCTCTATATATTTAAG
stSG3644	40	T C ---	---	ACATATGTAAGTCCATTAGTAGCCATATTAGGATGAGAT[C/G]GATTGAGAGGCATGAACCAAGG ATGCGTAATAATCAATTATGAATAATAAGTTATCTGGGGAACGGCCATTTGTCCAACATTTACTAA GTGCTCTACTA
stSG3646	70	G A ---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATGATGATAACAATAATATGTCTTACT GGT[G/A]ATATTAACTTTGATACCTTGGTTAAGATGGTGTCTGCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA

stSG3646 b	55 A G ---	---	CTCATAATTAGATTGAGATTGTCATTTGGCAAGAATATATGATGATAACAATA/GJ/TATGTCTT ACTGGTGATATTAACTTTGATACTTGGTTAAGATGGTGTCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3646 a	43 A T ---	---	CTCATAATTAGATTGAGATTGTCATTTGGCAAGAATATATG/JT/GATAACAATAATATGTCTT ACTGGTGATATTAACTTTGATACTTGGTTAAGATGGTGTCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3693 b	85 A C ---	---	ATTGTTTCCCTGAACATTCCTGGTGTCTCCCTCTGAAAGCCGATGACCATCCAAACCCTGGACTCACCT GAAATATCTACGAGGC/JCTCGCCCTCCGAGACTGACGATTATTAAACCCACACGGAAGG
stSG3693 a	30 C T ---	---	ATTGTTTCCCTGAACATTCCTGGTGTCTCC/JT/CTGAAAGCCGATGACCATCCAAACCCTGGACTCA CCTGAAATATCTACGAGGCATCGCCCTCCGAGACTGACGATTATTAAACCCACACGGAAGG
stSG3698 b	145 G A ---	---	TCTTGCCCTTTGTGTACCCCTAGAGAGATGGCACCCCAATCCCAAGGTTGCTCTCTGACTTCCACCAT TCACTGACTTTTATTGCCAGAGGAGCTCCCAAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTAAGTCT TTATTGGG/GAJA/GAATACCCACCCACCTTCCCTCACTGCAGA
stSG3698 a	51 C G ---	---	TCTTGCCCTTTGTGTACCCCTAGAGAGATGGCACCCCAATCCCAAGGTTG/JT/CTCTGACTTCCA CCATTCACTGACTTTTATTGCCAGAGAGCTCCCAAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTA AGTCTTTATTGGGGAGATAACCCACCCACCTTCCCTCACTGCAGA
stSG3724	107 C T ---	---	ACCAGCCTCATGTGCAGAGGGTCTCTGCTGGATCCCAACTGGAGCCATCCCTGGGCCCTAGACTTCT GTCTCCCTCACTTCTAAATGAGTGTCTCAGTGATGTGAAG/JT/JACACAGGAGTCCCTCAGGGCAAAA GTGGCTATGCTGGTGCT
stSG3725	104 G A ---	---	GCCAAAACAAAAGATCTTTGGAGTTTACTGACGGCAGCAGTTAATAGCACAGTCAACAGCATTTAA ATCAAAATATATTATACCAGCCCAACAGCAACAGCCCC/GAJ/AGCAGGAATCGGCACATAGTCATAA ATAACATCAGGGTAAATAACGGCACATTTA
stSG3751	128 G A ---	---	CGGAAGAAAGAAACACAATCCACAGGAACAATCTATGTTTCATACCTTTTGAAGAAGATGATTTTG AGGGCTTCAGTATTTAAAGGGGAAAGCAGGCTGGAGGGGAAAGAGAGAGGATATGGTCCC/GAJ/JT GCTGACTCCATGTGTTGCAAGAG
stSG3787	49 T A ---	---	TTCTGTGCAAAAGAAATCCACATCATTTGTTGGTAGCAGAGGATCTTAT/JA/AAAGTTCCCTAAGA CACTGAGGGCATAAACCAACAAAATAAAATAAGGAGTGTAGGCTAAAGCAGTATCTTCCCT
stSG3880 b	115 G C ---	---	GACAAGAGGAAGAGATGCGCCAGAGAACAGGGCTGGGCAGCTGGGGTCCCTGAGTGCCAGGGCG CACCACAGTCTCTGTGGGTCAAGGCCCTCTCTGGGGAGCAGGCTA/GC/JG/CACGGAGGATGCAG GGCTGGAGGGGACCCACCTCGGGGACCCAAAGGAGTCCATTTCTGCCCT

siSG3880 a	36 G C ---			GACAAGAGGGAAGAGATGCGCCAGAGACCAGGGCTG[C]GCGCAGCTGGGGTCCCTGAGTGCCAGG CGCCACCACACGTCCTGTGGGTCAAGGCCCCCTCTCTGGGAGCAGGTAGGGCAGGGAGGATGCAG GGCTGGAGGGGACCCACCTCGGGGACCCAAAAGGAGTCCATTTCTGCCCT
siSG3895	44 A G ---			AATCAGCCATTGTACACATTGCAGCTATGTATTGTAGTGTGT[G]G/TTTTTTTTCCATTAACTAA TACATGCCCTCATAGATATATTCAATTAGTGTATCACCATTGGAACAAGATGCTGATTGTCAACTG AAAAT
siSG3902	104 T C ---			TCGTGTGAGACTGGAGAGACCAGGTACCAAGCACCCGACTCTGGTGGAACTGGCTTCCTGATAACA TCATCTATTTACCTAAATGTGAACCTGCTTCTTTCTG[C]TCAGCTCAATAGCTTAACATCTAATTC ATGTTTGTCTCCCTTGTCTGGACAAT
siSG3935	50 G A ---			GGGTGTCTGACGGACAGGCACCCAGCAGTTTCAACAAGCAATTTGTCC[G/A]CTAGTGTGCAGGC TCCTCCCCAGTTTCCACAGGCTGAGTACTATGGGGTCACAACCTTCCTGGACGT
siSG40	25 A G ---			GAGGAAGAGGTTGAAGAAGTGTGA[G/G]AAATATATTTAAGATTTCCTTGGGGAGAAATCTCGTGC CCAAACCTGGTGATGGATCCCTTACTATTTAGAATAAGGAACAAAATAAACCCCTTGTGTATGTATCA CCCAA
siSG4009	32 A G ---			GTGTGGGCTGTCTGATGATGAATGGCGCGCTC[G]G/TACTCTTTACGGTCTTACACTTTTATGCTCCT ATGAATCTCTGATGGCTTTAAGGGCTGAACCATATCTGAAGGTTTTCCTCACACTGCTTACA
siSG4033	123 T C ---			AGAAAGCTTGGGACAATGGCAGTGCCCTTTCTGAGTAGACATGAATGCCATCTGGAGGATCCATT TGAACCTACAGTGCAGTAACCAAGAACCTAATGTTTTCAAGCATAAAGGTACTTT[C]TGTGAAC AGGTGGGCAACAC
siSG4038 a	29 G A ---			GCTGAGAGCACGTGTACAGCCACGCCCTGT[G/A]JCGCAGGCCACTCTGTGCAATAAACATGTTCTGCC CATGTTCTCAGTCAGGAGGTTTCAGGCTCCCGGAGAGCACCTGAGGGTCCATCACT
siSG406	53 T C ---			ACTGTGGTTCAACAGTATTGCGTTGTGACACTAGGAAAGCTAAACGAACAAAAT[C]GGTTTTAGTT TTGCTGAAGACTGGCCTTATTAATGGACAGCTTTCCTAACAAGAGATTATTAACTTTTATCAGGTGTT AACATCTGTTTCAGGAACATGGCA
siSG4095 b	55 G T ---			ATCTGGGCTGAATTAGTCAAGCAGGTCAGATACTATTGCTGCTAGATGTATTAG[G/T]ATAAAAA GTTTGCTTCTGTAATACCTTTAAAGCTTGCTTATCTCATCTGTAACCTATGTCTTGAGAATCAAG CCTTTGGACTAACCCAGGGCATTGCCCTTCATCCTGG
siSG4095 a	27 A C ---			ATCTGGGCTGAATTAGTCAAGCAGGTC[C]GATACTATTGCTGCTAGATGTATTAGGATAAAAA GTTTGCTTCTGTAATACCTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTCTTGAGAATCAAG CCTTTGGACTAACCCAGGGCATTGCCCTTCATCCTGG
siSG4120	65 G A ---			TGCATGTTCCACATCTTTTCAACAGCAAAATGTAATAATAAACCTACGTACTTATGGATAATCAC[G/ A]CTTTTTCCCTCAGAGAGCCACAGTTAAACAGTTCCAGCACACCACTTAATCCACCGAGCT

stSG4128	54	A G ---			---	CTTGGCAGATAAGGGACTCGTTTGCAGATATGACTTTCCTTTGTGTACATTCTTGA/GTATATTT TACTTCTTGAAATGCCACATAAATTTGCAATAAATGATTCACTCCTTAGCTCCAAAAGCAAGTCC TTATCAAAATGCAAATGTTCCAGAGGG
stSG4209 b	128	G A ---			---	CACGAAACAGATGCAGCCTACACAGTCTGTAGGACCGAGGCTCACAACATCCACATGGCACAAAG AGGCCGGCCACTCCAGGCAACGAAAGCCACCCCGAACCTTGCAGAGGCCGCACTCCCTC[G/A]GC AGGGGACCACGGAGCGACAGGTGCTTTGATGCCCTCGAAGAGCTGAGCTCCATTCCA
stSG4209 a	65	G A ---			---	CACGAAACAGATGCAGCCTACACAGTCTGTAGGACCGAGGCTCACAACATCCACATGGCACAA[G /A]CAGGCCGGCCACTCCAGGCAACGAAAGCCACCCCGAACCTTGCAGAGGCCGCACTCCCTCGCG AGGGGACCACGGAGCGACAGGTGCTTTGATGCCCTCGAAGAGCTGAGCTCCATTCCA
stSG4254 b	31	G A ---			---	CATTACCCAGAACGCCATGGAGGACAGAGC[G/A]CCACGCCCGGAGCTCCCGCATGGCTGGGGGG GCTATGGCTCTGACAAGAGGATGAGCGAGGGCGGGGGTGCCTCCTCCCCCAGGGGCAGACGTGAC TGGGGGACCATGGCCGAAGAGAGGATGACCGGTGATG
stSG4301	81	T G ---			---	TGCAACAGCTCTGAGAGGAAATCCTTGGCAGATCAAAAGAGAGGGTAGTGGCTCCACACTTCCCAT TTAAGCAAATAAATT/GIAGCTTCTGAGTAGTTGTCCAGTTTCAACCAACATTTTG
stSG4331 b	71	T G ---			---	CTCACAAGGCCAACACAGAAAAAGATACAAATACATTCATCCAGCTAATATTTAGTTTTATGACAC AGAGT/GTTTTCAAACAAGTTTAAGTGTACCTGAAGAGCATGTTAAAAAGTTTAAGTTATCATT GGAGACAGATTCTTGGCTCGCCCTTGTGATTCGTGTTGAGGGGTGTC
stSG4340	76	G A ---			---	TTTTGCAACAACATGGATGGACCTGGAGGCCATTAAAGTGAAGTAATGATACAGAAAAGTCAAAAACC ACATGTTCT[G/A]TAAGTGGGAGATAAACAAATGTGTACACCTGGACGTGGAGAGCAGAA
stSG4361 b	109	A C ---			---	TTCCCAACCATTAGTGACAGAGCTCAGTCATGACAGAACTCAGGTTTGCATGACTCAAATTAGGCAC AAGTCTTGAAATTTCCATAAGGGATAACTGCATCTTTTG[C/A]CCTTCACAACCTAGAAAACGACTO AGCGACTTTTCTGTGAGCAAATGTCGAGG
stSG4361 a	24	T C ---			---	TTCCCAACCATTAGTGACAGAGCT/C]CAGTCATGCAGAACTCAGGTTTGCATGACTCAAATTAGG CACAAATCTTGAAATTTCCATAAGGGATAACTGCATCTTTTGACCTTCACAACCTAGAAAACGACTO AGCGACTTTTCTGTGAGCAAATGTCGAGG
stSG4376	73	A G ---			---	TTTCACTGCTACTGGTTTCGGTGTCTGAGTCCTCAAACCTGCTTTGCAAGTGCCTCTCCAAGGGGAG AACAG[G/CT]GGAACCTCGGGCTCTGCAAGAGCCATTCTTTCCAAAGCCATTCTCTCTCAGCTGC
stSG4381	50	T C ---			---	GAAGGCCACAAACACTCCATAGCCAGAGAATGACAACATACGATTTCTTT/C]TCAGTCTTGAGT ATCCACAGTAGTGATGCTGTCCATGTACAAGTGTCTGTCCAGAACCCCATTAATTCATGCC
stSG4410	79	A G ---			---	ACCAATGGTTCTGCTATGTGATCCGATATTTTGGCCGATCTGAAATACTGCAAGGGCTTAACCAT TCAACACCCG[A/G]TGACAACGAAACCCAGTGGACTGTGAAACTCAGGCTGCAGGAGGGGTGCTGT CAGCTGGGT

stSG443	65 C T ---	---	AGCAGATCAGTCAGCCACTTGCTCTCTCTCTTTAGGGAGAGGCTAGGCAGTGAACACATCA/C/
stSG4430	54 A G ---	---	TGTATGCAATGAGAAATAACCAACTGGTAGGATGGGGAGGGGAGGAGGAGGGAATAGGCAC
a			AAATGGAATCTATCCTGGCTGCTCTCTCAGGTC
stSG4448	99 G A ---	---	ATGCACATTAATGAATGGCTTAACCTACTGGAACTTTAGTAGTCTTAAGGTJA/GJATTAAACATA
			GGTAGGATCCAGTTCTATGACAGGCTGCTGAAGGAACAGATATAGGCATCAAGAGGGCCATTTT
			CCTCCCTTCCCTTCCCTTCCCTTCCAGTCTTTCCATACTGTTCCCTCCCTCCCTCCCTCCCTCT
			CGCCTAGCCCTGCCCTCTGGGGTCACTGC/G/ATJGGGTTAGGCCCCCAAAAA
stSG4449	92 T C ---	---	ATTAGCCATTGATCTTGAACAATTGCTTTACTGTAACTAAGAGTACTGTACTGATGATGTTTACAAT
			TAACCTTTGGACAACITTAACCTTA/T/CJTAGTGACATTTGCTGTCTAATAATCAAAATACCTCATCATA
			GGCTGAACATAATTATTAAAGAGCAAAAGTTACCCCTCCC
			CAGACATGAGGGATGCCCTGTCTCTCTGGGACAGAGCCCTCA/CJAGATGATGTCCATGTTTGTGT
stSG4467	42 C A ---	---	GAATGAACTCAACACTCTTCAGTTTTAGATCATTTTCTGGTATCGAGCGCACACCGAGGAG
			CACACCTGCTTCCAAGGCTGCTGCCCTCTGCACACAGT
stSG4475	21 A C ---	---	ACATGTCAATTCCTGACCAGG/A/CJATTAAATAGTTTATTAGAAGAAATGAGTTGAAGTGAGCGGA
			TAAAGAGACACAAACTGGACTTTTGTTTTCTTTTACTGTAGCACCCAGGTTTCATG
			GTAACATCTGGGGTGGGGTGAGACAACAACA/JGJATGAACCAATAATTAATTACAATTATACATTT
			TCAAGGAGACTTTTAATCTAGGTTAATGTAACGACGACCATCAATGTTTGTGAGGAAAAGGAGGA
stSG4477	32 A G ---	---	TGAAGTCTGCTCTGGGCAACGTTTGGCCCTCATTCAGTCAGACTTGGC
			TGAACCTAGAGCTGGTGGGAGCTGCAGGCGGGGAGGCTGGGGCCAGATGAGCGCGCGGGA
			CAGCAGCGTCG/CJGCCACGTCCTGGCGTTGGTAGAAGAGGACATAGGCTGCTTGGACTCGATCT
stSG4531	79 C T ---	---	GATTCATTTGACAGGGGAGACGCTGTGTCATCAA
stSG4550	86 G A ---	---	TGCATTAAAGGAATGATACGGCATATTTGGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT
b			AAAAGAGACAGTGGGCACC/CJCAATTGGAGGGGAAGCGGGGCGAGGGTTTTAGAGAAC
stSG4550	85 C G ---	---	TGCATTAAAGGAATGATACGGCATATTTGGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT
a			AAAAGAGACAGTGGGCACC/CJGCAATTGGAGGGGAAGCGGGGCGAGGGTTTTAGAGAAC
stSG4590	47 A G ---	---	AATCAGGCACAAGCTCGGGAGAGAGCCCAACAAAGCTCTTCGCAC/JGJATGGGAGGGAGACAC
			CATTGAAAAGGCATGCTCTCTTCATGCAAGCGAGGCGCTGGCTCCACAGGCATGGTCTCCTTG
			AATCTGTATCACCCAGCGTGG/JCJCAATGTACTAGTACTTCCACAGGGAATTTTTATACTATTC
			CTATAAGGTTTTATCATGAATAAAAAGCTCACAACCTTTTCAGCCATTGCAGATTCACATTTATCT
stSG4623	22 T C ---	---	TAATATTCCTGTTCAAGATGCTCTGGAG
			TAAAAAAAACAACCCCCCAAAAAACACCCAGAAGTTTTGAGTTTTATGTTTTTTCAGATTTAAAG
stSG4843	102 A C ---	---	GTATTTCTTTCTTAGCTCTCTAAATTTTGGATCAT/JCJATCAGAAAAGCTTCCCTACTCCAAAGGTGA
			GAAAGGA







stSG8145	97	CT	---			TTGTGGACTTCAAATCTTTCCCTCAGATTTTAAATGACATTATGCATGTACATATTTTAAATTT AGACACATTTAGAGAACAAATTTGTGAA[C/T]ACAAATCTAAGAAATGAATGAGATGTTCTGAAA TCTGATCAAACACTTATCTTAACTGACTCTGTCAATCCTCTGCTGTGAAGG
stSG8150	36	AG	---			ATTGTTCTTGCAATTGCTTGGATTTTTCAGAAATAGTGA/GATATAATAAATACGGGAATCCTAGGCAT TCGTGTTTCTATGTTTTTAACAGGATTTCTCTAATGTTTCGCTATTAAATACCATGCAGGAAATT GGGAAAT
stSG8340	30	CT	---			AGAGGATTATGGAGAGAGCTGGGCAGGATC/TCAACATTATGACCCCTGAACCTCCAGAACTGGAT TCACTAGAAGGAGAGAGAGAAAAACGCTCATCAAAA
stSG8466	111	GA	---			TGTGATTGGGTGACTGTAGCCTAAGGATAAATGAAATAAATGACAGCAATGTTTATAAGCAGTGGGA GGAGTGAACCTGGGAATACTTGGTTACAAGGTATTTGCACTACCT[G/A]TGAAGCAGCACAGCATTAT TTGAAAG
ESTD-ACE	--	--	---			GATCAAGCAGTGCACACGGTACGATGGACCAGCTCTCCACAGTGCACCATGAGATGGGCATATA CAGTACTACCTGCAGTACAAGGATCTGCCCCGTCTCCCTGGTGGGGGCCAACCCCGCTTCCATGA GGCCATTGGGACGTGCTGGCGCTCTCGGTCTCCACTCTGAACATCTGCACAAAAATCGGCCTGC
ESTD-ADA	--	--	---			ACCATCTTACTATGGCAGGTAACTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGGCCCTGGGGAATCCAGGGTCACTGTCTCTCTCTGCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAACTGGGACTGTGAGGACATGGAGGCTCGGCACTGAGCTGCAGACCC GCAGACCAACTCCTGAGCTTCTGGGCCCTGAGTCTTGCTCTC
ESTD-AK-168	--	--	---			GGGAGTGACAGCTAGAGCACCAAGGGGGGCTCTACAGCTGTGTTCTCATGGAGGACAGGCTTCTGCTC ATTCTGG
ESTD-ALB	--	--	---			AATCCCAGCACITTTAGGAGGCTGAGGCAGGCATATACACAGAGGTGAGGATTTGAGACCAGTCTGA CCAAATGGTGAAACCCCATCTCTACTATAAAATACAAAATTAGCCAGGATGGTGGTGCATGCCTGT AATCCCAGGAGGCTGAGGCAGGAGAAATCGCTTGAACCTGGGAGCGAAGTTGTGGTGAGCCGAGAT GGCACCAITGCACCTCCAGCCTGGGCAACAAGAGTAAACTCTGCTCTC
ESTD-ANT1	--	--	---			TCCTCTGTCAATTCCTACTOCAATTAGTTCAAAGGTCAAGTGAAGAACTGGGGCAATTAACCAAGTAATCA TGGACTGCCCAACTCGGAAACAAGAGGGCGCAGTGGAGCAGGAGTATTATGCTACGCGGTACCTCTT TTTTATGGAGGACCGAACTGAGGCTGAGCTCAGATGATCCTGT
ESTD-APOA2	--	--	---			CCAGGTGTTGTGGCAGTGCCTGTAATCCAGCTACTCGGGAGACTGAGGCATGAGAAATCTTTTGAAC CGGGAGGGCGGAGTTGCAGTGAGCTGACATCGCGCACCTGCACCTCCAGCTAGGTGACAGAGCAAG ACTCC
ESTD-ARS3	--	--	---			GGAAGAAATGGAGCCTGTGGAAAGGAGCGGTCCGAGGGGTGGGCTTTGTGGCAAGCCCTTGCTGA AGCAGAAGGGCGTGAAGAACCGGGAGCTCATCCACATCTCTGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTTCGACGTGTGGAAAAACCATCAGTGAA GGAAGCCCATCCCCAGAAATTGAGCTGCTGCATAATATTGACCCCAAC

[illegible]

ESTD-C7	--	--	--	---	---	---	ATATCGTGGCCTTAGTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD-CB22	--	--	--	---	---	---	GGCAAGTTTTATTGATAGAGAGGAAATCAAATAATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGATGGACAGACAATGGCAGTGCACCAATAGGGCGGATACAAAGAC AGGCAAGGAAGGGTAGAACCATCAAAGAGGAATAGGCTGGTGAACCCAAAGGAAGGAGACCTAG TAACATAATTGTGCTTCATTATGGTCTCTTCCCGGCTTCTCTCACACAC
ESTD-CB23	--	--	--	---	---	---	TAGAACCATCAAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCAATTATGGTCTTCCCGGCTTCTCTCACACATACACAGAGCCCTACCAGGACCAGACAGCT CTCAGAGCAACCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAAAAACGTGTTCCACCCGA GGTGGCTGTGTTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAA
ESTD-CB24	--	--	--	---	---	---	ACCAGGACCAGACAGCTCTCAGAGCAACCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAA AAACGTGTTCCACACCGAGGTGCTGTTTGGAGCATCAGAAGCAGAGATCTCCACACCCAAAAAG GCCACACTGGTATGCTGGCCACAGGCTTCTACCCGACCACTGGAGCTGAGTGGTGGTGAATGG GAAGGAGGTGCACAGTGGGTGACAGACAGACCCGACGCCCTCAAGGAG
ESTD-CB25	--	--	--	---	---	---	GTTTTCTTTCAGACTGTGGCTTCACTCCGGTAAGTGAGTCTCTCTTCTCTCTATCTTTCGCCGTG TCTGCTCTCGAACAGGGCATGGAGATCCACGGACACAGGGCGTGAGGGAGGCCAGAGCACTG TGCACAGGTACCTACATGCTCTGTTCTTGTCACAGAGTCTTACCAGCAAGGGTCTGTCTGCCAOC ATCCTCTATGAGATCTTGCTAGGGAAGGCCACCTTGATGCCGTG
ESTD-CB27	--	--	--	---	---	---	TTTTCTGTTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT TGTTGTTGGGCTGGTTGCATTCAGGAGTGCTGTGGAGTTCGTGCTCATCACTGACCTATCTCTGA TTTAGGGAAGCAGCATTCCTTGGACATCTGAAGTGACAGCCCTCTTCTCTCCACCAATGCTGCT TTCTCCTGTTCACTGATGGAAGTCTCAACACCATTTCCATACC
ESTD-COL2A1c	--	--	--	---	---	---	AGAAATGTATATAGTCTCAAACTGGCCATCTCCATTTTCAAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTATGCTCTCTTCCCTGTCATTTCAAGGTGTTCAAGGTGGAAAAGGT GAACAGGGTCCCGCTGGTCTCCAGGCTTCCAGGTAAGTCAACTCAAGCATATACAATACTGCCTTTG GTCAGCCCTATTGAGCTGTAATCACCATAACCGTACCT
ESTD-COL2A1d	--	--	--	---	---	---	TGAGAGAACACCTAGTCTCCATCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGCTGGGACCTGGAACACTGGACTTCTTCTACTGCAGCAGACAAGACTTACCC AAGAGAGATTAAATGGCAAGATATACAATATTTTATTGACCAAAACACTATCATGGAACAGC ATT
ESTD-CPT2	--	--	--	---	---	---	GCCGCAATGCCCGGGAGTTTCTCCAATGTGTGGAGAGGCCCTTAGAAGACATGTTTGTATGCCTTAGAA GGCAAAATCCATCAAAGTTAACTTCTGGGAGATGAAAGCTACCATCACTTCTCATCATGAAAC TGGGAGGCCGGGCATAGTCTCATGCCTGTATCCAGCATTTTGAGAGGCTGAGGGGGTGGATCAC TTGAGGTCAGGAGTTTGAGACCAACCTGGCCAACAT

ESTD- CTLA-4	--	--	---	---	ATGGCTTGCCCTTGGAATTCAGCGGCAAGGCTCAGCTGAACCTGGCTACAGGACCTGGCCCTGCAC TCTCCTGTTTTCTTCTCTTCATCCCTGCTTCTGCAAGCAATGCACGTGGCCAGCCTGCTGTGGT ACTGGCCAGCAGCCGAGGCATGCCAGCTTGIGTGAGTATGCATCTCCAGGCAAGCCAC
ESTD- CYP2D6	--	--	---	---	CAGGCCAGCGTGGTCGAGGTGGTCAACCATCCGGCAGAGAACAGGTCAGCCACCACTATGCACAGGT TCTCATCATTTGAAGCTGCTCTCAGGGTTCCCTTGGCCTGAGCAGGGCCGAGAGCATACTCGG
ESTD- D11S1873	--	--	---	---	AAAAAACATTTTAACACCCTTTCAATCATATACACCAATAAATTTCCATTTTTCACATAAGTCAGTT TGAGCTGAGTTTTCCAATTACTTGCAATCTAAATGTCTAACTGATTAAATGCAAGTTCAACAGACA ACTTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATATGCCCATAT CTGCATGTC
ESTD- D17S33	--	--	---	---	CATCCCAAGCCCATCTCTTAGCCACTGGCAATTTTTGCCGCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACATCCAGGGGGCCCTACCTTTGATGCCATGGAAAGGCTCCTCTGGGGCCGTG GGGTTGTGGCTATGTGGTCTTTGTGTAGACGGGGCTTTGGTTTCAGTTGCACATTGCGTTATT GCAGATTGCTTTGTCTTCCACCTGAGCGAGCCCTC
ESTD- D18S8	--	--	---	---	TTTGAGACCACCCCTGGCCAAACATGGCGAATCACATCTACCAAAATACAAAAATTAGCTGGGTGT GGTGGTACATGCCATCTGTAATCCAGCTACATCGGAGGCTGAGCAGGAGAAATTGCTTGAACCCA GGAGCGAGAGCTTGCAGTGAGCCCAAGATCACACCACCTGCACCTACAGCCTGGGTGACACAGTGGAGA CTCTGTCTCAA
ESTD- D3S11	--	--	---	---	AACTGATTAGAACCTGAAATACATATTTTATCTGAAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCATTAATAAATCCAAATAAGTACACTGTAATAAGAAATTTAACAGAAATATCATTTGT TTATTCAAACTATTTATCATTATTTTATTGGTAAGCCATACTAAATCTAAAGCATGTTTCTGAAAG TTTTA
ESTD- D3S12	--	--	---	---	AGGTTCCACATTATTGCTGATGTTTGTGATGTTTCCAGGAGCCTTGATGTCACTCTGTATCTCCTCAG GTATCCCACCTTGAGACGTACTTTTCAAAAACCTCTCTACAGCCGTTGTTGTTATTAATTCAGGTTGA ACATAAAGTA
ESTD- D3S2	--	--	---	---	GATCATGTGGCCCCAAGTGGCAGAGCTACTTATACCATGCCAGACCTGCTAGCAGAACATTTCTCTGC TGAGTCTTATTCAAAACTGACAGCCATTATGCCACCTGAAATATGGTCAGGTTACAGCTGATTTCCC AGAAGTGAACATACTGCTCTAGAACGCCAGAGCTACTGGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAATAATAATAATCTGTCTCTTTATTGGAAGGATGCCGGTATGT
ESTD- D4S338	--	--	---	---	TTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATATGAAATGTATTT CTTAAACAAATAAECTTGAAGTCCAAAAATTACTCCTTGATCCATGGACTGCAGAAATAAATGTTATTT TAGCTGTCAGAAAAACAATACTAATCTTGCAATATGTTTCATCAGAGCCCTTGGGTGACCAGGTGTTT GCCAATAAGCAGTAATATTTGAGAGGAATCTTGTTTTCAATGCAGTAG
ESTD- D4S95	--	--	---	---	CTTTTCATGCACGATAGGCTTCTCTACTAATCACAGAAATTTTGAGAAGAGCAAAACAACTTTCAAGG ATAATGGGCAATCATTCTTTCTCTTTAGAGTCTACCGG

ESTD- D7S399	--	--	--	---	---	TGAATCTTAATTGCTATCTCTACAAAATGTATAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCAGTCTCCTACATCATCCTTTACAAACATTTTCATCCATGGACTCCATACCTAG AATATTTGAAGAAACAACATGACAAACATTTTC
ESTD-DM	--	--	--	---	---	GTGGGACACCCGAGGGCTCCAGGCTGGGCTTGACAGTGTGGCTCAAGCAGCTGCTGGCTCCACT TCCATGGGTGTGGGCTGGGACTCACTGTCTGGGAGAGAGGAGGTGGGAGGGAGACA GAATGCTGATTATCTGGTGAGAACCAAGAACTTTCTGGCTGTGGTGGGAGGAGCTGCTTCCAGACC TCTGATTTGAGGAAGGGAGCAGCAGAGCGAAGAGAACAGAT
ESTD- DRD1	--	--	--	---	---	TCCCAGCCCTATCGGTCAATTTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAAACCATCAC ACAAAACGGTCAGCACCCCAACCTGAACCTCGCAGATGAATCCTGCCACACATGCTCATCCCAAAAGCT AGAGGAGATTGCTCTGGGCTCGCTATTAAAGAACTAAGGTAC
ESTD- DRD2	--	--	--	---	---	TCTGCTTTGTGACAGAGGCTGCCGGCAGAGCCAGGAGTGGAGTGGATGCTCTCCAGCACCA GCCAACCGAGAGACCCGGTACAGCCCATCCACCCAGCCACCACTGACTCTCCCGGACCCG TCCACCAAGGCTCTCCAGCACTCCCGACAGCCCGCCCAACCCAGAGAGAATGGGCATGCCAAAG ACCAACCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	--	--	--	---	---	AAGACGATGGCCAGGATGAGCGCGCAGTAGGAGAGGGGCATAGTAGCATGTGGCGGGCTGGCTGG CACCTGTGGAGTTCTCTGCCACACAGGTGTAGTTTCAGGTGGCACTCAGCTGGCTCAGAGATGCCATA GCCAGAGGGAGGTGGTGATGCCAAGGGCTTCTGTGAGGAGA
ESTD- ERB82	--	--	--	---	---	TCTTCAGGATCCGATCTGCGCTGTGGCTGCTCCGCTAGGTGTCAGCGGCTCCACAGCTGG GGTAGGGGGTGGTGGTCACTGCCGGGGCCGGTGCAGACCCACCGGGCTGGGAGGACTTCAOCC CGCCTCACTCCGTTTCTGACGAGTCTCCGCTATCGTACT
ESTD- ETS2	--	--	--	---	---	ACTCACAGTCTTTAAGTGAAATGGTCGAGAAAGAGGACCCAGGAAGCCGCTCCTGGCGCCTGGCA GTCCGTGGGACGGATGTTCTGGCTGTTTGAGATCTCAAGGAGCGAGCATGCTGTGGACACACAC AGACTATTTTAGATTTCTTTGCTTTTGCCTTTTGCACCCAGGAACAGCAATGCAAAAACCTCTTTGAGAGG GTAGGAGGTGGGAAGGAACAACCATGTCATTTCAGAAAGTTAGTTG
ESTD-F2	--	--	--	---	---	GATAAGTACACTGAGGCCCCAGGAGGTTATTGCCCTAGTAGCCCAACTGTGTCATGCACGCTTAACCTCT GCACCAATGGCTCCAGGCCCGTAGGGGAACCTGGGGATCTAGGGATGGGTGAGGAATGGCC AGCCAGTCCCGGGCTGCTGGTCCCAACAGAGGAGGCCGTGGAGGAGGAGACAGGAGATGGGC TGGATGAG
ESTD-F9	--	--	--	---	---	AGATCCTGATGATTTTTTCTCTATTTTTTCTAAATGTTTTACAGTTTGAAGTTTAGATTTATGCCCCA TGCTCCATTTGAGTTAATATTTGTGTAAGATGATGTTTAACTCAAACTCATTTTTTTTCCATA GGTATGTCCAAATTTATCCAGCACAAATTTGTTAAACAAAAAC

ESTD- G2H	--	--	--	---	---	---	CGCAGACCGGTAGTGGGGTGGGAGTGTGAGGGAAGGAGGAGAACTGGGGTTTAGGGACT TTCCGGGTGACTTTCCCGTTCTGTGCTTGCAGAGAAAGCGGGAGAACACAGAGCCAACTGGCTAA GTGTAAGGGACCTCTGGTGCACCGTGTCTGCTGCCCTGTTCAGCTGTCTGCTGCCGACGTGGA CTCTGTCCCGGAAATTCGAGAGCT
ESTD-GCK	--	--	--	---	---	---	GTTTTATGATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCCTGGTCACCATGAC AACCACAGGCCCTCTCAGGAACACAGTAAGCCCTGGCAGGAGAAATCCCCACCCACACCTGGCTGG AGCAGGAATGCCAGCGGCCCTGAGCCCCAGGGAAGCAGGCTAGGATGTGAGAGACACAGTCACC TGCAGCCTAATTACTCAAAGCTGTCCCCAGGTCACAG
ESTD- GNAT2	--	--	--	---	---	---	GACCTGAGTACCTCCCTAGTGAGCAAGATGTCTCCGATCCAGGGTCAAAACCACAGGCATCATTG AAACCAAGTTTTCCGTCAAAGACTTGAATTCAGGTAAGTCATGGTTCCTAGG
ESTD- GPPK2L	--	--	--	---	---	---	AGTCTTCATCTGCGGTGCCAGGTAGATCCCTTTCACGCCGAGAACTGCTCGATATC
ESTD- HRAS	--	--	--	---	---	---	CTGGGCTGCCCCGAGCAGCTGCTGGCACCTGGACGGCGGCCAGGCTCACTCTATAGTGGGGTGG TATTCGTCCACAAAATGCATCTGGATCAGCT
ESTD- HSD3B1	--	--	--	---	---	---	TTGGAAGTTCTCCACTGTTAACCAGTCTATGTTGGCAATGTGGCCTGGGCCACATTCCTGGCCTTG AGGCCCTGAGGACCCCAAGAGGCCCAAGCATCGAGGACAGTTCTACTATATCTCAGATGACA CGCTCACCAAGCTATGATAACCTTAATTACACCTGAGCAAGAGTTGGCCCTCCGGCTTGATTCC AGATGGAGCTTCCCTTATCCCTGATGATGGATTGGCTTCCCTGCTG
ESTD-HT2	--	--	--	---	---	---	GGGCTAAAATTTCCGAGCAACTTTCATAGACTGTTTTATTGACTTTGACAGGATGCTAGAGATAGG CAGGGAGAGGAAGATGTTACAGTTTGTACAGAGAGATAAAAGGATAACCTGGGGTTTTCTGTGC TTTGCTTCTCACATCCCTGGGGAGTTAATAGCTGCAATTTTCAAGAACGGTATACAGGGACAGCA AAGCGCAGTCGTGAAGTTTTCAAAACAGACACACCTT
ESTD-HT4	--	--	--	---	---	---	ACCAAGAGCGCGGATACAGACACTCTTAAGTTTTGCCCTAAGGCTCATTCAAATCATTAGGCATTTT CTGATAAACTAGTTCTTGGGTGCCCTTCTATCGGCAAGAAATGCGTACTTATTTGAATAGAGGTAA ACCACAGCCCCCAAGAGTCACTGAGACTGGCAGCTTCTGCAGCAGGCGTGAACCCCGTAGCCTAAA TGACAGCCGAAGAGGCGCCGAAGACATGCAGATGTGC
ESTD-HT5	--	--	--	---	---	---	AACACAAAGCCCCAGCGAGAAATTGAACCTCGGACCCCTGGTTTACAAGACAGTGTCTAACCCCT GAGCTATGGAGCCCTGCTGCTGTTGGTTTTCTTCCCTTTCATCTTATAGATTGATGTTATGCTCCTA GCATTCGGGCTACCGAATAGGATGTAGCTTGAGTAAATTCAGGATATTCCTCTACAAAATGAAA ACATTTTCGTGCTCTGTAATCCCTCGAAAAGGTTCT
ESTD- IGFBP1	--	--	--	---	---	---	ACCCAGTGGAGCCCCGCTCATTCGACGGTCTTGGCAGGAGGTGCCCTGGGAGAGAAGGAAGATGTTCT CAGGGCACACATAGCTTAGTGGAGACTC



ESTD- IGHV4-6	--	--	--	---	---	---	TTTACTATTTCAATGATACAGAAATTGTGGAGTCACTATATTCTATGAACAAAAATTCAGATTT CAGTGTTAAGTAATGTTGCCTACATTGTGTGAGTGACGGGAGTGGTGATCCGAGAGTGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGAAAGATGAGTATCTATGATACGAACTGAAAGT ATGTAATACTTCACAAAATACTATAAACGGAGTTGAATATAAAACCCA
ESTD-IL1A	--	--	--	---	---	---	CAAAGTAAGCACCCCAATAATGTTAGCTATTACTATCATATTATTATTATTTATTTTTTTG AGATGGAGTCTGGCTCTGCACCCAGGCTGGAGTGCAGTGGCACAATCTCGGCTCACTGCAAGCTCTG CCTCCTGGGTTTCATGCCATTCTCCTGCCCTCAGCCTCCCGAGTAGCTGGGAATACAGGCCACCCGCCACT GTTCCCGGCTAATTTTGTATTTTAGTAGAGACGGAGTTCACCGT
ESTD-IL1B	--	--	--	---	---	---	CCACTACAGATGGATAAATGGGTACAATGAAGGCCAATAGCCCTCCCTGCTGTATTGAGGGTGT GGGTCCTACCTTGGGTGCTCTCTGCTCAGGAGCTCTCTGCAATTGCAGG
ESTD- KRT10	--	--	--	---	---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAAAATGCAATTTAAAGTAACGTGCTAAGGTTTTTCCATTAAACCACATATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTCTC TGCCACAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT8	--	--	--	---	---	---	ACCTCACCCCTCCCTTAGCCGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCCTGACATGAGACCTCAGACAGAACTTCTAGAGTT TGCTAGAGGTCAAGGTCAAGACTAAAGAGGGGCCAGATGTTAAGTACAAAAAGTGAGGCCCATAG GCTGCCTATCTCTCCGCTCAGGTTTACCACGTCACATTGACACA
ESTD- LF79	--	--	--	---	---	---	GGGTGATTTGAGGCTCAGTTAATATTCAAAATTTGAACGTAGCAAACTGCATTGGTATTAGA AAAAATAAAAAATTTCCAATATGTAGTGTGTATTACCTGCCTCTGCCATCGCATCATAGCCTGT GGGAACCCAGGAGGCTTCCCTTACCACCCAGA
ESTD- LMP2	--	--	--	---	---	---	TACACACTTTCCTTACCCATTCACTGAAAACGACTCGCAAACTGGAGCCTTGTAGGAATGGAGTTGA CCTTCCCAAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	--	--	--	---	---	---	TGTCAGTGTCCCTAGGGCACTCACCACTCCAGCTTCTCAGCTCTGCCCTGCTGCTGCTGCTGCA AGGTTTTGCTTAATTCGAATCAATGTCTCTTCATCTTTAGCAGCTGTGGGTTTTGTTGTTTC TTCTGTTTTGCTTAGTATCTGACTACTTTTTTAATTATAAAAGAGATGTATCTAAACAAAAATAGAG ATTGTTATCAGAAGTTCACAACATTTTAAAAATTTTTCACCTG
ESTD-MCC	--	--	--	---	---	---	TTGTCAGGAGTGTGCTGATGCTGCCCTCCCAAGCTCTGTCCCTAGCCGAACCTTCAGGACAACGTGCAG CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCCCCGAA TCTCAGGAAGTCTCTGCTTCCCAAGGTTTGGTCAAGTGTCTGATTACCCGGATTTTCTGACGATC TTTCAACTGCTAGAGCATCTGGTTCCTGTTTTCGATGG
ESTD-NF1	--	--	--	---	---	---	ATTATCCAGATGAATTTACAAAATAATACCAGATCCACAGACTGATATGGCTGGT

ESTD- NFKB1	--	--	--	---	---	AACATGGACTTGATATTTGTACAAAAAAGTTTATTTTCTAAAAAAGAAAAAAGAAAAA AAATTTAAGGGTGACTATATCCACACTGCACACTGCCTAGCCCCAAACGCTTATTGTGGTAGG ATCAGCCCTCATTTTGTGTTTGTGAACTTTTGTAGGGGACGAGAAAGATCATTTGAAATTTCTGAG AAACTTCTTTAAACCTCACCTTTGTGGGTTTGTGAGAAAGTTATCA
ESTD- NPPA	--	--	--	---	---	TGTCCTAGGCCAGCCCTGCTTGTCTCCCTGGCTGTTATCTTCAGTACTGCAAAGAGAACACAGAC AT
ESTD- NRAMP	--	--	--	---	---	GGAGCAGGAGGTGGGAGGGGTCTGTCTGCTCCAGGTCCACAGAACAGAGAGGGGCTCAGTG TATCCCAACCCCAATGTGGCGCTGGAGATGAAGAGAGTTGATGCAGGT
ESTD- NRAS	--	--	--	---	---	GTGTTTCTTAATCTTTCCAGGAACACAGTGACCATATTTCTTTCTGCAGGCATATAGAAATTTGGT GGTTTCTTTATGTAGGTGATATTGGATCTTTTGTGTTGTGATTATATAGCAATTTGAGGG ACAAACCAGATAGGCAGAAATGGGCTTGAATAGTGTATGCTTATTTAACCTTGGCAATAGCATTGC ATCCCTGTGGTTTATAAAAAAT
ESTD-OTC	--	--	--	---	---	GTGACCTTCTCACTTTAAAAACTTTACCGGAGAGAAATTAATATATGCTATGGCTATCAGCAGA TCTGAAATTTAGGATAAAACAGAAAGGAGAGGTATGTAACA
ESTD-PAI1	--	--	--	---	---	GCCACCACACCCACCCAGCACACCTCCACCTCAGCCAGACAAGTTGTTGACACAAGAGAGCCCC TCAGGGGCACAGAGAGTCTGGACACGTGGGAGTCAAGCGTGTATCATCGGAGCGCGCGGGCAC ATGGCAGGATGAGGGAAGACCAAGAGTCTCTGTGGCCCCAAGTCTAGACAGACAAAAACCTAG ACAATCACGTGGCTGGCT
ESTD-PAR	--	--	--	---	---	CTCTTCAGGAACCCAGCTCTTACCAAACAGCACTTATGCTGTCGAGAGGTACAACCCGTAGA ACTTCTCCTAACTGTAATTTAGTTAAAGGAATCGAACTGGCTCTGAAGACATGGAGATACTGCCT AATCGACTGGCTTTCATTAGCTGTGAGTGTTTCTTTCACTTTCTGTGTTCTAGAACGTTTCTAG GACTGGCAGTTTAACTTCACTTAGGCTTCTGTATACCCATGCC
ESTD- PBDA	--	--	--	---	---	CCTTCTCATGCCAGATGGAATTCAGTCCCTTCAGGATCTGCCTAACCTGTGACAGTCTAAAGAGT CTGAGCGTGGCTGGGAAGGCGAGCACTAATCCAAATCTTACCCGAGCTTGCTCGCATACAGACG GACAGTGTGGTGGCAACATTGAAGCCTCGTACC
ESTD-PS-1	--	--	--	---	---	GGGGAGTAAACTTGGATTGGAGATTTCATTTCTACAGTGTCTGGTTGGTAAAGCCTCAGCAACA GCCAGTGGAGACTGGAACACACCATAGCCTATTCTGTAGCCATATTAATGGTTTGTGCCCTTACATT ATTACTCTTGCCATTTCAAGAAAGCATTCAGCAGCTCTCCAAATCCATCCATCACCCTTTGGGCTTGT CTACTTGGCACAGATTATCTGTA
ESTD- PXMP1	--	--	--	---	---	ATGAACATGGTCTTTAATTTATGATATGTTTATAGCTATCTTAAAGGGCTTCTTTTTTTTA ATGCAGAAAGAGGGGAAAGAGCGAGCTGTGGTGGACAAGGTGTTTTCTCAAGGCTCATACAGA TTCTGAAATCATGGTCCCTAGAACATTTTGAAGAGGTAACTTATGAAATATAATCTT
ESTD- Per/RDS	--	--	--	---	---	ACCTACAGACGTGCTGGATGGTGTGTGTCACCCGAGGAATCTGAGAGCGAGAGCGGCTGGCTG CTGGAGAAGAGCGTGGCGGAGACCTGGAAGGCT

ESTD-FDS	--	--	--	---	---	---	CCCGAGGAATCTGAGCGGAGCGAGGGCTGGCTGCTGGAGAAAGAGCGTGCCGGAGACCTGGAAGG CCTTTCTGAGAGTGTGAAGAGCTGGCAAGGGCAACAGGCTGGAAGCCGAGGGCGCAGACGCGAGG CCAGGCCCAAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCGAACACTGAGAAATAGTGCACCT CCAAGAAACGTGGATCTCCCCCTCATCCAACTCCGAAAGTCIGAA
ESTD- RYRI	--	--	--	---	---	---	CTTCGTGACGGGAGGTACGTCCTCCGCCCTCTTCATGGACATATGGATGAGTGTCTGACCATTTCCOC CTGCTGACAGTGTATGACCGCGCAGACTTGTCTACTATGAGAGGGGAGCTGTGTCACACTCATGCCCCGC TCCCTCTGGAGGCTGGAGCCACTGAGAAATCAGCTGGAGTGGAGCCACCTGCGCTGGGGCCAGCCACT CCGAGTCCGGCATGTCACTACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD- SPTB	--	--	--	---	---	---	TGAACACCTGTGTGTCGGAGCCAGTTGTGTTCTCCTGGAGCCTGAGGAGTTTGTGTGTGTG CAGTCCCGCGCCACCTGCTGTTGAGCCTGGACATACACCTTCACTCCTTTGCCCGGAGAGAC ATTTACCCACCTGGCCATGTCCCTGGCCTGTTGTGCACACCTCTGTGAAGACCCCAACCCCTGCCCTCC CCACCCAGGCCAGTTCTAGCAAGGGCAGGAC
ESTD- SSA1	--	--	--	---	---	---	TTACATTTGTGGATTGTTCTTTTGTGTGTCGACGACCTTTTCAACATGATGTATCCCATTTGTCCAAG TTTGCTTTGGCTGCCCTGTGCTGTGGGATATTTGAAGAGATCTTTGCCAGTCCCAATGTCTTAGAGAG TTTTCCCAATGTTTCTTGTAAATAGTTTTCATAGTTTGAGGCCCTTAGATTTAAGTCTTTAATCCATTTTG ATTGTATTTCTGTA
ESTD-TAT	--	--	--	---	---	---	AAATGGTCAGGACCTGATCCACAAGAGTGTACCAATTCATCAGGGCCATCAGTTCATTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTCATCTTAAATGACTTGTGGGACAGGATCA ATTTCTCTCACCTAGAACGTTTGTTTACAACCTTTCTTCCAGTATGGATGGGATATGATGGGGGG GAGAAACAAATTTTAAATAGGACCCCATGAGACACATCA
ESTD- THRB	--	--	--	---	---	---	TGCGGCCCTTCTCCGGCAGGGTAGACTTCTTACTTGGCTGTTGATTTCCAAAGAGAAAGAGTCCCAAG CACACGAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAATCACACAGGATCACTTCATCCA CACTGGATTGGCCCAACAAAGTCTGAGTGCAGCCAGGACTCAACGGTCCCTGTAGATGGG
ESTD- TNFA	--	--	--	---	---	---	TTCTGCATCCTGTCTGGAAGTTAGAAGGAAACAGACCACAGACCTGGTCCCCCAAAAGAAATGGAGG CAATAGTTTGTAGGGGCATGAGGACGGGTTGAGCCTCCAGGGTCTACACACAAATCAGTCAGTG GCCCAGAGACCCCTCAGATCGGAGCAGGGAGGATGGGGAGTGTGAGGGGTATCCTTGTATGCTT GTGTGTCCTCCAACTTTCCAAATCCCCCGCCCGGATGG
ESTD-TYR	--	--	--	---	---	---	TAGTGAAGTTTTCATCTCCTGTGAGCTTCTGGAATTTCTTCTCCACCGCAACAAGAGTCTATGC CAAGGCAGAAAGCTGGTCTTCATGGGCAAAATCAATGCTCTCCAGATTTCCAGATCCCCCAAGCA GTGCATCCATTGACACATAATAATGCATCCAGACAAGAGGTGTCATAAATATTGATGTCGTAAACAT GGGTGTGATCCATTTTTCATTTGGCCCATAGGTCCCTATGGGATGACA

[illegible]

EST11458 6	--	--	--	---	---	CCACTTTGGTAGTGCCAGTGTGACTCATCCACAATGATTTCTCCAGTGTCTCATCTTGTTCTCGAGTTTCTCTGCCATGTTGCTATTGCAGGACGGACCTGTCCCAAGCCAGATGATTTACCAATTTCCACAGTGGTCCCATTAAACAATTCTATGAGCCAGGAGAGAGATTACGTATTCCTGCAAGCCGGGCTATGTGTCCCGAGGAGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC
EST39852 8	--	--	--	---	---	CGGCTTCTCTCCAGGATTGTTGCAGAAGGCCGAGATGACCTCTATGTCTCAGATGCATTCATTAAGGCATTTCTGAGGTGAGTACACCTTCCCACCTCTCTACGGTACAGAAAGGAGATGCATGAACAGCAGGAACACGTGGAAAAGGCCCTGTTTCCAGTGTTAAGGCATGCAAAAGGCCCTCCACAGGCTGCTATAATACAGCCCT
EST62448 0	--	--	--	---	---	ACCTGGTGTGCTGGTGTGGGTGAACCTGGTCTCTTGGCATTTGCCGGCCCTCTCTGGGGCCCGTGGTCTCTGGTGTGGGTAGTCTCTGGAGTCAACGGTCTCTAGTGAAGCTGGTCTGTGATGGCAACCCTGGGAACGATGGTCCCCCAGGTGCGGATGGTCAACCCGGACACAAAGGAGAGCGCGGTTACCCCTGGCAATAT
EST36027 2	--	--	--	---	---	AGTGACTTCCAAGGAAATGGCTACCCAACTTGCCTTCATGCGCCTGCTGGCCAACTATGCCTCTCAGAACATCACCTACCACCTGCAAGAACAGCATTGCATACATGGATGAGGAGACTGGAACCTGAAAAAGGCTGTCAATTCTACAGGGCTCTAATGATGTTGAACCTGTTGCTGAGGGCAACAGCAGGTTCACTTACACTGTCTTTGTAGATGGCTGCTCTAAAAAGACAAATGAATGGGGAAGACAA
EST12274 0	--	--	--	---	---	CCCCAGTTGCAGCCACTGCTCTAGACTAAGTTCTTGCTTCCAAATAGAGCCTTACCAAAGTGTATTACATAAAGAAGTCAAGTGGTTTACTCTCATGACCAAAATATCTTCCCTCTAGGATGAGGTGATAGTAAATGACCGATGGGTGAGAACTGTTCTGTCCACCATGGAGGATACTATAACTGTGAAGATAAATTCAAGCCACAGAGCTTGCCAGATC
EST76807 EST44438 7	--	--	--	---	---	ATGCTAAGGGGATCGACATGAAGGACCTGTGAGCCGATTGTCTCTATCTCCAGCGGCCCTGTCTATCAGCTCACTCATCAATGGGGCAGTCAGGCCAGGCACTGGGCTCCGGAGGACTCACCACTGCCCCCTGCTGCCATGTGGACTGGTGCAAGTTGAGGACTTCTTG
EST12839 3	--	--	--	---	---	GCAGCCAGGAGCCGCTGCACCATGCCCGCATAGATGCGGACCTCAAGCTCGACTTCAAGGACGTCCTGCTCCGACCTAAGCGGAGCAGCCTCAAGAGCCGAGCGGTGGG
EST54419 8	--	--	--	---	---	TGCAAAACACACAAAATCTTCTCCAGATGCCCTATGGCTGTGGAGGAGCAGAATATGGTCTCTTGCTCCTAACATCTATGTACTGGATTATCTAAATGAACACAGCAGCTTACTCCAGAGATCAAGTCCAAAGGCCATTGGCTATCTCAACACTGGTGAAGTACTTGAAGTAAAGGAACTTGAATGTTATTCAACTGGATTTCCAGTAGGTTTCAGTTACTTATGAATATTAATGATACCTAGCTTAG
	--	--	--	---	---	CTTCTGCCTAATTTGAATGATATTGCTGTGGGACCTGAGCACTTTTATGGCACAATGATCACTATTTTCTTGACCCCTACTTACAATCCTGGGAGATGTTATTTGGGTTTAGCGTGTGCTGATGTTGCTACTATAGTCCAAGTGAA

EST10398 2	---	---	---	---	---	TGCTGGGGTGGCAAGGCTGCAAAAGAGGAGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGATGATGTTACATTTTGGGCTTGACTTTCCACACGGAGAAAG CATTGTTTCTTGGGCCAAGAAGGTATCTACCAATAGTGTCTATTAGGCAITTTG
EST36751 7	---	---	---	---	---	CCAAAGTCGTTCAATTTTAGCTTTCAGGTTTAACTCGATTACTTTTTCTATTCAAATCTCTGTAAAA TTGAAATATGAACCTTAGTTTTCTGATCTATGTTTCAAGTTAAACAG
EST40562	---	---	---	---	---	CACGTGGAAGAGCTATTTTGGAGGCTTTAAGAGTAAAGATCTGCCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAGTTTTCACCTGGATGCATTAATAACAAATATTTTACCTTTTGAAAAATAAATG AAGGATTTGACCTGCTTGGCTCTGGAAGAGTATCCGTACCGTCTGACGTTTGAACAAATACAGAT GCCTTCCCTTGTAGCAGTTTTCAGCCTCTCTACCTA
EST18288 3	---	---	---	---	---	GCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAA GATTGACAGGTTTCAGCAGGCTGTGACAGGATGGAAGACTGGCTGCTCCCTGACGGGAGCCAGTGTGG ACAGCACCTGGCTTCAACACCTACGTCCACTTCCAAGGTAAAGCAACCTCTCTGCTGGCTCTGGC CCTAGGACTTAGTATCC
EST70523 3	---	---	---	---	---	TTCCCGCCAGCCCCCATCTTGGCACCTGGTCCCTCAGGGGCCACCCCGGCGCACTCACCGCTCT CGCTCTCGGTAAACATCGGGCGGGCGGCTCTTGAACATAGCTGGACCGTTCCGTATAGGAGG ACCGTGTAGGCTTCTGTCGGGCTTGGCAGGGGCCAGGCTGCAGAGAGAGGGTCCCTGTGGT TGAGCTGAACACAGCTGTGGAGTGTCTCCACGCTG
EST58707 7	---	---	---	---	---	CAGTGTATCTGGAAGCCTACAGGACACCAAAATAACCTTAATCATCAATTGGTTACAGGAGCTTT AAGTTGAGCATCTTTGGCTCACATGAAGGCCAAATTCGAGAGACCCTAGAAGATACACGAGACCGA ATGTATCAATGGACATTCAGCAGGAACCTTCAACGATACCTGCTCTGTGGTGGCCAGGTTTATAGCA CACTTGTCACTACATTTCTGATTGGTGGACTCTTGTCTGCTAAGAACCTT
EST74167 6	---	---	---	---	---	AGACCATGAAGAGTTGAAGGCTACAAATCGGAACCTGGAGGAACAACCTGACCCCGGTGGCGGAGG AGACCGGGCACGGCTGTCCAAGGAGCTGCAGGGCGGCGAGCCCGGCTGGGCGGGACATGGAGGA CGTGGCGGCGGCTGTGTCAGTACCGGGCGGAGGTGCAGGCCATGCTGGCCAGAGCACCGGAGGAGC TGCGGGTGGGCTGGCTCCCACTGGCAAGCTGGCTAAGCGGCTCCTC
EST43211 8	---	---	---	---	---	CGCCTGGTGCAGTACCGGGCGAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGGGGTGGG CCTCGCTCCCACTGCGCAAGCTGCGTAAGCGGCTCTCCGGATGCCGATGACCTGCAGAAAGCGOC TGGCAGTGTACAGGCGGGGCGCGAGGGCGCGAGCGGCGCTCAGCGCCATCCGCGAGGCGCTG GGGCCCCGTGGTGAACAGGGCGCGCTGGCGGCGCGCACTGTGGGCTC
EST36770 4	---	---	---	---	---	TGTAGCCAAAGTCACCTGCATCATCTTGGCTGCTGGCAGGCTTGGCCAGTTGCCAGCTATAATCC ATCGAAATGTATTTTTCATTGAGAACACCAATATTACAGTTTGTGCTTCCATTATGAGTCCCAAAAT TCAACCCCTCCGATAGGGCTGGGCTGACCAAAATATACTGGTTTCTGTTCTCTTCTGTATCAT TCTTACAAGTTATCTCTTATTGGAAGGCCCTAAAGAGGCTTATG

EST26021 1	..	--	--	---	---	TAATGTAAGCTCATCCACCAAGAAGCCTGCACCATGTTTTAGGTTGAGTGACATGTTGGAACCTGTTCCATAAGTAATTTGTGAAAGAGGAGCAAGAGAACATTCCTCTGCAGCATTCTACTACCAATGAGCATTAAGCTACTTTTCAGAAATTGAAGGAGAAATGCAATTATGTGACTGAACCGACTTTTCTAAAGCTCTGAACAAAAGCTTTTCTTCTTTGCAACAAGACAAAGCAAGGCC
EST51212 0	--	--	--	---	---	ATCCTGAGCTGCGCAATAAGCTTCTTGGTTCTACTTCTCTCTCCACAAGCCCCAATTCACTTTCTCA GAGGAAATCCCAAGCTTAGGAGCCCTGGAGCCTTGTGCTCCCACTCAATAACAAAAGGCCCTCTCT ACATCT
EST20118 2	--	--	--	---	---	GTTCGGAATCCTCCTCTGAAAGTGCCGGGTTTAATCTGCTCATGACGCTGCGGCTGTGGTCCAGCT GAGGTGAGGGCCCTTGAAGCTGGAGTGGGTTTAGGACGCGGGTCTCTGGGTGCATCCTAAGCTCT GAGAGCAACCTTCCCTTGAAGCTGGGAGTGGGTTTAGGACGCGGGTCTCTGCGTGCATCCTAAGCT CTGAGA
EST53018 6	--	--	--	---	---	ACAATCCAGGTCACACATTCAGAAAGAGGGGTGGTCAAGTGGGTAGGTCCAGTAATCCA AGGATTGAGGAAGGAGGCCACGAGGATCGAAGTTAGTGAAGTC
EST68787 5	--	--	--	---	---	CTTCCTATGGGATTGACITTTATTTCTCCATTGCTTACCTTTACAGGTGTTAATATAGTGAAAAG GAAGCTTGAGCTCATGACAAATTTGAAGCTGACAAATTACAGAAGAGGAAATAAATTCACAGTCAA AGAATCAAGCACTTTTCGAAACATTGAAGTTGTTTTGAACTTGGTGTACCTTTAATTACAAACCTAG CAGACGGAACCTGAACCTCAGGTAAGAAT
EST34088 2	--	--	--	---	---	GTGGGGCAACAGTGGGAGAGAAGGGGCCAGGGTATAAAGGGGCCACAAGAGACCGGCTCAAGG ATCCCAAGGCCCCAACTCCCCGAACCACTCAGGGTCTGTGGACAGCTCACTAGCTGCAATGGCTACA GGTAAG
EST37382 5	--	--	--	---	---	CTGAGAAACAATTGGCAAAATAAAGGAATTTGGCACTCCCCACCCCTCTTCTCTCTCCCTTGGGA CTTTGAGTCAAAATGGCCTGGACTTGAGTCCCTGAACCAGCAAGAGAAAGAGGCCCCAGAAAT CACAGGTGGGCACGTGCGTCTACCGCCATCTCCCTTCTACGGGAATTTTCAGGGTAAACT
EST74082 0	--	--	--	---	---	TCCAGGTGGCTGGACCCCAAGGCCCAAGCTCTGACGAGGAGGACGTGGCTGGCTGCTGAAGCATG TGGGGGTAGCCAGGGGGCCCCAAGGCAGGCACTGGCTTACGCTGCTCAGCCCTGCTGCTGCTGCTC CCAGATCACTGCTCTTCTGCCATGGCCCTGTGGATGCGCTCTGCCCCCTGCTGGCGCTGCTGGCCCTC TGGGACCTGACCCAGCCGACGCTTTTGTGAACCAACACCTGTGCG
EST45311 0	--	--	--	---	---	GCCCTCCTCTCTTCCAAATCTGTCCCTATAGTTTTCTCTATTAAGTGAACATGACATTCCTTTAGT GGATAGATGCACACAACACACAAGCCATTATGGGAAGGATCCAGGTGTGGCCATATTGTAACA CATTTTCTGCAAAATCACCTCTTTCATTTAACAGGCCCTTATCAATGGCCCTTTTCTTTTTCAGTAGTA CATACACATCTGTGTCATTTGTGAAT

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EST65258 8							TGCCCATCACGCGCGGAGACATGGCTTGCACAGCTCTTGAGGATGTCACCAATTAACCCAGAAAT CCAGTTATTTCCACCTCAAAATGACAGCCATGCCCGCGGGTCTTCTGGGGCTCGTCGGGGGG ACAGCTCCACTCTGACTGGCACAGCTTTGCATGGAGACTTGAGGAGGGGCTTGAGGTTGGTGAG GTTAGGTGCGTGTCTCTGTCAAGTCAGGACATCAGTCTGATTAAA
EST38216 3							ATGCAGGATGAAGGTGGACAGGGAGGAGGGGCAACCTGTGATCCAGGGCTGCAGATGTCGCTG GACTATGGGTTTGACCCCACTGACCTCCATGAGCATCAGGG
							ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATATTAGCATTTGTTTAGCATTAACCTAA TTTTTCTCTGCTCCATGCAGACTGTAGCTTTACCTTAAATGCTTATTTTAAATGACAGTGGAAAG TTTTTTTCTCGAAGTGCCAGTATCCAGAGTTTGGTTTTTGAACCTAGCAATGCCTGTGAAAAA GAACTGAATACCTAAGATTTCTGTCTGGGGTTTTTGGTGCATGCA
EST62782 --							GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATTCTCCCAATCTGTGCGTCCACCGATG GAACTGCCGGCAATCTGACACGTGTGCACCCAGGCTGTACCCAAATTAGGTGAACATGGCTTCGAG AGAGTTGAACAGATTCTCGAAGACACAGCAGCGGGATGGGGCAGGAGAGCTGCCTGGATGAA
EST35879 9							GGAAAGAGATTTAAGAAGCTTGATTGGACAATCTGTGTTCTTTGAGTGTGGAAGAGTTTCATGTCTCT GCCTGAGTTACAACAGAAATCCTTTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAATGGA GAAGTAGACTTTAAAGTAAGAAAGTAGTATTTTTTA
EST68308 5							GGAAATTTAAATAATTTTAAATACCTCCATTTTGCTTATCCTTTTAGTGAAGATGATACCTGCAA AAGACATGGCTAAAGTTATGATTGTGATGTGGCAATTTGTTTCTTACAAAATCGGATGGGAAATCT GTTAAGTAAGTACTGTTTGGCTTGGAAATGGATTTTAAATGTGACTTTATCAT
EST52908 0							ATCACAGGTCTCTGGTCTCTGGCCATCATTTCTCTGGGAGAGATGGATGGTGTCTGCAAGCCCTTTGG CAATGTGAGATTTGATG
EST19590 --							AGGAGAAGCTGAGGAGGGGAAGAGAGACAAGAATGACATTGATGAGTGAAGATGTCGGCTCAGGAT GCCGGAAATGAC
EST76136 --							TGAAGCTTCTGCCAGCTTGCCATTGTTTCTAGGAGAACCCGCGTCATACCTTTATCTATAGCCTTCCCC TAGGTCTT
EST58607 0							CTCTGGATGGTTACAGGTGGCAGGCACAGCCAGTCCATCCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCTCACTGGAGAACAGGACAGCCACATGGCGGGGATGGCGGGGAGTTCTGGT TGCGGCACCGCTGTGGCTCTGTTGTAACGGTAGCCTTTGCGGTTGCGATGCCTAAACCTTTGTTTCT TGGCCAAGGAGGGGGGGTGCCTGCTGAGATGTAGATGGGCC
							Legend: 1=Marker 2=PM Position 3=Reference Allele 4=Altered Allele 5=SNP Forward Primer 6=SNP Reverse Primer 7=Sequence



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## EQUIVALENTS

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that

5 various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the

10 specific embodiments of the invention described specifically herein. Such equivalents are intended to be encompassed in the scope of the claims.

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## CLAIMS

WE CLAIM:

1. A nucleic acid segment shown in column 7 of the Table,  
or a portion thereof which includes a polymorphic site,  
5 or the complement of the segment or portion thereof.
2. The nucleic acid segment of claim 1 that is DNA.
3. The nucleic acid segment of claim 1 that is RNA.
4. The segment of claim 1 that is less than 100 bases.
5. The segment of claim 1 that is less than 50 bases.
- 10 6. The segment of claim 1 that is less than 20 bases.
7. The segment of claim 1, wherein the polymorphic site is  
biallelic.
8. The segment of claim 1, wherein the polymorphic form  
occupying the polymorphic site is the reference base  
15 for the fragment listed in the Table, column 3.
9. The segment of claim 1, wherein the polymorphic form  
occupying the polymorphic site is an alternative form  
for the fragment listed in the Table, column 4.
10. An allele-specific oligonucleotide that hybridizes to a  
20 segment of a fragment shown in the Table, column 7 or  
its complement.
11. The allele-specific oligonucleotide of claim 10 that is  
a probe.

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12. The allele-specific oligonucleotide of claim 10,  
wherein a central position of the probe aligns with the  
polymorphic site of the fragment.
13. The allele-specific oligonucleotide of claim 10 that is  
5 a primer.
14. The allele-specific oligonucleotide of claim 13,  
wherein the 3' end of the primer aligns with the  
polymorphic site of the fragment.
15. The allele-specific oligonucleotide of Claim 10, which  
10 is selected from the group consisting of the nucleotide  
sequences of the Table, column 5.
16. The allele-specific oligonucleotide of Claim 10, which  
is selected from the group consisting of the nucleotide  
sequences of the Table, column 6.
- 15 17. An isolated nucleic acid comprising a sequence of the  
Table, column 7 or the complement thereof, wherein the  
polymorphic site within the sequence or complement is  
occupied by a base other than the reference base shown  
in the Table, column 3.
- 20 18. A method of analyzing a nucleic acid, comprising  
obtaining the nucleic acid from an individual; and  
determining a base occupying any one of the polymorphic  
sites shown in the Table.
19. The method of claim 18, wherein the determining  
25 comprises determining a set of bases occupying a set of  
the polymorphic sites shown in the Table.

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20. The method of claim 18, wherein the nucleic acid is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and the method  
5 further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.